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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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461.5
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Match Length DB
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Gapop 10.0 , Gapext 0.5
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2626
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                                                                                                                                     SwissProt_41:*
   GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
   ANIA REIGO
NIR RHOSH
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Q53239 rhodobacter
P25006 achromobact
Q01537 rhizobium g
Q06006 pseudomonas
Q92229 rhizobium m
Q60214 rhizobium h
P38501 alcaligenes
                             Q8zbk0
Q02079
P43561
Q12541
Q51705
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P00123	Q9a5f0	Q53692	Q02075	Q9uy49	Q53047	P21333	Q45754	Q12542	Q12717	Q61147	Q8kg93	
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ALIGNMENTS

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M97/ A492/ IKBW Pro; Pro; PFO/ PFO/ DT; P	his SWIS etween he Europ se by odified ntities r send a	SEQUENCE FROM N.A. STRAIN=ATCC 33084 / F62; STRAIN=93014188; PubMed=1398981; Hoehn G.T., Clark V.L.; Hoehn G.T., Clark V.L.; Hoehn G.T., Clark V.L.; infects. Immun. 60:4704-4708 (1992)i- SUBCELLULAR LOCATION: Attached anchor (Probable)i- INDUCTION: BY ANAEROBIOSISi- SIMILARITY: Contains 2 plastoc:	sseria; teria; sseria; sseria; I_TaxII DUENCE PAIN=R1; hn G.T colation or ana or ana	-ANIA NEIGO Q02219; Q1-JUN-1994 Q1-JUN-1994 Q1-JUN-1994 15-SEP-2003 Major outer ANIA.
926; AAA25462. 08; A49208. 1; 27-FEB-02. 1PR001117; Cu 1PR001187; Cu 10394; Cu-oxida R00695; CUNOZR PS00013; PROKA uter membrane, 18 19 19 19	, сонк	INLEATICE FROM N.A. INLEATICE 33084 / P62; INLE 93014188; PubMed=13989 IN G.T., Clark V.L.; INDUCTION: BY ANAEROBIOSÍS SIMILARITY: Contains 2 pla SIMILARITY: Contains 2 pla	rogonorrhoeae. Proteobacteria; Proteobacteria; D=485; D=485; EROM N.A. 0; 0; 0; 10; 10; 10; 10; 10; 10; 10; 10	STANDARD; (Rel. 29, Cr (Rel. 29, La (Rel. 42, La .membrane pro
ים טייטסי	y is copyright. It is nestitute of Bioinforma rematics Institute. The institutions as long attenent is not removed license agreement (See license@isb-slb.ch).	/ F62; V.L; V.L; pically induc is a lipop 1, is a lipop 14704-4708(19 9CATION: Atta 1202) NAMAEROBIOSÍS NAMAEROBIOSÍS	Deae. acteria; Betaprot isseria. PubMed=1383156; V.L.; V.L.; clectide sequence ly induced outer 14695-4703(1992).	0 tt tb
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RESULT 2

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15-SEP-2003
                                                                                   MEDLINE=97175533; PubMed=9023188;
Tosques I.E., Kwiatkowski A.V., Shi J., Shapleigh J.P.;
Teductase in Rhodobacter sphaeroides 2.4.3.";
J. Bacteriol. 179.1090-1095(1997)
J. Bacteriol. 199.1090
J. Bac
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Matches 133
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PRINTS; PR00695; CUNUZKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U62291; AAB05767.1; -. HSSP; P25006; INIF.
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nitrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001287; CuN02_reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Periplasmic (By similarity).
DOMAIN: THE TYPE I COPPER SITE IN NIR PLAYS A CRUCIAL
ELECTRON TRANSFER FROM PSEUDOAZURIN TO THE TYPE II COF
OF NIR, WHICH COMPRISES THE CATALYTIC CENTER OF NIR FC
REDUCTION OF NITRITE.
SIMILARITY: Contains 2 plastocyanin-like domains.
                        340
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                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       assimilation;
                                                                                                                                                                                                                             VHKGATASVLVEGEWDNDL----MEQVWPPVG
                       FNKGALGILKVEGEENHEIYSHKQTDAVYLPEG 372
                                                   RPHLIGGHGDLV-WETGKFHNAPERDLETWFIRGGTAGAALYKFLQPGVYAYVNHNLIEA
                                                                            SFHVIGEIFDKVHFEGGKGEN---HNIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRA
                                                                                                  PFDMEKAIRED-------ABYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNLTS
                                                                                                                                                           PMIPWHVVSGMAGCIMVLPRDGLKDHEGKPVRYDTVYYIGESDHYIPKDEDGTY-----M
                                                                                                                                                                                  ----MHIANGMYGLILVEPKEGLP-----KVDKEYYVMQGDFY----TKGKYGEQGLQ
                                                                                                                                                                                                               LTLINPPENTMPHNIDFHAATGALGGGGLTLINPGEKVVLRFKATRAGAFVYHC--APGG
                                                                                                                                                                                                                                                                  PPFAHAHEQVAASGPVINEFEMRIIEKEVQLDEDAYLQAMTFDGSIPGPLMIVHEGDYVE
                                                                                                                                                                                                                                                                                          PPVDRDH-----PAKVVVKMETVEKVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASTOCYANIN-LIKE 1
PLASTOCYANIN-LIKE 2
COPPER (TYPE 1) (BY
COPPER (TYPE 2) (BY
COPPER (TYPE 2) (BY
COPPER (TYPE 1) (BY
COPPER (TYPE 1) (BY
COPPER (TYPE 1) (BY
COPPER (TYPE 1) (BY
COPPER (TYPE 2) (BY
COPPER (TYPE 2) (BY
                                                                                                                                                                                                                                                                                                                                                                       Score 468; DB
Pred. No. 1.2e
52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Periplasmic; Signal.
POTENTIAL.
COPPER-CONTAINING NITRITE REDUCTASE.
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.2e-25;
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RESULT 3
NIR ACHCY
ID NIR ACHCY
AC P25006;

STANDARD;

PRT;

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EMBL; Z48635; CAA88564
PIR; JC4648; JC4648.
PDB; 2NRD; 07-DEC-95.
PDB; 1NIA; 07-DEC-95.
PDB; 1NIG; 07-DEC-95.
PDB; 1NIC; 07-DEC-95.
PDB; 1NIC; 07-DEC-95.
PDB; 1NIC; 07-DEC-95.
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01-NOV-1997
15-SEP-2003
                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Payne W.J., le Gall J.;
"The 2.3-A X-ray structure cycloclastes.";
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                                                                                                                                                                                                                                                                                                                                                   +
                                                                                                                                                                                                                                                                                                                                                               copper depleted.";
J. Biol. Chem. 270
                                                                                                                                                                                                                                                                                                                                                                                       cycloclastes at
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96070866; PubMed=7499203; Adman E.T., Godden J.W., Turley S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE=91320115; PubMed=1862344;
Godden J.W., Turlay S., Teller D.C., Adman E.T., Liu
Payne W.J., le Gall J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Amino acid sequence of nitrite reductase: a copper protein from Achromobacter cycloclastes."; Biochemistry 30:7180-7185(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 39-378.
STRAIN-IAM 1013;
MEDLINE=91308101; PubMed=1830217;
Fenderson F.F., Kumar S., Adman E.T.,
le Gall J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning, characterization, and expression of the nitric generating nitrite reductase and of the blue copper prote Achromobacter cycloclastes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=IAM 1013;
MEDLINE=96193667; PubMed=8605003;
Chen J.-Y., Chang W.-C., Chang T.,
le Gall J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alcaligenaceae; Achromobacter.
NCBI_TaxID=223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copper-containing NIRK.
                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 253:438-442(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Achromobacter cycloclastes
                                                                                                                                                                                                          REDUCTION OF NITRITE. SIMILARITY: Contains 2 plastocyanin-like domains.
                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Periplasmic.

SUBCELLULAR LOCATION: Periplasmic.

DOMAIN: THE TYPE I COPPER SITE IN NIR PLAYS A CRUCIAL ROLE FOR ELECTRON TRANSFER FROM PSEUDOAZURIN TO THE TYPE II COPPER SITE OF NIR, WHICH COMPRISES THE CATALYTIC CENTER OF NIR FOR THE
                                                                                                                                                                                                                                                                                      II COPPER; FAD.
PATHWAY: Nitrate assimilation (denitrification).
SUBUNIT: Homotrimer.
                                                                                                                                                                                                                                                                                                                       Biol. Chem. 270:27458-27474(1995).

CATALYTIC ACTIVITY: Nitric oxide + H(2)O + ferric nitrite + ferrocytochrome c.

COFACTOR: CONTAINS ONE ATOM OF TYPE I COPPER AND
                                                                                                                                                                                                                                                                                                                                                                                     structure of copper-nitrite reductase from Achromobacter oclastes at five pH values, with NO2-bound and with type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 21, Created)
(Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
aining nitrite reductase precursor
                                                                                       CAA88564.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Commun. 219:423-428(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chang T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of nitrite reductase from Achromobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu M.-Y., Payne W.J.,
                                                                                                                                                                                                                                                                                                                                                  H(2)O + ferricytochrome
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SIGNAL
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TIGREAMS; TIGRO1409; TAT signal seq; 1.
Oxidoreductase; Copper; Metal-binding; Flav
Nitrate assimilation; Repeat; Periplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00394; Cu-oxidase; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDB, INIF, 07-DEC-95
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001287; CuNO2 reductase.
InterPro; IPR006311; Tat.
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PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
COPPER (TYPE 1).
COPPER (TYPE 2).
COPPER (TYPE 1).
COPPER (TYPE 1).
COPPER (TYPE 1).
COPPER (TYPE 1).
COPPER (TYPE 2).
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Best Local :
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SEQUENCE
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01-FEB-1995
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                  NIR_RHIGA
Q01537;
                                                                                                                                                      WEDLINE=93175864, PubMed=8439151;
Ye R.W.; Fries M.R., Bezborodnikov S.G.,
"Characterization of the structural gene
nitrite reductase and homology of this ge
                                                                                                                                                                                                                                                             Rhizobium galegae.
Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium/Aç
                                                                                                                                                                                                                                                                                                   Copper-containing NIRU.
            -
                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=G-179;
                                                                                                                                          denitrifiers.";
                                                                                                                                                                                                                                              NCBI_TaxID=399;
                                                                                    CATALYTIC ACTIVITY: Nitric oxide + H(2)O + ferricytochrome c nitrite + ferrocytochrome c.

COFACTOR: CONTAINS ONE ATOM OF TYPE I COPPER AND ONE ATOM OF COPACTOR.
                                   II COPPER; FAD. TYPE 1 COPPER IS BOUND WITHIN A SINGLE MONOMER, WHILE TYPE 2 COPPER IS HELD BY RESIDUES FROM EACH OF TWO MONOMERS OF THE TRIRITE IS BOUND TO THE TYPE 2 COPPER SITE.

PSEUDOAZURIN IS THE PHYSIOLOGICAL ELECTRON DONOR FOR THE CU-NIR II
PATHWAY: Nitrate assimilation (denitrification) SUBUNIT: Homotrimer (By similarity).
                         VITRO (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350
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                                                                                                                               Environ. Microbiol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLAGAALAG--AVAPLIHTAQAHAAGAAAAGAAPVDISTLPRVKVDL-----VKPPFVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLSGCSNQADKAAQPKSSTVDAAAKTANADNAASQEHQGELPVIDAIVTHAPEVPPPVDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YV-WATGKFRNPPDLDQETWLIPGGTAGAAFYTFRQPGVYAYVNHNLIEAFELGAAGHFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVHFEGGKGENH----NIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAVKAMRTLTPTHIVFNGAVGALTGDHALTAAVGE--RVLVVHSQANRDTRPHLIGGHGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DMEKAIRE-DAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNLTSSFHVIGEIFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HVTSGMNGAIMVLPRDGLKDEKGQPLTYDKIYYVGEQDFYVPKDEAGNYKKYETPGEAYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIANGMYGLILVEPKEGLP-----KVDKEYYVMQGDFYTK-----GKYGEQGLQPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NHPDSKMPHNVDFHAATGPGGGAEASFTAPGHTSTFSFKALQPGLYVYHCAVAPVGM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AHDQVAKTGPRVVEFTMTIEEKKLVIDREGTEIHAMTFNGSVPGPLMVVHENDYVELRLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DH-----PAKVVVKMETVEKVMRL-ADGVEYQFWTFGGQVPGQMIRVREGDTIEVQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                VTGEWNDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGEENHEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPDTNTLLHNI DFHAATGALGGGALTQVNPGEETTLRFKATKPGVFVYHC--APEGNVPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325
337
351
355
                                                                                                                                                                                                                                                                                                             (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 42, Last annotation update)
aining nitrite reductase precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                            teobacteria; Alphaproteobacteria; Rhizobiales; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Æ,
                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332
343
350
361
368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40771 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.6%;
36.3%;
                                                                                                                59:250-254(1993).
itric oxide + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A70B52B814090EA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461.5;
No. 3.
                                                                                                                                                                                                                                                                                                                                                                               379
                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .3e-25
                                                                                                                                                       encoding a copper-containing ene to DNA of other
                                                                                                                                                                                 Averill B.A.,
                                                                                                                                                                                                                                                                                                                                                                               ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                               (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                 1.7.2.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                   Tiedje J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41;
                                                                                                                                                                                                                                                                                                                  (Cu-NIR)
                                        CU-NIR IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                       METAL
METAL
METAL
METAL
METAL
METAL
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Oxidoreductase; Copper; Metal-binding
Nitrate assimilation; Repeat; Peripl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M97294; AAC79132.1; -. PIR; A48936; A48936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P25006; 1NIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00695; CUNO2RDTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00394; Cu-oxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001287; CuNO2_reductase.
InterPro; IPR006311; Tat.
                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Periplasmic.

DOMAIN: THE TYPE I COPPER SITE IN NIR PLAYS A CRUCIAL ROLE FOR ELECTRON TRANSFER FROM PSEUDOAZURIN TO THE TYPE II COPPER SITE OF NIR, WHICH COMPRISES THE CATALYTIC CENTER OF NIR FOR THE REDUCTION OF NITRITE.

SIMILARITY: Contains 2 plastocyanin-like domains.

CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-12 IS THE INITIATOR.
                                                                                                                                                       177
                                                                                                                                                                                                       119
                         343
                                                  295
                                                                                                   237
                                                                                                                                                                             184
354
                                                                                                                            227
                                                                                                                                                                                                                                124
                                                                                                                                                                                                                                                        59
                                                                                                                                                                                                                                                                          72 VPPPVDRDH------PAKVVVKMETVEKVMRLAD-GVEYQFWTFGGQVPGQMIRVREGD
                                                                          VIGEIFDKVHFEGGKGENH---NIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNK 342
                                                                                                                                                                                                     YVELTLVNPDTNELQHNIDFHSATGALGGGALTVVNPGDTAVLRFKATKAGVFVYHC--A
                                                                                                                                                                                                                            TIEVQFSNHPDSKMPHNVDFHAATGPGGGAEASFTAPGHTSTFSFKALQPGLYVYHCAVA
GAAGHFKVTGDWNDDL
                       GALGILKVEGEENHEI
                                                 LIGGHGDYV-WATGKFANPPELDQETWFIPGGAAGAAYYTFQQPGIYAYVNHNLIEAFEL
                                                                                                   SAGEAYPDVLEAMKTLTPTHVVFNGAVGALTGDNALQAKVGD-
                                                                                                                          EQGLQPFDMEKAIRE-DAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNLTSSFH
                                                                                                                                                     PAGMVPWHVTSGMNGAIMVLPRDGLKDHKGHELVYDKVYYVGEQDFYVPKDENGKFKKYE
                                                                                                                                                                        PVGM---HIANGMYGLILVEPKEGLPK------VDKEYYVMQGDFYTK------GKYG
                                                                                                                                                                                                                                                        VKPPFVHAHTQKAEGEPKVVEFKMTIQEKKIVVDDKGTEVHAMTFDGSVPGPMMIVHQDD
                                                                                                                                                                                                                                                                                                                                                           379
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                    215
134
139
174
175
184
189
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                                                                                                                                                                                                                                                                                                                                                                                      379
214
279
134
139
174
178
184
                                                                                                                                                                                                                                                                                                                  17.3%;
                                                                                                                                                                                                                                                                                                                                                            MW.
                         358
                                                                                                                                                                                                                                                                                                          45;
                                                                                                                                                                                                                                                                                                         *Score 453; DB
Pred. No. 1.3e
45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   COPPER
COPPER
COPPER
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COPPER
COPPER
                                                                                                                                                                                                                                                                                                                                                                        COPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COPPER-CONTAINING NITRITE PLASTOCYANIN-LIKE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLASTOCYANIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                            090A3CBF6662F62F
                                                                                                                                                                                                                                                                                                                                                                        (TYPE 1)
(TYPE 2)
(TYPE 2)
(TYPE 1)
(TYPE 1)
(TYPE 1)
(TYPE 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flavoprotein;
                                                                                                                                                                                                                                                                                                                     DB 1;
.3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal
                                                                                                                                                                                                                                                                                                           119;
                                                                                                                                                                                                                                                                                                                                                                    IKE 2.

(BY SIMILARITY).

(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                 Length 379;
                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                      RVLILHSQANRDTRPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL
                                                                                                                                                                                                                                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Вņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collaboration
L outstation -
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                commerc
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                                                                                                                               285
                                                                                                                                                       236
                                                                                                                                                                                226
                                                                                                                                                                                                                                                                                    123
                                                                                                       294
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RESULT 5
NIR_PSECL
ID NIR_PSECL
AC Q06006;

STANDARD;

PRT;

363

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01-FEB-1995 01-FEB-1995 15-SEP-2003

(Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 42, Last annotation update)
aining nitrite reductase precursor

(E)

1.7.2.1) (Cu-NIR).

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                                                                                                           Query Match
Best Local S
Matches 124
                                                                                                        METAL
METAL
SEQUENCE
                                                                                                                                               DOMAIN
DOMAIN
METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                              InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001287; CuNO2_reductase
Pfam; PF00394; Cu-oxidase; 2.
                                                                                                                                                                                                                                                                                                                                                    EMBL; Z21945; CAA79939.1; -. PIR; S32112; S32112. HSSP; P38501; 1AS8.
                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of Pseudomonas stutzeri.";
Arch. Microbiol. 160:18-26(1993).
                                                                                                                                                                                                                                                                                  Oxidoreductase; Copper; Metal-binding; Flavoprotein;
                                                                                                                                                                                                                                                                                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glockner A.B., Juengst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93356602; PubMed=8352648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                functional in a mutationally cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glockner A.B., Juengst A., Zumft W.G.,
Copper-containing nitrite reductase f
                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Periplasmic.

DOMAIN: THE TYPE I COPPER SITE IN NIR PLAYS A CRUCIAL ELECTRON TRANSFER FROM PSEUDOAZURIN TO THE TYPE II COF NIR, WHICH COMPRISES THE CATALYTIC CENTER OF NIR EX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Nitric oxide + H(2)O + ferricytochrome c = nitrite + ferrocytochrome c.

COPACTOR: CONTAINS ONE ATOM OF TYPE I COPPER AND ONE ATOM OF TYPE II COPPER; FAD. TYPE 1 COPPER IS BOUND WITHIN A SINGLE MONOMER, WHILE TYPE 2 COPPER IS HELD BY RESIDUES FROM EACH OF TWO MONOMERS OF THE TRIMER. NITRITE IS BOUND TO THE TYPE 2 COPPER SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 2 plastocyanin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: Nitrate assimilation (denitrification) SUBUNIT: Homotrimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSEUDOAZURIN IS THE PHYSIOLOGICAL ELECTRON DONOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REDUCTION OF NITRITE.
 8
                            72
                                                                  Similarity
                                                                                                                                                                                                                                                                                                PR00695;
VAPPLVHPHEQVVSGPPKVVQFRMSIEEKKMVIDDQGTTLQAMTFNGSMPGPTLVVHEGD
                     VPPPVDRDH-----PAKVV-VKMETVEKVMIKLAD-GVEYQFWTFGGQVPGQMIRVREGD
                                                                                                        25
25
194
113
118
118
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324
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                                                     Conservative
                                                                                                                                                                                                                                                                                                  CUNO2RDTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas.
                                                                                                                       363
113
118
153
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168
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193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND
                                                               17.2%;
                                                                                                                                                                                                                                                                      Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Pseudomonas aureofaciens)
                                                                                                         M.
                                                                                                     PLASTOCYANIN-LIKE 2
COPPER (TYPE 1) (BY
COPPER (TYPE 2) (BY
COPPER (TYPE 2) (BY
COPPER (TYPE 1) (BY
COPPER (TYPE 1) (BY
COPPER (TYPE 1) (BY
COPPER (TYPE 1) (BY
COPPER (TYPE 2) (BY
COPPER (TYPE 2) (BY
                                                  Score 451; DB
Pred. No. 1.7e
#1; Mismatches
                                                                                                                                                                                                                              COPPER-CONTAINING NITRITE REDUCTASE PLASTOCYANIN-LIKE 1.
                                                                                                                                                                                                                                                                      Periplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ဝ္ဂ
                                                                                                                  R (TYPE 1) (BY SIMILARITY).

R (TYPE 2) (BY SIMILARITY).

R (TYPE 2) (BY SIMILARITY).

R (TYPE 1) (BY SIMILARITY).

R (TYPE 1) (BY SIMILARITY).

R (TYPE 1) (BY SIMILARITY).

R (TYPE 2) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from
                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                               DB 1;
.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cdl-free background (NirS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aureofaciens
                                                                                                                                                                                                                                                                       Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonadales;
                                                                             Length
                                                    Indels
                                                                                                                                                                                                                                                                                    FAD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CU-NIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITE
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
                         123
97
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RESULT
NIRK_RH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RX MEDLINE=21396509; PubMed=11481432;

RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

RA Barnoy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,

RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,

RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,

RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

RA Kalman S., Keating D.H., Palm C., Surzycki R., Wells D.H.,

RA Kalman S., Keating D.H., Palm C., Surzycki R., Wells D.H.,

RA Kalman S., Keating D.H., Palm C., Surzycki R., Wells D.H.,

RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,

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RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn M.L.,

RA Gurjal M., Hong A., Hyman R.W., Kahn M.L.,

RA Gurjal M., Long S., Kahn M.L.,

RA Gur
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Q92Z29;
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                              use by non-profit institutions as long as its cont
modified and this statement is not removed. Usage by
entities requires a license agreement (See http://www.
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15-SEP-2003 (Rel.
15-SEP-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Nitrate assimilation (denitrification).
SUBUNIT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Periplasmic (By similarity).
DOMAIN: THE TYPE I COPPER SITE IN NIR PLAYS A CRUCIAL ROLE
ELECTRON TRANSFER FROM PSEUDOAZURIN TO THE TYPE II COPPER S
OF NIR, WHICH COMPRISES THE CATALYTIC CENTER OF NIR FOR THE
                                                                                                                                                                                                                                                                             REDUCTION OF NITRITE.
SIMILARITY: Contains 2 plastocyanin-like domains.
                                                                 SWISS-PROT entry is copyright. It is produced through reen the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content field and this statement is not removed. Usage by and
                                                                                                                                              European
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sae; Sinorhizobium/Ensifer group; Sino
email to license@isb-sib.ch)
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PIR; A95347; A95347.

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TIGRFAMB; TIGR01409; TAT_signal_seq; 1.
Oxidoreductase; Copper; Metal-binding;
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InterPro; IPR001287; CuNO2_reductase
InterPro; IPR006311; Tat.
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                                                                         Rhizobium hedysari.
Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium/A;
NCBI_TaxID=50338;
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01-NOV-1997 (Rel. 35,
15-SEP-2003 (Rel. 42,
Copper-containing nitr
MEDLINE=97055705; PubMed=8899992;
                                        SEQUENCE FROM N.A.
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                                                                                                teobacteria; Alphaproteobacteria;
Rhizobium/Agrobacterium group; Rl
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Pred. No. 1.2e
52; Mismatches
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R (TYPE 1) (B
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R (TYPE 1) (B
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(BY SIMILARITY).

(BY SIMILARITY).

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(BY SIMILARITY).

(BY SIMILARITY).
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                                                                                                         Rhizobium.
                                                                                                                                                                                         (EC 1.7.2.1) (Cu-NIR)
                                                                                                                          Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
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165

KAGVFVYHC--APPGMVPWHVTSGMNGAIMVLPREGLTDGHGKELVYDKVYYLGEQDFYI

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Best Local :
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InterPro; IPR001287; CuNO2_reductase.
InterPro; IPR006311; Tat.
Pfam; PF00394; Cu-oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U65658;
HSSP; P38501;
InterPro; IPRO
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
Oxidoreductase; Copper; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00695;
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RICHIEL + FERROCYCOCHROME C.

ROPACTOR: CONTAINS ONE ATOM OF TYPE I COPPER AND ONE ATOM OF TYPE I COPPER; FAD. TYPE 1 COPPER IS BOUND WITHIN A SINGLE MONOMER, WHILE TYPE 2 COPPER IS HELD BY RESIDUES FROM EACH OF TWO MONOMERS OF THE TRIMER. NITRITE IS BOUND TO THE TYPE 2 COPPER SITE.

OF THE TRIMER. NITRITE IS BOUND TO THE TYPE 2 COPPER SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: Nitrate assimilation (denitrification).
SUBUNIT: Homotrimer (By similarity).
SUBCELULIAR LOCATION: Periplasmic (By similarity).
DOMAIN: THE TYPE I COPPER SITE IN NIR PLAYS A CRUCIAL
ELECTRON TRANSFER FROM PSEUDOAZURIN TO THE TYPE II COP
OF NIR, WHICH COMPRISES THE CATALYTIC CENTER OF NIR FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. Environ. Microbiol. 62:4019-4025(1996).
CATALYTIC ACTIVITY: Nitric oxide + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REDUCTION OF NITRITE. SIMILARITY: Contains 2 plastocyanin-like domains.
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                                                                                                                                                                                                                        Similarity
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  QPGLYYYHCAVAPVGM---HIANGMYGLILVEPKEGLPK------VDKEYYVMQGDFY-
                                  VPGPLIVVHQDDYVEVTLVNPETNTLQHNIDFHSATGALGGGALTVVNPGESAVLRFKAT
                                                            VPGQMIRVREGDTIEVQFSNHPDSKMPHNVDFHAATGPGGGAEASFTAPGHTSTFSFKAL
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                                                                                                                      PVIDAIVTHAPEVPPPVDRDHP-----AKVVVKMETVEKVMRLAD--GVEYQFWTFGGQ
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                                                                                                                                                                                                                                                                             COPPER CONTAINING NITRITE REDUCTASE.
PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
COPPER (TYPE 1) (BY SIMILARITY).
COPPER (TYPE 2) (BY SIMILARITY).
COPPER (TYPE 2) (BY SIMILARITY).
COPPER (TYPE 1) (BY SIMILARITY).
COPPER (TYPE 2) (BY SIMILARITY).
                                                                                                                                                                                                                        Score 437; DB 1;
Pred. No. 1.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Periplasmic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            seq; 1.
Thating: Flavoprotein;
                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal.
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6 outstation -
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RESULT 8
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01-OCT-1994
01-OCT-1994
                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

MEDLINE=98019216; PubMed=9353305;

Murphy M.E., Turley S., Adman E.T.;

"Structure of nitrite bound to copper-containing nitrite reductase from Alcaligenes faecalis. Mechanistic implications.";

J. Biol. Chem. 272:28455-28460(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ul-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Copper-containing nitrite reductase precursor
NIRK OR NIR.
                                                                                                                                                                                                                                                                                                                                                                                      Murphy M.E., Turley S., Kukimoto M., Nishiyama M., Horinouchi S., Sasaki H., Tanokura M., Adman E.T., "Structure of Alcaligenes faecalis nitrite reductase and a copper site mutant, M150E, that contains zinc."; Biochemistry 34:12107-12117(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning and characterization of a nitrite Alcaligenes faecalis and its expression in J. Gen. Microbiol. 139:725-733(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kukimoto M., Nishiyama M., Murphy M.E.P., Turley S., Adman E.T., Horinouchi S., Beppu T.;
"X-ray structure and site-directed mutagenesis of a nitrite reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIR_ALCFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemistry 33:5246-5252(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96032602; PubMed=7547950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S-6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alcaligenaceae; Alcaligenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93294530; PubMed=8515232;
                                                                                              CATALYTIC ACTIVITY: Nitric oxide + H(2)O + ferricytochrome c = nitrite + ferrocytochrome c.

COPACTOR: CONTAINS ONE ATOM OF TYPE I COPPER AND ONE ATOM OF TYPE II COPPER; FAD. TYPE 1 COPPER IS BOUND WITHIN A SINGLE MONOMER, WHILE TYPE 2 COPPER IS HELD BY RESIDUES FROM EACH OF TWO MONOMERS OF THE TRIMER. NITRITE IS BOUND TO THE TYPE 2 COPPER SITE.

PSEUDOAZURIN IS THE PHYSIOLOGICAL ELECTRON DONOR FOR THE CU-NIR IN
                       PATHWAY: Nitrate assimilation (denitrification) SUBUNIT: Homotrimer. SUBCELLULAR LOCATION: Periplasmic.
                                                                                   VITRO (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alcaligenes faecalis S-6: roles of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274
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  UNDER ANAEROBIC GROWTH CONDITIONS AND BY NITRITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kukimoto M., Ohnuki T., Horinouchi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GGHGEYVWRTGKFVNVPDRDQETWFIPGPTRGAAYY
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                                                                                                        CU-NIR IN
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    Pfam; PF00394; cu-value prints; PR00595; CUNOZRDTASE.
TIGRPAMS; TIGR01409; ATT signal seq; 1.
Oxidoreductase; Copper; Metal-binding; Flavoprotein; Oxidoreductase; Copper; Metal-binding; Flavoprotein; Nitrate assimilation; Repeat; Periplasmic; Signal; 31
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PIR; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 1ET7; 24-AUG-00.
; 1ET8; 24-AUG-00.
erPro; IPR001117; Cu-oxidase.
erPro; IPR001287; CuNO2_reductase.
erPro; IPR006311; Tat.
m; PF00394; Cu-oxidase; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 2 plastocyanin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; D13155; BAA02440.1; -. 139582; I39582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-NOV-96.
25-FEB-98.
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25-FEB-98.
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59
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91
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COPPER (TYPE 2).

COPPER (TYPE 2).

COPPER (TYPE 1).

COPPER (TYPE 1).

COPPER (TYPE 1).

COPPER (TYPE 2).

COPPER (TYPE 2).

M->K: LOOSES NITRITE-REDUCING ACTIVITY.

AND FALLS TO CATALYZE THE REDUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRROLIDONE COPPER (TYPE COPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COPPER-CONTAINING NITRITE REDUCTASE. PLASTOCYANIN-LIKE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLASTOCYANIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOXYLIC
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3D-structure;
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                                                                                                                                                                                                           Similarity
                                                                                                                                                        EVPPPVDRDHPAKVVVKMETVEKVMRLAD-GVEYQFWTFGGQVPGQMIRVREGDTIEVQF
                                             DKVHFEGGKGENHNI--QTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILK
                                                            EDTVKVMRTLTPTHVVFNGAVGALTGDKAMTAAVGE--KVLIVHSQANRDTRPHLIGGHG
                                                                         FDMEKAIRE-DAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNLTSSFHVIGEIF
                                                                                                                               SNHPDSKMPHNVDFHAATGPGGGAEASFTAPGHTSTFSFKALQPGLYVYHCAVAPVGM--
                                                                                                                                             S---QVAEGGPKVVEFTMVIEEKKIVIDDAGTEVHAMAFNGTVPGPLMVVHQDDYLELTL
                                                                                                                                                                        LAGAALAG-----ALAPVLATTSAWGQGAVRKATAAEIAALPRQ-KVELVDPPFVHAH
                                                                                                                                                                                      LSALMLSGCSNQADKAAQPKSSTVDA----AAKTANADNAASQEHQGELPVIDAIVTHAP
                  VEGEENHEIYSHKQTDAVYLPEG
                                DYVWATGKFNTPPDVDQETWFIPGGAAGAAFYTPQQPGIYAYVNHNLIEAFELGAAAHFK
                                                                                       WHVVSGMNGAIMVLPREGLHDGKGKALTYDKIYYVGEQDFYVPRDENGKYKKYEAPGDAY
                                                                                                     -HIANGMYGLILVEPKEGLP-----KVDKEYYVMQGDFYT----KGKYGE---QGLQP
                                                                                                                   INPETNTLMHNIDFHAATGALGGGGLTEINPGEKTILRFKATKPGVFVYHC--APPGMVP
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                         16.3%;
                                                                                                                                                                                                                                40332 MW;
      -SVLAPSG
                                                                                                                                                                                                    51;
                                                                                                                                                                                                           Score 427.5;
Pred. No. 8.1
                                                                                                                                                                                                                                OAD918988301BF29 CRC64;
                                                                                                                                                                                                     Mismatches
                   372
                                                                                                                                                                                                    1.1e-23;
les 158;
                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                  Length 376;
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                     45;
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                                                                                                                                 187
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P81445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel.
28-FEB-2003 (Rel.
15-SEP-2003 (Rel.
                                                                                                                                                                                                                                              METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: Nitric oxide + H(2)O + ferricytochrome c = nitrite + ferrocytochrome c.

-i- COPACTOR: CONTAINS ONE ATOM OF TYPE I COPPER AND ONE ATOM OF TYPE I COPPER; FAD. TYPE 1 COPPER IS BOUND WITHIN A SINGLE MONOMER, WHILE TYPE 2 COPPER IS HELD BY RESIDUES FROM EACH OF TWO MONOMERS OF THE TRIMER. NITRITE IS BOUND TO THE TYPE 2 COPPER SITE.

PSEUDOAZURIN IS THE PHYSIOLOGICAL ELECTRON DONOR FOR THE CU-NIR-IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94059002; PubMed=8240262;
Abraham Z.H.L., Lowe D.J., Smith B.E.;
"Purification and characterization of the dissimilatory nitrite
reductase from Alcaligenes xylosoxidans subsp. xylosoxidans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copper-containing NIRK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001287; CuNO2_reductase.
Pfam; PF00394; Cu-oxidase; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
STRAIN=NCIMB 11015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS)
STRAIN=NCIMB 11015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alcaligenaceae;
NCBI_TaxID=515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alcaligenes xylosoxydans xylosoxydans (Achromobacter
                                                                                                                                                                                                                                                                                                                                                                                                                    Nitrate assimilation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF NITRITE.
-!- SIMILARITY: Contains 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dodd F.E., Hasnain S.S., Abraham Z.H.L., Eady R.R., "Structures of a blue-copper nitrite reductase and
                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reductase from Alcaligenes xylosoxidans subsp. xylosoxidans (N.C.I.M.B. 11015): evidence for the presence of both type 1 and
                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          copper centres.";
iochem. J. 295:587-593(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Nitrate assimilation (denitrification).

SUBUNIT: Homotrimer.

SUBECLULAR LOCATION: Periplasmic (By similarity).

DOMAIN: THE TYPE I COPPER SITE IN NIR PLAYS A CRUCIAL ROLE FOR ELECTRON TRANSFER FROM PSEUDOAZURIN TO THE TYPE II COPPER SITE NIR, WHICH COMPRISES THE CATALYTIC CENTER OF NIR FOR THE REDUCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALCXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDR; 07-JUL-97.
INDS; 07-JUL-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crystallogr.
  124 TIEVQFSNHPDSKMPHNVDFHAATGPGGGAEASFTAPGHTSTFSFKALQPGLYVYHCAVA
                                                                                                                                   116;
                                             10
                                                                                      72
                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR00695;
                                             VAPPLVHPHSQVAAGAPKVVQFRMSIEEKKWVADDDGTTAQAMTFNGSVPGPTLVVHEGD
                                                                                      VPPPVDRDH-----PAKVVVKMETVEKVMRL-ADGVEYQFWTFGGQVPGQMIRVREGD
                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Achromobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUNO2RDTASE
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41, Last sequence update)
42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nitrite reductase
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34413
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330
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125
126
140
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                                                                                                                                                          16.1%;
35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                  Metal-binding; Flavoprotein; FAL
epeat; Periplasmic; 3D-structure.
PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Betaproteobacteria;
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                                                                                                                                 36;
                                                                                                                                                                                                                                              COPPER
COPPER
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                                                                                                                                                                              Score 424;
                                                                                                                                                          Pred.
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                                                                                                                                      Mismatches
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(EC 1.7.2.1)
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                                                                                                                                                          1; DB 1;
1.2e-22;
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                                                                                                                                                                              Length 330;
                                                                                                                                                                                                                              CRC64;
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                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xylosoxidans).
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                                                                                                                                          56
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                                                                                                                                        Gaps
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                                                      69
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CRC64; Length Indels

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Gaps

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                      SIGNAL
CHAIN
                                                                                    TIGRFAMS; TIGRO1480; copper res A; 1.
TIGRFAMS; TIGRO1409; TAT signal seq; 1.
PROSITE; PS00079; MULTICOPPER OXIDASE1;
PROSITE; PS00080; MULTICOPPER OXIDASE2;
                                                                                                                                                    InterPro; IPR006376; CopA.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR00235; MultiCu_oxidse2.
InterPro; IPR006311; Tat.
Pfam; PF00394; Cu-oxidase; 2.
                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a celebrate the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brown N.L., Barrett S.R., Camakaris J., Lee B.T.O., Rouch D.A.; "Molecular genetics and transport analysis of the copper-resistance determinant (pco) from Escherichia coli plasmid pRJ1004.";
                                                                                                                                                                                                                                                                  EMBL; X83541; CAA58525.1; PIR; S70159; S52253.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=K12 / ED8739;
MEDLINE=96130847; PubMed=8594334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammap
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
Plasmid pRJ1004.
Bacteria; Protec
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16-OCT-2001 (Rel.
Copper resistance
                                                        Periplasmic.
                                                                       Oxidoreductase;
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                                                                                                                                                                                                                                                                                                                     tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: REQUIRED FOR THE COPPER-INDUCIBLE EXPRESSION RESISTANCE. WAY HAVE OXIDASE ACTIVITY (BY SIMILARITY). SUBCELLULAR LOCATION: Periplasmic (Potential). SUBCELLULAR LOCATION: Periplasmic (Potential). SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDA:
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   TANDEM REPEATS OF D-H-X-X-M-X-
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Plasmid; Metal-binding;
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P37064;
01-JUN-1994 (Rel. 2
01-JUN-1994 (Rel. 2
28-FEB-2003 (Rel. 4
                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
101-JUN-1994 (Rel. 29, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
L-ascorbate oxidase (EC 1.10.3.3) (Ascorbase) (ASO).
Cucurbita pepo var. melopepo (Zucchini).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosiderrosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
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                               X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

MEDLINE=92194315; PubMed=1548698;

Messerschmidt A., Ladenstein R., Huber R., Bolognesi M.,

Messerschmidt A., Radenstein R., Finazzi-Agro A.;

Avigliano L., Petruzzelli R., Rossi A., Finazzi-Agro A.;

"Refined crystal structure of ascorbate oxidase at 1.9-A

"In Mol. Biol. 224:179-205(1992).
X-RAY CRYSTALLOGRAPHY
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PDB; 1AOZ; 31-OCT-93.
PDB; 1ASO; 31-JAN-94.
PDB; 1ASO; 31-JAN-94.
PDB; 1ASO; 31-JAN-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89236417; PubMed=2716059; Messerschmidt A., Rossi A., Ladenstein R., Huber R., Bolognesi M., Gatti G., Marchesini A., Petruzzelli R., Finazzi-Agro A.; "X-ray crystal structure of the blue oxidase ascorbate oxidase from "zucchini. Analysis of the polypeptide fold and a model of the copper sites and ligands.", J. Mol. Biol. 206:513-529(1989).
METAL 
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DISULFID
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PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.

PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.

PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.

PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.

PLASTOCYANIN-LIKE 1.

DOMAIN 134 300 PLASTOCYANIN-LIKE 2.

DOMAIN 344 523 PLASTOCYANIN-LIKE 3.
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InterPro; IPR002355; MultiCu_oxi
Pfam; PF00394; Cu-oxidase; 3.
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GlycoSuiteDB; P37064;
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COFACTOR:
CONTAIN TH
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CATALYTIC ACTIVITY: 2 L-ascorbate +
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FUNCTION: MAY BE INVOLVED IN A REDOX SYSTEM INVOLVING ASCORBIC
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Matches 81; Conser
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Pred. No. 0.00016;
7; Mismatches 129;
                                                                                                                                                          24660B0F47AB54B4 CRC64;
                                                                                                                  Length
                                                                                  Indels
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                                                                                Gaps
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18; 148

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RESULT 12
ASO_CUCMA
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P24792; Q39539;
01-MAR-1992 (Rel
01-NOV-1997 (Rel
                    EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                   Kisu Y., Harada Y., Goto M., Esaka M.; "Cloning of the pumpkin ascorbate oxidase gene acting region involved in induction by auxin.", plant Cell Physiol. 38:631-637 (1997).

-i- FUNCTION: MAY BE INVOLVED IN A REDOX SYSTEM
                                                                                              entities requires a or send an email to
                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Ebisu Nankin;
MEDLINE=90361033; PubMed=2143984;
MEBSAKA M., Hattorī T., Pujisawa K., Sakajo S., Asi
Esaka M., Hattorī T., Pujisawa K., Sakajo S., Asi
Esaka M., Hattorī T., Pujisawa K., Sakajo S., Asi
MEDLINE Colored Strain Sakajo S., Asi
MEDLINE SAKAJO S., Asi
MEDLINE SAKAJO SAKAJO S., Asi
MEDLINE SAKAJO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=97354114; PubMed=9210335;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cuturbita maxima (Pumpkin) (Winter squash)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003
                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                          COPACTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASE CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR. SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES SIMILARITY: Contains 3 plastocyanin-like domains.
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COFACTOR:
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CATALYTIC ACTIVITY: 2 L-ascorbate +
                  D55677;
P37064;
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                                                                                          non-profit institutions as long d and this statement is not removed. s requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTRARHPNTPPGLTLLNYLPNSVSK-LPTSPPPQTPA
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(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
oxidase precursor (EC 1.10.3.3) (
                  CAA39300.1;
BAA09528.1;
1AOZ.
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Cu-oxidase
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Pseudomonas syri
Plasmid pPT23D.
Bacteria; Protec
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P12374;
01-OCT-1989
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83; Conserv
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PS00079; MULTICOPPER OXIDASE1;
PS00080; MULTICOPPER OXIDASE2;
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                  Proteobacteria;
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(Rel.
                                                     syringae
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12, Created)
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42, Last annotation upon
42 protein A precursor.

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PLASTOCYANIN-LIKE 2
PLASTOCYANIN-LIKE 3
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Pred.
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Query Match
Best Local Similarity
Matches 89; Conserv
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InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2.
InterPro; IPR006311; Tat.
InterPro; IPR006311; Tat.
Pfam; Pr00394; Cu-oxidase; 2.
Pfam; Pr00394; Cu-oxidase; 2.
TIGRPAMB; TIGR01480; copper_res A; 1.
TIGRPAMB; TIGR01409; TAT_signal_seq; 1.
PROSITE; PS00079; MULTICOPPER_OXIDASE2; 1.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
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SEQUENCE
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mellano M.A., Cooksey D.A.;
"Nucleotide sequence and organization
"Recubercial syringae pv. tomato.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=PT23.2;
MEDLINE=88227880; PubMed=3372485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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HSSP; P36649; 1KV7.
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Natl. Acad. Sci. U.S.A. 88:8915-8919(1991).
FUNCTION: MEDIATES COPPER RESISTANCE BY SEQUESTRATION OF THE PERIPLASM ALONG WITH THE COPPER-BINDING PROTEIN COPC.
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170:2879-2883(1988)
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COPPER (TYPE 3) (BY
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COPPER (TYPE 2) (POT
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COPPER (TYPE 3) (POT
COPPER (TYPE 1) (POT
COPPER (TYPE 
   Score 164.5; DB 1;
Pred: No. 0.00044;
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                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Takeda Y., Shimizu T.;
Takeda Y., Shimizu T.;
"Cloning and sequencing of the gene
"Cloning and sequencing of the gene
from Gluconabacter suboxydans.";
from Bloeng. 72:1-6(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                   Q47945; O08083;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alcohol dehydrogenase cytochrome c subunit precursor
553) (C553) (G3-ADH subunit II).
                        This
                                                               bound alcohol dehydrogenase from Gluconobacter suboxydans expression in Acetobacter pasteurianus.";
Appl Environ. Microbiol. 63:1131-1138(1997).
-!- FUNCTION: DEHYDRATION OF PRIMARY ALCOHOLS (EXCEPTION:
-!- SUBUNIT: HETEROTRIMER (DEHYDROGENASE, CYTOCHROME AND E-ADHS), THAT FORMS THE ALCOHOL DEHYDROGENASE COMPLEX:
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING THE PERIL SPACE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                Gluconobacter oxydans (Gluconobacter suboxydans)
Bacteria; Proteobacteria; Alphaproteobacteria; R
Acetobacteraceae; Gluconobacter.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
STRAIN=IFO 12528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYCA_GLUOX
                                                                                                                                                                                Kondo K., Horinouchi S.;
"Characterization of the genes encoding
                                                      -!- PTM: BINDS THREE HEME GROUPS PER MOLECULE (POTENTIAL).
                                                                                                                                                                                                           MEDLINE=97208225; PubMed=9055427;
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=442;
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             ROT entry is copy
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bacter suboxydans and their
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DE L-ascorbate c
GN AAO.
OS Nicotiana tab
OC Eukaryota; Vi
OC Spermatophyta
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RN [1]
RP SEQUENCE FROM
RX MEDLINE=96194
RA KATO N., ESAM
RT "CDNA cloning
RL Plant, Mol. Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches 49
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InterPro; IPR003239; Cyt_Cadh.
InterPro; IPR003219; CytC_adh.
InterPro; IPR003215; CytC_heme_bind.
InterPro; IPR000345; CytC_heme_bind.
Pfam; PF00034; cytochrome_C; 1.
PRINTS; PR00605; CYTCHROMECI.
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PROSITE; PS00190; CYTOCHROME_C; 3.
Electron transport; Oxidoreductase; Si
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EMBL; D86375;
HSSP; P04164;
                                                                                       Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; eudicotyla
Asteridae; lamiids; Solanales; Solanacea
SEQUENCE FROM N.A.
MEDIJUS=96194464; PubMed=8624413;
Kato N., Esaka M.;
"CDNA Cloning and gene expression
Plant Mol. Biol. 30:833-837(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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(Rel. 35, Last sequence update)
(Rel. 38, Last snnotation update)
oxidase precursor (EC 1.10.3.3) (
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BAA19754.1; -.
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30:833-837(1996)
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              oxidase
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InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2
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CATALYTIC
H(2)O.
COFACTOR:
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TISSUE SPECIFICITY: HIGHLY EXPRESSED IN YOUNG AND GROWING SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES. SIMILARITY: Contains 3 plastocyanin-like domains.
 259
                     151
                                                                               149
                                                                                                                                         104;
                                                           94
                                                                                                   37
                                                                                                                     91
                                                                                                                                                   Similarity
                     GEGEKEPFHYDGEFNLLLSDWWHKGSHE---
                                                           IGTPWADGTAAISQCAINPGETFLYRFKVDKAGTYFYH--
                                                                               PG----
                                                                                                                     VEKVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSN--HPDSKMPHNVDFHAATG
NALKAKVGETVRLFV-GNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNI
                                      KEGLPK----VDKEYYVMQGDFYTKGKYGEQGLQPFDMEKAIREDAEYVVFNGSVGALTGE
                                                                                                  VEYIHWSPDGEESVVMGINGQFPGPT:
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PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
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BY SIMILARITY.
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COPPER (TYPE 3) (BY S.
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N-LINKED (GLCNAC. .
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OR BLUE,
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NPLR-WIGEPQTLLLINGRGQYNCSLAARFSKPPLPQCKLRGGEQYAPQILRVRPNKIYRL

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RESULT 16
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ID C552_THEFH
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ID C552_THEFH
AC P04164;
DT 20-MAR-1
RX SEQUENCI
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                                                                                                                                                                                                                                                                    "Integrity of Thermus thermophilus cytochrome c552 s
Bscherichia coli cells expressing the host-specific
maturation genes, ccmABCDEFGH: biochemical, spectral
characterization of the recombinant protein.";
Protein Sci. 9:2074-2084(2000).
                                                                                                                                                                                                                                                                                                                                                                                                      Fee J.A., Chen Y., Todaro T.R., Bren K.L., Patel K. Gomez-Moran E., Loehr T.M., Ai J., Thony-Meyer L., Stura E., Sridhar V., McRee D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Thermus thermophilus cytochrome-c552: a new highly thermostable cytochrome-c structure obtained by MAD phasing.";
J. Mol. Biol. 271:629-644(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97428333; PubMed=9281430, Than M.E., Hof P., Huber R., Boul Soulimane T.;
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MEDLINE=85199131; PubMed=2986626;
Titani K., Ericsson L.H., Hon-Nami K., Miyazawa
"Amino acid sequence of cytochrome c-552 from Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-1987
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=HB8 / ATCC 27634;
MEDLINE=21025441; PubMed=11152119;
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                                                                                                                                                                                         FUNCTION: THIS MONOHEME BASIC PROTEIN APPEARS TO FUNCTION & ELECTRON DONOR TO CYTOCHROME OXIDASE IN T.THERMOPHILUS; IT BE A C2-TYPE CYTOCHROME BUT IS DISTANTLY RELATED TO OTHER
                                                                                                                                                                   CYTOCHROMES.
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7 (Rel. 35, Last sequence update)
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c-552 precursor (C552).
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                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                   QADGAKIYAQCAGCHQQNGQGIPGAFPPLAGHVAEILAKEGGREYLILVLLYGLQGQIEV
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A homolog precursor
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by non-profit institutions as long
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SEQUENCE FROM N.A.

Pseudomonadaceae;

Pseudomonas.

NCBI_TaxID=323;

COPA OR PSPTO3914.

Pseudomonas syringae (pv. tomato). Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

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"Complete sequence of Pseudomonas syringae.";
Submitteed (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Could be involved in copper resistance. May have ox activity (By Similarity).
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TO THE FAMILY OF MULTICOPPER OXIDASES.
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15-JUL-1999
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InterPro; IPR002355; MultiCu_oxi
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Ohkawa J., Okada N., Shinmyo A., Takano M.;
"Primary structure of cucumber (Cucumis sativus) ascorbate oxidase deduced from cDNA sequence: homology with blue copper proteins and
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
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Proc. Natl. Acad. Sci. U.S.A.
-!- FUNCTION: MAY BE INVOLVED
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Matches 49
InterPro; IPR003088; Cyt_CI.
InterPro; IPR002329; Cyt_CIC.
InterPro; IPR002329; CytC_adh.
InterPro; IPR00345; CytC_heme_bind.
Pfam; PF00034; cytcothrome_c; 1.
PRINTS; PR00605; CYTCHROMECIC.
PRODOm; PD011584; CytC_adh; 1.
PROSITE; PS00190; CYTOCHROME_C; 3.
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01-OCT-1993
01-OCT-1993
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tamaki T., Fukaya M., Takemura H., Tayama K., Okumura H., Kawamura Y., Nishiyama M., Horinouchi S., Bepu T.; "Cloning and sequencing of the gene cluster encoding two subunits membrane-bound alcohol dehydrogenase from Acetobacter polyoxogenes Biochim. Biophys. Acta 1088:292-300(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENC SPECIES-A.polyoxogenes, STRAIN=NBI1028; MEDLINE=91159482; PubMed=2001402;
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01-OCT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alcohol dehydrogenase cytochrome C subunit precursor.
                                                                                                                                                                                                                                   EMBL; D00635; BAA00529.1; -.
EMBL; Y09480; CAA70689.1; -.
EMBL; S14271; S14271.
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SUBCELLULAR LOCATION:
SPACE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: DEHYDRATION OF PRIMARY ALCOHOLS (EXCEPTION: METHANOL)
SUBUNIT: HETEROTETRAMER (DEHYDROGENASE, CYTOCHROME, AND TWO
SMALLER UNKNOWN SUBUNITS) THAT FORMS THE ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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2:331-342(1992).

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RESULT 20
ASO_BRANA
  RETTER RECEPTOR OF THE REST OF
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Q00624;
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tobacco plant J.
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                                                                                                                                                                                                                                     Brassica napus (Rape).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside
eurosids II; Brassicales; Brassicaceae; Brassica.
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                "A Brassica napus gene family which ascorbate oxidase is expressed in de characterization and analysis of protobacco plants."
                                                                                                                                   STRAIN=cv. Westar;
MEDLINE=93272050; PubMed=1303799;
                                                                                                                                                                                                                                                                                                                     BP10
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                                                                                              Albani D., Sardana R.,
Fabijanski S.F.;
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                                                                                                                                                                                                                NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                       L-ascorbate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84;
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197
                                                                                                                                                                                                                                                                                                                                     oxidase homolog
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(Rel. 24, Last sequence update)
(Rel. 40, Last annotation updat
oxidase homolog precursor (EC 1
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HEME 2 (COV.
IRON (HEME
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Pred. No. 0.0062;
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                                                               Molecular
                                                                                                                    P.G.,
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                                                                                                                                                                                                                                                             Rosidae;
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RESULT
FA5_BOV
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Best Local S
Matches 71
                                                                                                                                                 SULT 21
      Bos taurus (Bovine).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Cet
Movidae; Bovinae; Bos.
                                                                                                FA5 BOVIN S
Q28107; Q28108;
Q1-NOV-1997 (Rel
Q1-NOV-1997 (Rel
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PIR; S23763; S23763.
TPR001117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                        Coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00394; Cu-oxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COPACTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WHICH CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR.
SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
SIMILARITY: TO CERULOPLASMIN AND LACCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H(2)0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Eleuropean Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                              321
                                                                                                                                                                                                                                                        212
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                                                                                                                                                                                                                                                                                                                                                                                      153
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                                                                                                                                                                                                                                                                                                                                                                                                              43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X64257; CAA45554.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                       (Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
factor V precursor (Activated pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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1 23 POTENTIAL.

24 555 LASCORBATE OXIDASE HOMOLOG.

444 444 COPPER (TYPE 2) (PROBABLE).

33 31 N-LINKED (GLCNAC. ...) (POTENTIAL).

61 61 N-LINKED (GLCNAC. ...) (POTENTIAL).

110 110 N-LINKED (GLCNAC. ...) (POTENTIAL).

110 110 N-LINKED (GLCNAC. ...) (POTENTIAL).

33 30 N-LINKED (GLCNAC. ...) (POTENTIAL).

35 30 N-LINKED (GLCNAC. ...) (POTENTIAL).

422 N-LINKED (GLCNAC. ...) (POTENTIAL).

55 AA; 62130 MW; 5BF23C9D73EA6C6A CRC64;
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                      Chordata; Crania
Cetartiodactyla;
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Pred. No. 0.009
37; Mismatches
                      Craniata; Vertebra
actyla; Ruminantia;
                                                                                                                                        PRT;
                                                                                                                                        2211 AA
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                       Vertebrata; Eutel
minantia; Pecora;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92147638; PubMed=1737753;
Guinto E.R., Esmon C.T., Mann K.G., Macgillivray R.T.;
"The complete cDNA sequence of bovine coagulation factor V.";
J. Biol. Chem. 267:2971-2978(1992).
-i- FUNCTION: COAGULATION FACTOR V IS A COFACTOR THAT PARTICIPATES
WITH FACTOR XA TO ACTIVATE PROTHROMBIN TO THROMBIN.
-i- SUBUNIT: Factor Va is composed of a heavy chain and a light chain, noncovalently bound. The interaction between the two checked the coadact.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
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SEQUENCE FROM N.A.
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M81440; AAA30512.1; -. EMBL; M81441; AAA30513.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified
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- PYM: SULFATION IS REQUIRED FOR EFFICIENT THROMBIN CLEAVAGE AND ACTIVATION AND FOR FULL PROCOAGULANT ACTIVITY (BY SIMILARITY).

- SIMILARITY: Contains 3 F5/8 type A domains.

- SIMILARITY: Contains 2 F5/8 type C domains.

- SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coagulation;
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; PS01285; FA58C_1; 2.

; PS01286; FA58C_2; 2.

; PS50022; FA58C_3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00079; MULTICOPPER OXIDASE1; 2.
agulation; Glycoprotein; Sulfation; Calcium;
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ACTIVATION PEPTIDE (CONNECTING REGION)
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PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
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PLASTOCYANIN-LIKE
Score 143.5; D
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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AC Q9GLP1;

AC Q9GLP1;

DT 16-OCT-2001

DT 15-SEP-2003
                     MEDLINE=21121490; PubMed=11229814; Grimm D.R., Colter M.B., Braunschw Kim H.K.W.;
                                                                                                                                                                                                                               Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                     protein modeling domains.";
                                                                                                                                                                   TISSUE=Liver;
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is calcium-dependent.

DOMAIN: Domain B contains 41 X 9 AA tandem repeats. Domains
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r V precursor (Activated protein C
                                                                                                 cDNA cloning, gene
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and C2 may be involved in membrane binding.

PTM: Thrombin activates factor V proteolytically to cofactor, factor Va (formation of a heavy chain at terminus and a light chain at the C-terminus).

SIMILARITY: Contains 3 F5/8 type A domains.

SIMILARITY: Contains 2 F5/8 type C domains.

SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.

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InterPro; IPR001117; Cu-oxidase.
InterPro; IPR000421; FA58_C.
Pfam; PF00394; Cu-oxidase; 3.
Pfam; PF00754; F5_F8_type_C; 2.
SMART; SM00231; FA58C; 2.
PROSITE; PS01285; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
PROSITE; PS01287; FA58C_3; 2.
PROSITE; PS00079; MULTICOPPER OXID
Blood coagulation; Glycoprotein; S
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COAGULATION FACTOR V.

COAGULATION FACTOR V.

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(BY SIMILARITY).

LIGHT CHAIN (BY SIMILARITY).

F5/8 TYPE A 1.

PLASTOCYANIN-LIKE 1.

PLASTOCYANIN-LIKE 2.

F5/8 TYPE A 2.

PLASTOCYANIN-LIKE 3.

PLASTOCYANIN-LIKE 4.
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41 X 9 AA APPROXIMATE TANDEM T-L-S-P-D-L-[GS]-[HQ]-T.
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MEDLINE-96/71523; PubMed-8598061;
Mahleithner J.A., Xu F., Brown K.M., Brown S.H., Golightly E.J.,
Halkier T., Kauppinen S., Pederson A., Schneider P.;
"The identification and characterization of four laccases from the
plant pathogenic fungus Rhizoctonia solani.";
Curr. Genet. 29:395-403(1996).
-!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
PRODUCTS (PROBABLE). THIS ISOZYME SHOWS OPTIMAL ACTIVITY AT PH 6.
-!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
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                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thanatephorus cucumeris (Black scurf of potato)
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetidae; Ceratobasidiales; Cerato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=R22
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CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPI
3 OR COUPLED BINUCLEAR (BY SIMILARITY).
SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: IN MYCELLA, AT A LOWER LEVEL THAN LCC4
SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
SIMILARITY: Contains 3 plastocyanin-like domains.
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                ; Z54275; -; NOT_ANNOTATED_CDS
S68117; S68117.
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an email to license@isb-sib.c
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97 (Rel. 35, Last annotation update)
97 (Rel. 35, Last annotation update)
precursor (EC 1.10.3.2) (Benzenediol:oxygen
oxidase) (Diphenol oxidase).
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PLASTOCYANIN-LIKE 3
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COPPER (TYPE 3) (B)
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Pred. No. 0.
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(AC. .) (POTENTIAL).
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STANDARD;

PRT;

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EMBL; Z54277; CAA91042.1; -.

PIR; S68120; S68120.

InterPro; IPR001117; Cu-oxidase.

InterPro; IPR002355; MultiCu_oxidse2.

Pfam; PF00394; Cu-oxidase; 3.

PROSITE; PS00079; MULTICOPPER_OXIDASE1;

PROSITE; PS00080; MULTICOPPER_OXIDASE2;
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Wahleithner J.A., Xu F., Brown K.M., Brown S.H., Golightly E.J.,
Halkier T., Kauppinen S., Pederson A., Schneider P.;
"The identification and characterization of four laccases from the
plant pathogenic fungus Rhizoctonia solani.";
Curr. Genet. 29:395-403(1996).
-i- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
PRODUCTS (PROBABLE). THIS ISOZYME SHOWS OPTIMAL ACTIVITY AT PH 7.
-i- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Heterobasidiomycetidae;
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PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
uctase; Signal; Copper; Metal-binding; Glycoprotein;
egradation; Multigene family; Polymorphism.
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(Rel. 35, Last sequence update)
(Rel. 38, Last annotation update)
recursor (EC 1.10.3.2) (Benzenediol:oxygen
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P12759; Q14285;
01-OCT-1989 (Rel. 1
01-FEB-1994 (Rel. 2
15-SEP-2003 (Rel. 4
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01-FEB-1994 (Rel. 28, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Coagulation factor V precursor (Activated F.F.
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Mammalia; Eutheria; Primates;
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                               M., Kaufman D.D., Toole J.J.,
M., Kaufman R.J., Mann K.G.;
CDNA and derived amino acid
1. Acad. Sci. U.S.A. 84:4846
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Pred. No. 0.08:
54; Mismatches
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P -> S.
H -> R.
                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata;
Catarrhini; Hominidae
  AND
                                       84:4846-4850(1987).
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  GLU-925
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  AND
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  ILE-1285
                                                                                                 R.A.,
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VARIANT MET-1764.

VARIANT MET-1764.

MEDLINE-95179146; PubMed=7874144;

MEDLINE-95179146; PubMed=7874144;

Bayeston T.A., Ireland H., Olds R.J., Theiler T. T., Theiler T.
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                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94217810; PubMed=8164741; Bertina R.M., Koeleman B.P.C., Koster T., Rosendaal F.R., Dirven R.J., de Ronde H., van der Velden P.A., Reitsma P.H.; "Mutation in blood coagulation factor V associated with resi activated protein C."; Nature 369:64-67(1994).
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Edgington T.
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VARIANT APCR GLY-334, AND VARIANT LYS-513
WEDLINE=98122763; PubMed=9454741;
Chan W.P., Lee C.K., Kwong Y.L., Lam C.K.
"A novel mutation of Arg306 of factor V g
                                                                                                                                                                                                                                                                           VARIANTS ILE-1285 AND MEDLINE=96351768; PubM Lunghi B., Iacoviello Pinotti M., Castaman G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94264012; PubMed
Pittman D.D., Tomkinson
Kaufman R.J.;
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                                                                                                                                                  "Detection of new polymorphic markers association with factor V levels in p. Thromb. Haemost. 75:45-48(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Crystal structures of the coagulation factor V.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20052169; PubMed=10586886; Macedo-Ribeiro S., Bode W., Huber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombin cleavage and activation and Biochemistry 33:6952-6959(1994).
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Bourenkov G.P.,
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3; PubMed=8713778;
viello L., Gemmati D
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S.-T., Pyati J.,
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kinson K.N., Mic
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Bartunik H.D., Stubbs
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C., Liang R.;
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G., Marchetti
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MEDLINE=99318093; Fubmeu-1007. Sklar P., Ardlie K., Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Daley
EMBL;
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Shaw N., La
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ILE-1820 AND GLY-2222, AND VARIANT
MEDLINE=99318093; PubMed=10391209;
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Blood 91:1140-1144(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98122764; PubMed=9454742;
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                                                                                                                                                                                                                     send
                                                                                                                                                                                                                                                                                                                            implantation.
- SIMILARITY: Contains 3
- SIMILARITY: Contains 2
- SIMILARITY: STRONG, TO
                                                                                                                                                                                                                                                                                                                                                                              PTM: Thrombin activates factor V proteolytically to the active cofactor, factor Va (formation of a heavy chain at the N-terminus and a light chain at the C-terminus).

PTM: SULFATION IS REQUIRED FOR EFFICIENT THROMBIN CLEAVAGE AND ACTIVATION AND FOR FULL PROCOAGULANT ACTIVITY.

DISEASE: Defects in F5 are the cause of Owren parahemophilia [MIM:227400], an hemorrhagic diastesis.

DISEASE: Defects in F5 are the cause of resistance to activate protein C (APCR) [MIM:188055], a form of thrombophilia. The AP mutation is found in about 5% of the population which suggest a slight thrombotic tendency may confer some advantage in feta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Factor Va is composed of a heavy chain and chain, noncovalently bound. The interaction between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: COAGULATION FACTOR V IS A COFACTOR THAT PARTICIPATES WITH FACTOR XA TO ACTIVATE PROTHROMBIN TO THROMBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is calcium-dependent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genet. 23:373-373(1999)
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                                                                                                                                                   L32757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes
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; AAB59401.1;
; AAB59401.1;
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                                                                                                                                                                                                                     license agreement (S license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single-nucleotide
                                                                                                                                                                                                                                                                                                                            s 3 F5/8 type A domains.
s 2 F5/8 type C domains.
TO COAGULATION FACTOR VIII.
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VAL-1749; MET-1764;
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Best Local :
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GO; GO:0003801; F:blood coagulation; Tag
GO; GO:0007596; P:blood coagulation; Tag
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR000421; FA58_C.

Pfam; PF00394; Cu-oxidase; 3.

Pfam; PF00754; F5 F8 type_C; 2.

SMART; SM00231; FA58C; 2.
                                      CUEO YERPE STANDARD; PRT; 533 AA. (98.2BK0; 98.2BK0; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 28-FEB-2003 (Rel. 41, Last annotation update) Blue copper oxidase cueO precursor (Copper ef CUEO OR YPO3499 OR Y0777.
                       Yersinia
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M16967;
M14335;
1CZS; 26:
1CZT; 26;
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1FV4; 17;
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; 26-NOV-99.
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; 17-JAN-01.
NC:3542; F5.
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19.7%;
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Gammaproteobacteria;
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Pred.
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Enterobacteriales;
                                                                   oxidase)
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THEFFE THE TWO DESCRIBED DOUGHOOF CONTROL OF CONTROL OF THE THEFFE THE TRANSPORT OF THE 
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J. Bacteriol. 184:4601-4611(2002).

-!- FUNCTION: Probably involved in periplasmic detoxification of copper by oxidizing Cu(I) to Cu(II) and thus preventing its into the cytoplasm. Possesses phenoloxidase and ferroxidase activities and might be involved in the production of polyphonogonals and the prevention of oxidative damage in the peri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                        TIGREAMS; TIGRO1409; TAT signal seq; 1. PROSITE; PS00080; MULTICOPPER OXIDASE2; Oxidoreductase; Copper; Metal-binding; F
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ414157; CAC92639.1; EMBL; AE013680; AAM84364.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21470413; PubMed=11586360; Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamilin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Versinia pestis, the causative agent of plague."
                                                                                                                                                                                                                                                                                                       Pfam; PF00394; Cu-oxidase;
                                                                                                                                                                                                                                                                                                                                                                              PIR; AC0414; AC0414.
InterPro; IPR001117; Cu-oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=KIM5 / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CO-92 / Biovar Orientalis
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NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                      nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (By similarity).

(By similarity).

(By similarity).

(COPACTOR: This protein belongs to the multicopper oxidases of the contain three distinct Cu centers known as type 1 or blue, contain three distinct Cu centers known as type 1 or blue, or normal, and type 3 or coupled binuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: The methionine-rich domain could provide binding exogenous copper ions. This methionine-rich region is probimportant for copper tolerance in bacteria.

SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 3 plastocyanin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or normal, and type 3 or coupled binuclear (By similarity) SUBUNIT: Monomer (Probable).
SUBCELLULAR LOCATION: Periplasmic. It is exported via the
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  (Probable).
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IPR006311; Tat.
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                                                                       BY SIMILARITY,
BLUE COPPER OXIDASE (
PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
                            MET-RICH
COPPER (1
  Sdal)
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(See http://www.isb-sib.ch/announce/
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                                                                                                                   Halkier T., Kauppinen S., Pederson A., Schneider "The identification and characterization of four plant pathogenic fungus Rhizoctonia solani."; Curr Genet 29:395-403(1996).
                                                                                                                                                                                                                       Eukaryota; Fungi; Basidiomycoca; nymenomyocco; Ceratobasidiaceae; Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiaceae;
                                                                                                                                                                                                                                      Thanatephorus cucumeris (Black scurf of potato)
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
                                                                                                                                                                                                                                                                                                                            LAC3
                                                                                                                                                         MEDLINE=96171523; PubMed=8598061; Wahleithner J.A., Xu F., Brown K.M.,
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                                                                                                                                                                                                                     Thanatephorus.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
Laccase 3 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Diphenol oxidase).
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COPACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISCOPACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISCOPPACTOR: BINDCLEAR (BY SIMILARITY).

3 OR COUPLED BINUCLEAR (BY SIMILARITY).

SUBUNIT: Homodimer (By similarity).

SUBCELLULAR LOCATION: Secreted.

TISSUE SPECIFICITY: IN MYCELLA, AT A LOWER LEVEL SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER SIMILARITY: Contains 3 plastocyanin-like domains.
                                                                                        FUNCTION: LIGNIN DEGRADATION AND DETOXIF PRODUCTS (PROBABLE).
CATALYTIC ACTIVITY: 4 benzenediol + O(2)
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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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OXIDOTEQUICLESE; Signal; Copper; Metal-binding. Clinin degradation.
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                                                                                                                                                           HIANGMYG-LILVEPKEGLPKV----DKEYYVMQGDFY-TKGK----YGEQGLQPFDMEK
                                                                                                                                                                                 RTTSIHWHGLLQHRNADDDGPAFVTQCPI-VPQASYTYTMPLGDQTGTYWYH---SHLSS
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                   KVEGEENHEIYSHKOTDAVYLPEGAPQAIDTQEAPKT---PAP-ANLQEQIKAGKATYDS
                                                                 EIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGIL
                                                                                        ----ATINGK-GREDPDNTPANPNTLYTLKVKRGKRYRLRVINS--SAIASE----
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PLASTOCYANIN-LIKE 1
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MEDLINE=95400292; PubMed=7670463;
Murakami Y., Naitou M., Hagiwara H., Sh
Sasanuma·S.-I., Sasanuma M., Tsuchiya Y
Yamazaki M., Tashiro H., Bki T.;
"Analysis of the nucleotide sequence of
Saccharomyces corevisiae.";
Nat. Genet. 10:261-268(1995).
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MEDLINE=98075360; PubMed=941343y;

Spizzo T. Byersdorfer C., Duesterhoeft S., Eide D.;

Spizzo T. Byersdorfer C. Duesterhoeft S., Eide D.;

"The yeast FET5 gene encodes a FET3-related multicopper oxid implicated in iron transport.";

Mol. Gene. Genet. 256:547-556(1997).

-!- FUNCTION: IRON TRANSPORT MULTICOPPER OXIDASE, WHICH IS !

-!- FUNCTION: IRON HIGH AFFINITY UPTAKE. MAY BE REQUIRED ON TRANSPORT MULTICOPPER OXIDASE.
                                            Glycoprotein;
Copper; Repeat
SIGNAL
CHAIN
DOMAIN
TRANSMEM
57
DOMAIN
59
                                                                                                                                                                                                                                 EMBL; D50617; BAA09199.1; -.
PIR, S56214; S56214.
HSSP; P37064; IASQ.
SGD; S001853; FETTS.
GO; GO:0004322; F:multicopper ferroxidase iron transport medi.
GO; GO:0006826; P:iron ion transport; IMP.
InterPro; IPR001317; Cu-oxidase.
InterPro; IPR001355; MultiCu_oxidse2.
                                                                                                                                                   InterPro; irnvector, providase; 3.

Pfam; PF00394; Cu-oxidase; 3.

PROSITE; PS00079; MULTICOPPER OXIDASE; 1.

PROSITE; PS00080; MULTICOPPER OXIDASE; 1.

PROSITE; PS00080; MULTICOPPER OXIDASE; 1.

Transport;
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by non-profit institutions as for 
modified and this statement is not removed. 
entitles requires a license agreement (See 
or send an email to license@isb-sib.ch).
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28-FEB-2003
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., Eki T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5341;
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SIGNAL
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PROSITE; PS00080; MULTICOPPER_OXIDASE2;
Oxidoreductase; Signal; Copper; Metal-b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2.
Pfam; PF00394; Cu-oxidase; 3.
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CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2
3 OR COUPLED BINUCLEAR (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted.
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FUNCTION: LIGNIN DEGRADATION AND D
PRODUCTS (PROBABLE)
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larity 26.6%;
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PLASTOCYANIN-LIKE 2
PLASTOCYANIN-LIKE 3
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COPPER
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Pred. No. 0.91;
28; Mismatches
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943DB3F23297B891
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_PARDE
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SIGNAL
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"Sequence and expression of the gene encoding the respiratory
nitrous-oxide reductase from Paracoccus denitrificans. New and
conserved structural and regulatory motifs.";
Eur. J. Biochem. 218:49-57(1993).
I FUNCTION: NITROUS-OXIDE REDUCTASE IS PART OF A BACTERIAL
RESPIRATORY SYSTEM WHICH IS ACTIVATED UNDER ANAEROBIC
CONDITIONS IN THE PRESENCE OF NITRATE OR NITROUS OXIDE.
                                                                                      METAL
SEQUENCE
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a cheveen the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and to
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
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28-FEB-2003
                                                                                                                                                                                                                                                               or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=NL1B8944;
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COPACTOR: COPPER (BY SIMILARITY).

SUBUNIT: HOMODIMER; EACH SUBUNIT CO
CENTERS A AND Z. Z IS THOUGHT TO BE
REDICTION (BY SIMILARITY).

SUBCELLULAR LOCATION: Periplasmic.
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                                                       Similarity
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an email to license@isb-sib.ch).
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Last annotation
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rerminal section,
                                             18;
                       DRDHPAKVVVKMETVEKVMRLADGVEYQFWTFGGQVPGQMIR
                                            Score 116; DB
Pred. No. 1.2;
L8; Mismatches
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01-DEC-1992
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01-NOV-1997
                                                                     CARBOHYD
SEQUENCE
                                                                                                                                                                                                     Signal;
SIGNAL
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                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              van Herpen M., Schrauwen J., Wullems G.;
"Characterization of a pollen-specific cDNA clone fr
tabacum expressed during microgametogenesis and germ
plant Mol. Biol. 18:1101-1111(1992).
-i- FUNCTION: PRECISE FUNCTION UNKNOWN BUT PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Petit Havana SR1; TISSUE=Pollen; MEDLINE=92283302; PubMed=1600146; Weterings K., Reijnen W., van Aarseen R., K van Herpen M., Schrauwen J., Wullems G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotiana tabacum (Common tobacco),
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence updated)
01-NOV-1997 (Rel. 35, Last annotation upd
Pollen-specific protein NTP303 precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4097;
                                                                                                                                                                                                                                        nterPro;
                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ROLE DURING GERMINATION AND/OR TUBE SUBCELLULAR LOCATION: Extracellular TISSUE SPECIFICITY: POLLEN.
                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 3
                                                                                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE:
ARE EXPRESSED DURING
                                                                                                                                                                                                                                                                                                                                                                                              INDUCTION: EXPRESSION REGULATED BY THE HAPLOID GAMETOPHYTE ITSELF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
                       91;
                                  Similarity
                                                                                                                                                                                                                Germination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTSTFSFKALQPGLYVYHCAVAPVGMHIANGMYGLILVEPKE
GVEYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTSSVTFVAANPGVYWYYCQWFCHALHME--MRGRMLVEPKE
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                                                                                                                                                                                                                                     IPR001117; Cu-oxidase.
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                       Conservative
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332
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                                                                      62033 MW;
                                  4.2%;
20.8%;
                                                                                                                                                                                                                Glycoprotein;
                      43;
                                                                                                                                                                                                                                                                                                                                                                                  plastocyanin-like domains.
                     Score 111.5;
Pred. No. 2;
i3; Mismatches
                                                                                N-LINKED
                                                                                                       N-LINKED
                                                                                                                              N-LINKED
                                                                                                                                                      PLASTOCYANIN-LIKE 2. PLASTOCYANIN-LIKE 3.
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                                                                                                                                                                                         POLLEN-SPECIFIC PROTEIN NTP303
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Q99056;
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                 "Cloning and characterization of three laccase genes from the white-rot basidiomycete Trametes villosa: genomic organization
                                                                                                                                                                                                                                                                                           MEDLINE=97128774; PubM
Yaver D.S., Golightly
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Basidiom
Aphyllophorales; Trametes.
                                                                                                                                                                                                                                          Gene
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                                                                                                                                                                                                                                                                                                                                                                                   Trametes villosa (White-rot
                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Laccase 5 precursor (EC 1.10.3.2) (Benzenediol:oxygen
                                                                                                                                                                                                                EVISIONS.
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lene 181:95-102(1996).
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                                          SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER
SIMILARITY: Contains 3 plastocyanin-like domains.
                                                                                               COFACTOR: BINDS 4 CU-IONS PER MOLECULE. CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
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S., Golightly E.J.;
and characterization of
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SIGNAL 1 23 POTENTIAL.
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HSSP; P37064; 1AOZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (so or send an email to license@isb-sib.ch).
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InterPro; IPR002355; MultiCu_oxidse2
Pfam; PF00394; Cu-oxidase; 3.
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                                                                              TAAKLG-----PAFPAGPDSVLING-LGRFSGD---
                                                                                                TKGKYGEQGLQPFDMEKAIREDAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNL
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                                                                                                                                                                                                  PVTDLTISNADVTP-
                                                                                                                                                                                                                    PVIDAIVTHAPEVPPPVDRDHPAKVVVKMETVEKVMRLADGVEYQFWTFGGQVPGQMIRV
                    TEFKVDVPGDYVL-----VDHAIFRAF-NKGAL-
                                        TVITVTQGKRYRFRLVSISCDPNFTFSIDGHNMTIIEVDGVNHEALDVDSIQIFAGQRY-
                                                                                                                     FTVPDQAGTFWYH--
                                                                                                                                        FKAL-QPGLYVYHCAVAPVGMHIANGMYGLILV----EPKEGLPKVDKEYYVMQ-GDFY-
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                                                          ------SSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGGAAI
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COPPER (TYPE 1) (B)
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Pred. No. 2.1;
63; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Johnson P.E., Joshi M.D., Tomme P., Kilburn D.G., McIntosh L.P.;

"structure of the N-terminal cellulose-binding domain of Cellulomonas
fimi CenC determined by nuclear magnetic resonance spectroscopy.";

Biochemistry 35:14381-14394(1996).

-i- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:

(1) ENDOGLUCANASES WHICH CUT INTERNAL BETA-1, 4-GLUCOSIDIC BONDS;

(2) EXOCELLOBIOHYDROLASES THAT CUT THE DISSACCHARIDE CELLOBIOSE
FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;

(3) BETA-1, 4-GLUCOSIDASES WHICH HYDROLYZE THE CELLOBIOSE AND OTHER

(3) BETA-1, 4-GLUCOSIDASES WHICH HYDROLYZE THE CELLOBIOSE AND OTHER

(3) SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
                                                                                                                                                                                                                                                                                                                   Protein
[5]
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MEDLINE=90103465; PubMed=2604391;
Moser B., Gilkes N.R., Kilburn D.G., Warren R.A.J.,
"Purification and characterization of endoglucanase fimi, cloning of the gene, and analysis of in vivo t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coutinho J.B., Moser B., Kilburn D.G., War "Nucleotide sequence of the endoglucanase Cellulomonas fimi, its high-level expressi characterization of its products."; Mol. Microbiol. 5:1221-1233(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endoglucanase (Cellulase C)
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                                                                                                                                                                                                                                                                                                                                          MEDLINE=97035265; PubMed=8880921;
Bateman A., Eddy S.R., Chothia C.;
"Members of the immunoglobulin superfamily
Protein Sci. 5:1939-1942(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The binding of Cellulomonas fimi and Sephadex is mediated by the N-Mol. Microbiol. 6:1243-1252(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coutinho J.B., G
Miller R.C. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92065819; Pul
Coutinho J.B., Moser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
STRAIN=ATCC 484;
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Micrococcineae; Cellulomor
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annotation update)
(EC 3.2.1.4) (Endo-1,4-beta-glucanase
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N-terminal repeats
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lucanase C of Cellulomonas
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Matches .

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Query Match
Best Local
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PDB; 10W; V1-AxP-97.

PDB; 1CX1; 03-APR-00.

PDB; 1GU3; 26-SEP-02.

InterPro; IPR003305; CBM_CenC.

InterPro; IPR003105; Glyco_hydro_9.

InterPro; IPR004197; Glyco_hydro_91g.

InterPro; IPR003199; Ig.

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InterPro; IPR003006; Ig_MHC.

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                                                                                                                                                                                                                                                                                                                                  Cellulose degradation;
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Similarity
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immunoglobulin-like domains.
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CELLULOSE-BINDING 1
CELLULOSE-BINDING 2
CATALYTIC.
IG-LIKE 1.
IG-LIKE 2.
BY SIMILARITY.
BY SIMILARITY.
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         SEQUENCE FROM N.A.

STRAIN-TLS / ATCC 49652 / DSM 12025;

XX MEDLINE-22103685; PubMed=12093901;

XX Elsen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

XX Elsen J.A., Nelson K.E., Paulsen I.T., Nelson W.C., Haft D.H.,

XX Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,

XX Hicky E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

XX Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,

XX Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

XX Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,

XX Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

XX Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

XX Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

XX Proc. Natl. Acad. Sci. U.S.A. 99:509-5514 (2002).

--- FUNCTION: This basic c-type monoheme cytochrome has been found

C. exclusively in the green photosynthetic bacteria, although its
                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 4
28-FEB-2003 (Rel. 4
28-FEB-2003 (Rel. 4
Cytochrome c-555 pr
                                                                                                                                                                                                                                                                                                                                                                                C555 CHLTE
Q8KG93;
28-FEB-2003
                                                                                                                                                                                                                                                                                                                       Cytochrome CT0075.
                                                                                                                                                                                                                                                        NCBI_TaxID=1097;
                                                                                                                                                                                                                                                                           Chlorobium.
                                                                                                                                                                                                                                                                                      Bacteria;
                                                                                                                                                                                                                                                                                                         Chlorobium
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in bacterial
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Chlorobi;
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                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                   precursor
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41,
                                                                                                                                                                                                                                                                                         Chlorobia; Chlorobiales;
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 photosynthesis
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                                                                                                                                                                                                                                                                                                                                     annotation (C555).
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                            has been found
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Query Match
Best Local S
Matches 27
                                                                                                                                                                                                                                                                               CERU MOUSE
Q61147;
Q611-NOV-1997
01-NOV-1997
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                       MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. use by non-profit institutions as l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE012787; AAM71323.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                          MEDLINE=96294736; PubMed=8690795; Klomp L.W.J., Farhangrazi Z.S., Dugan L.L., C "Ceruloplasmin gene expression in the murine J. Clin. Invest. 98:207-215(1996).
                                                                                                                                                               SEQUENCE FROM N.A. Klomp L.W.J., Farhangrazi Z Klomp L.W.J., Farhangrazi Z Submitted (MAR-1996) to the
                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                         -
                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                     Ceruloplasmin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
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InterPro; IPR002323; Cyt_CIE.
InterPro; IPR000345; CytC_heme_
                                                                                                                                          SSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with
FUNCTION: CERULOPLASMIN IS A BLUE, COPPER-BINDING (6-7 ATOMS PER MOLECULE) GLYCOPROTEIN FOUND IN PLASMA. FOUR POSSIBLE FUNCTIONS ARE FERROXIDASE ACTIVITY, ANIN COUPER TRANSPORT AND HOMEOSTASIS, AND SUPEROXIDE DISMUTASE ACTIVITY. COPPER TRANSPORT CATALYTIC ACTIVITY: 4 Fe(2+) + 4 H(+) + 0(2) = 4 Fe(3+) + 2 H(2)0. COPACTOR: BINDS 6 CU-IONS PER MOLECULE. THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES: WHICH CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unusually low redox potential compared with mitochondrial cytochrome c. It is reactive with cytochrome c oxidases b
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S; PR00607; CYTCHROMECIE
TE; PS00190; CYTOCHROME_C
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(Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
(Rel. 42, Ecc 1.16.3.1) (Ferroxidase).
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82
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108
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82
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2 BY SIMILARITY.
108 CYTOCHOME C-555.
36 HEME (COVALENT) (BY SIMILARITY).
39 HEME (COVALENT) (BY SIMILARITY).
40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
82 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
10892 MW; 9711CBOA43B8825C CRC64;
                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is not removed.
                                                                                                                                                                .S., Choi D.W., Gitlin J.D.;
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 109;
Pred. No. 0.
                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                  Gitlin
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MGD; MGI:84476; Cp.
InterPro; IPR0011117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2.
Iffam; PF00394; Cu-oxidase; 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; 3.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
Oxidoreductase; Copper; Metal-binding; Gl)
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or send an email to license@isb-sib.ch).
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TISSUE SPECIFICITY: MANY TISSUES, INCLUDING SIMILARITY: Contains 3 F5/8 type A domains.
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                                                                                                     163
                                                                                                                                        449
                                                                                                                                                                           114
                                                                                                                                                                                                             95;
                                                                                                                                                                                                                          Similarity
DVDKEFYLFPTVFDENESLLLDDNIRMFTHAPDQVDKEDEDFQESNKMHSMNGFMYGNQS
                                  KVDKEYYVM-----
                                                                     TFTYEWTVPKEMGPTYADPVCLSKMYYSAVDPT-KDIFTGLIGPMKICKKGSLLADGRQK
                                                                                                                                      GPVIWAEVGDTIKVTFHNKGQHHLSIQPMGVSFTAENEGTYYGPPGASSQQAASHVAPKX
                                                                                                                                                                         GQMIRVREGDTIEVQFSN---HPDSKMPHNVDFHAAT-----GPGGGAE---
                                                                                                                                                                                                                                                                               1036
1037
1041
1046
138
226
583
625
757
757
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1035
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          PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.

PROSITE; PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
Lignin degradation; Multigene family.
SIGNAL 1 23 POTENTIAL.
                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97464057; PubMed=9322748;
Ong E., Pollock W.B., Smith M.;
"Cloning and sequence analysis of two laccase complementary
the ligninolytic basidiomycete Trametes versicolor.";
Gene 196:113-119(1997).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Laccase 5 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Diphenol oxidase) (Laccase IV).
                                                                                                                            InterPro; IPRO01117; Cu-oxidase.
InterPro; IPRO02355; MultiCu_oxidse2.
Pfam; PF00394; Cu-oxidase; 3.
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
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COPACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTICOPACTOR: BINDS 4 TYPE 1 OR BLUE, TYPE 2 OR NORMAL,
3 OR COUPLED BINUCLEAR (BY SIMILARITY).

3 OR COUPLED BINUCLEAR (BY SIMILARITY).

SUBCELLULAR LOCATION: Secreted.

SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER O:
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CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 ber
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PLASTOCYANIN-LIKE 2
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Laccase II precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Diphenol oxidase).
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J. Gen. Microbiol. 139:1209-1218(1993)
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Agaricales; Agario
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InterPro; IPR002355;

    -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES
    -!- SIMILARITY: Contains 3 plastocyanin-like domains.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of two laccase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perry C.R., Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93367392;
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CATALYTIC ACTIVITY: 4 benzenediol + O(2)
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CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2
3 OR COUPLED BINUCLEAR (BY SIMILARITY).
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M., Britnell C.H.,
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                                             AND PARTIAL SEQUENCE
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MultiCu_oxidse2.
 4.1%;
20.5%;
                                                                                                                                                                                                                                                                                        Multigene
                                  MW;
                                                                                                   LACCASE II.
PLASTOCYANIN-LIKE 2
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                                   CRC64;
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                                                            modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                         Patent number EP0462721, 27-DEC-1991.
-!- FUNCTION: ENDOTOXIN WITH NEMATICIDAL ACTIVITY.
-!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PROPRULATION AND IS ACCUMULATED BOTH AS AN INCL
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.,
STRAIN=NRRL B-18244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales;
                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                              N-TERMINUS.
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                          genes encoding
                                                                                                                                                                                                                                                                                                                                            "Novel Bacillus thuringiensis microbes active against genes encoding novel nematode-active toxins cloned fro
                                                                                                                                                                                                                                                                                                                                                                              Sick A
                                                                                                                                                                                                                                                                                                                                                                                           Narva K.E., Payne J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRY12AA OR CRYXIIA(A) OR CRYVB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CryXIIA(a))
                            EMBL; L07027;
                                                                                                                                                                                                                              -!- MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                           thuringi.";
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                InterPro;
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                                                                                                               non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
crystal protein cry12Aa (Insecticidal delta-endotoxin
(Crystaline entomocidal protoxin) (142 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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endotoxin_N
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                                                                                                                                                                                              THE DELTA ENDOTOXIN FAMILY.
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                                                                                              Usage
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L outstation -
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RESULT 39
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Best Local
                                                                                                                    FLNA
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Pfam;
Toxin;
SEQUENCE FROM N.A., AND PARTIAL S: MEDLINE=90361737; PubMed=2391361; Gorlin J.B., Yamin R., Egan S., S. Kwiatkowski D.J., Hartwig J.H.;
                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                        01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Filamin A (Alpha-filamin) (Filamin 1) (Endothelial actin-binding
                                                                                                                                                                                                                        NAMUH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Toxin; Sporulation. SEQUENCE 1257 AA;
                                                                NCBI_TaxID=9606;
                                                                                                        Homo
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                                                                                                     sapiens (Human)
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PF03945;
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                                                                                                                                (ABP-280)
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                                                                                                                                                                                                                                                                                                                                                                                                   EAPKTPAPANLQEQIKAGKATYDSNCAACHQPDGKGVPNAFPPL-ANSDYLNADHARAAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRDFINVYTLISTPTINELSTEKIKGFP-AEKGYIKNQGIMKYYGKPEY-INGAQPVNLE
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                                                                                                                                                                                                                                                                        FASSAODTLASNVS
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                                                                                                                    OR FLN
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endotoxin_N;
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----IREDAEYVV-----FNGSVGALTGENA----
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                                                                                                                                (Nonmuscle
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                                                                             Chordata;
Primates;
                                      AND PARTIAL SEQUENCE
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19.2%;
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Pred. No. 11
                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                           PRT;
                                                                                                                                filamin)
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             Stewart M.,
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              Stossel T.P.
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MEDLINE=21423782; PubMed=11532987;
Sheen V.L., Dixon P.H., Fox J.W., Hong S.E., Kinton L., Sisodiy Sheen V.L., Dixon P.H., Fox J.W., Hong S.E., Kinton L., Sisodiy Duncan J.S., Dubeau F., Scheffer I.E., Schachter S.C., Wilner Allenchy R., Crino P., KamuroʻK., DiMario F., Berg M., Kuzniecky Cole A.J., Bromfield E., Biber M., Schomer D., Wheless J., Silv Mochida G.H., Berkovic S.F., Andermann F., Andermann E., Dobyns Wood N.W., Walsh C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         van der Flier A., Sonnenberg A.;
"Structural and functional aspects of filamins.";
Biochim. Biophys. Acta 1538:99-117(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                   "Mutations in the X-linked filamin 1 gene cause periv nodular heterotopia in males as well as in females."; Hum. Mol. Genet. 10:1775-1783(2001).
-i- FUNCTION: Promotes orthogonal branching of actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stossel T.P., Condeelis J., Schleicher M., Shapiro S.S. "Filamins as integrators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Human endothelial actin-binding protein (ABP-280, nonmuscle filamin): a molecular leaf spring.";
J. Cell Biol. 111:1089-1105(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mapping of two genes encoding isoforms of the actin binding protein ABP-280, a dystrophin like protein, to Xq28 and to chromosome 7."; Hum. Mol. Genet. 2:761-766(1993).
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Repetto M., Villa A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Long-range sequence analysis in Xq28: candidate genes in 219.4 kb of high GC
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                                                                                                                                                                                                                                                                                                 links actin filaments to membrane glycoproteins. Anchors variransmembrane proteins to the actin cytoskeleton and serves scaffold for a wide range of cytoplasmic signaling proteins. SUBUNIT: Homodimer. Interacts with cvHsp. Interacts with varocher binding partners in addition to filamentous actin. SUBCELLULAR LOCATION: PERIPHERAL CYTOPLASM.
                          surface. In heterozygous females these neurons presumably represent those cells that, after X-chromosome inactivation, contain the active X chromosome with the filamin mutation. Most hemizygous affected males die early during embryogenesis, whereas heterozygous females have normal intelligence but suffer from seizures and various manifestations outside the central nervous system, especially related to the vascular system. This implies that essential embryonic cell migration can only occur in FLNA-
                                                                                                                                                                PTM: The N-terminus is blocked.

DISEASE: Defects in FLNA are the cause of periventricular heterotopia (PH) also called nodular heterotopia, bilateral periventricular (NHBP or BPNH). PH is an X-linked developmental dominant disorder in which many neurons fail to migrate into the cerebral cortex. They remain as nodules lining the ventricular
                                                                                                                                                                                                                                                                                     PTM: PHOSPHORYLATION EXTENT CHANGES IN RESPONSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rev. Mol. Cell Biol. 2:138-145(2001).
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Y., Zollo M., Mazzarella R.A., Cic
Heiner C., Burough F.W., Ripetto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PH PHE-656 AND THR-1764
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deelis J., Cooley
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ACTIN-BINDING DOMAIN IS
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tto M., Schlessinger
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EMBL; L44110; AAA92644.1; -.
EMBL; X70082; CAA49687.1; -.
EMBL; X70085; CAA49690.1; -.
EMBL; X70085; CAA49690.1; -.
PIR; A37098; A37098.
HSSP; P13466; 1KSR.
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SMART; SM00557; IG FLMN; 24.
PROSITE; PS00019; ĀCTININ 1;
PROSITE; PS00020; ACTININ 2;
PROSITE; PS50021; CH; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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Actin-binding; Phosphorylation; Repeat;
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Pfam; PF00630; Filamin; 24.
VARIANT
                              VARIANT
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InterPro; IPR001715; Calponin-like.
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GO:0003780; F:actin cross-linking activity; TAS.
GO:0007012; P:actin cytoskeleton reorganization; TAS.
GO:0007399; P:neurogenesis; TAS.
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SIMILARITY: Contains 2 calponin-homology (CH) domains.
SIMILARITY: Contains 24 filamin repeats.
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1951
2042
2132
2233
2327
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FILAMIN 16.
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FILAMIN 21.
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FILAMIN 2.
FILAMIN 3.
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FILAMIN 14.
FILAMIN 15.
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FILAMIN
FILAMIN
                             SELF-ASSOCIATION SITE, TAIL. CLEAVAGE (BY CALPAIN).
V -> A (IN dbSNP:1064816).
                                                                                FILAMIN 24
             FTId=VAR
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                  01283
 dbSNP:1064817)
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Best Local Similarity
Matches 115; Conserv
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Q53047;
30-MAY-2000
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CONFLICT
SEQUENCE
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=783;
[1]
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                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                 antigen)
                                                                                                                                                 Outer membrane
                                                                 Rickettsia rickettsii.
                                                                                                                dwo<sub>z</sub>)
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                                                                                                 2001 (Rel. 40, Last annotation update)
mbrane protein B precursor (168 kDa surface-layer protein)
protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
[Contains: 120 kDa surface-exposed protein (Surface protein (120 kDa outer membrane protein ompB); 32 kDa beta peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYVTEID---QDKYAVRFIP-----RENGVYLIDVKFNGT--HIPG-SPFKIRVGEP
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                                                                                                                                                                                                                                                                                                                     HIPGSPYRVVVP 2647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKTPAPANLQEQIKAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVKMDCQECPEGYRVTYTPMAPGSYLISIKYGGPYHIGGSPFKA------KVTGPRL
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/FTId=VAR 012833.
L -> F (IN PH).
/FTId=VAR 01267.
A -> "
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A -> T (IN PH).
/FTId=VAR 012835.
A -> G (IN REF. 3).
H -> D (IN REF. 2).
MW; 6C1A07041DFA3D42 CRC64;
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Best Local Similarity
Matches 128; Conserv
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - MOI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X16353; CAA34403.1; -. PIR; S18227; S18227.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license
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TIGRFAMs; TIGR01414; autotrans_bar1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning, expression and sequence analysis of the gene encoding 120 kD surface-exposed protein of Rickettsia rickettsii."; Mol. Microbiol. 3:1579-1586(1989).
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SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVEREI
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QTTLI----PAGGAAITEFKVDVPGDYYLVDHAIFRAFNKGALGILKVEGE---ENHEIY 359
                                                                                                                    VGETVRLFVGNGGPN----
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                                                                                                                                                                                                                                                      --GAPA-----STLVFNLANP-----TTQKAPLILGDNAVIANGVNGTLNV-----
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                                                                 AGGTTINFTGTDGTGRLVLLSKHAAATNFNITGSLGGNLKGVIEFNTVAVDGQLTANAGA 317
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ative 65; Mismatches 228;
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32 kDa BETA PEPTIDE.
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                                                                                                                    -LTSSFHVIGEI--
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망	318 ANAVIGTNNGAGRAAGFVVSVDNGKVATIDGQVYAKDMVIQ 358
Qy	360 SHKQTDAVYLPEGAPQAIDTQEAPKTPAP396
8	359 SANATGOVNERHIVDVGADGTTAFKTAASKVTITQDSNEGNTDEGNLAAQIKVPNAITLT 418
Qy	397AGKATYDSNCAACHQPDGKGVPNAFPPLANSDYLNADHARAASIV 441
Вb	419 GNFTGDASNPGNTAGVITFDANGTLESASADANVAVTNNITAIEASGAGVVQLSGTHAAE 478
Qy	442 -ANGLSGKITVNGNQYESVMPAIALSDQQIANVITYTLNSFGNKGGQLSAD 491
DЬ	479 LRLGNAGSIFKLADGTVINGKVNQTALVGGALAAGTITLDGSATIT-GDIGNAGGAAALQ 537
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Db	538 RITLANDAKKT 548

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YOS1 SCHPO
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RPAZ THEVO
FUSI YEAGT
FRAL HUMAN
AROF ARATH
YAGB SCHPO
SYE METKA
YAGM RHISN
SYE METKA
SYE ARTICU
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InterPro; IPR001117; Cu-oxidase.
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                                                                      This SWISS-PROT entry is copyright. It is produced through a centre of the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                        MEDLINE=93014188; PubMed=1398981;
Hoehn G.T., Clark V.L.;
"The major anaerobically induced outer membrane
gonorrhoeae, Pan 1, is a lipoprotein.";
Infect. Immun. 60:4704-4708(1992).
-!- SUBCELLULAR LOCATION: Attached to the outer
                                                                                                                                                                                                                                                                 MEDLINE=93014187; PubMed=1383156; Hoehn G.T., Clark V.L.; "Isolation and nucleotide sequence major anaerobically induced outer m gonorrhoeae.";
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Biochem. J. 295:587-593(1993).

Biochem. J. 295:587-593(1993).

Biochem. J. 295:587-593(1993).

Biochem. J. 295:587-593(1993).

I COPACTOR: CONTAINS ONE ATOM OF TYPE I COPPER AND ONE ATOM OF TY II COPPER; FAD. TYPE 1 COPPER IS BOUND WITHIN A SINGLE MONOMER, WHILE TYPE 2 COPPER IS HELD BY RESIDUES FROM EACH OF TWO MONOME OF THE TRAMER. NITRITE IS BOUND TO THE TYPE 2 COPPER SITE.

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Abraham Z.H.L., Lowe D.J., Smith B.E.;
Purification and characterization of the dissimilatory nitrite
reductase from Alcaligenes xylosoxidans subsp. xylosoxidans
(N.C.I.M.B. 11015): evidence for the presence of both type 1 and
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              OF NITRITE.
SIMILARITY: Contains
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; 1NDS; 07-JUL-97.
                                                                                          PATHWAY: Nitrate assimilation (denitrification). SUBUNIT: Homotrimer.
SUBCELLULAR MOCATION: Periplasmic (By similarity DOMAIN: THE TYPE I COPPER SITE IN NIR PLAYS A CRELECTRON TRANSFER FROM PSEUDDAZURIN TO THE TYPE NIR, WHICH COMPRISES THE CATALYTIC CENTER OF NIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 YHCAVAPVGMHIANGMYGLILVEPKEGLPKVDKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Outer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR00695; CUNO2RDTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YHCAVAPVGMHIANGMYGLILVEPKEGLPKVDKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hasnain S.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 41, Crea
(Rel. 41, Last
(Rel. 42, Last
aining nitrite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    blue-copper nitrite
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387
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377
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100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53:406-418(1997).
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Cu-oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence up
Last annotation
rite reductase (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Abraham Z.H.L., Eauy ...
                                                    2 plastocyanin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X.
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N-ACYL DIGLYCERIDE (PR
PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
4 X 5 AA TANDEM REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB; Pred. No. 5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A4707CC87B923C97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA TANDEM REPEATS OF A-A-S-A-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on update)
(EC 1.7.2.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330
                                                                                          y similarity).
R PLAYS A CRUCIAL ROLE
TO THE TYPE II COPPER (
ENTER OF NIR FOR THE RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eady R.R., Smith B.E.;
uctase and its substrat
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                                                        domains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Cu-NIR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    substrate-bound
                                                                                                                                                                                                                                  SITE.
THE CU-NIR IN
                                                                                                                                                                                                                                                                         TWO MONOMERS
                                                                                                                                ROLE
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                                                                                                REDUCTION
                                                                                                                SITE
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RESULT 3
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Best Local S
Matches 12
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01-FEB-1995
01-FEB-1995
15-SEP-2003
EMBL;
                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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METAL
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                        functional in a mutationally cytochrome of Pseudomonas stutzeri.";
                                                                                                                                                                                                                                                                                                                                                          Glockner A.B., Juengst A., Zumft W.G.;
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93356602; PubMed=8352648
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas chlororaphis (Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copper-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nitrate assimilation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase; Copper; Metal-binding; Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                'Copper-containing nitrite reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                      PATHWAY: Nitrate assimilation (denitrification).
SUBUNIT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Periplasmic.
DOMAIN: THE TYPE I COPPER SITE IN NIR PLAYS A CRUCIAL ROLE FOR ELECTRON TRANSFER FROM PSEUDOAZURIN TO THE TYPE II COPPER SITE OF NIR, WHICH COMPRISES THE CATALYTIC CENTER OF NIR FOR THE
                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Nitric oxide + H(2)O + ferricytochrome c = nitrite + ferrocytochrome c.

COFACTOR: CONTAINS ONE ATOM OF TYPE I COPPER AND ONE ATOM OF TYPE II COPPER; FAD. TYPE I COPPER IS BOUND WITHIN A SINGLE MONOMER, WHILE TYPE 2 COPPER IS HELD BY RESIDUES FROM EACH OF TWO MONOMERS OF THE TRIMER. NITRITE IS BOUND TO THE TYPE 2 COPPER SITE.

PSEUDOAZURIN IS THE PHYSIOLOGICAL ELECTRON DONOR FOR THE CU-NIR IN
                                                                                                                    SIMILARITY: Contains
                                                                                                                              REDUCTION OF NITRITE.
                                                                                                                                                                                                                  VITRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSECL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 MPHNVDFHAATG 148
                                                                                                                                                                                                                                                                                                               Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00394; Cu-oxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00695;
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330
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(Rel. 31, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                  13985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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90
125
126
135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                           160:18-26(1993).
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330
90
125
125
135
140
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                                                                                                                                                                                                                                                                                                                                                                                                AND SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat; Periplasmic; 3D-structure.
5 PLASTOCYANIN-LIKE 1.
0 PLASTOCYANIN-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.4%;
                                                                                                                 2 plastocyanin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 12;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E2C38C3A2CEBFCE8 CRC64;
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(TYPE
(TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EC 1.7.2.1) (Cu-NIR)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 330;
                                                                                                                                                                                                                                                                                                                                    background
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                         a collaboration
                                                                                                                                                                                                                                                                                                                                    (Nirs-)
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                                  .ch/announce/
                                                                               outstation
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R_RHIHE
                                                                                                                                        Physical Phizobium 'hedysari ... 62:4017-32-18

Appl. Environ. Microbiol. 62:4017-32-18

Appl. Environ. Microbiol. 62:4017-32-18

Appl. Environ. Microbiol. 62:4017-32-18

-i- CATALYTIC ACTIVITY: Nitric oxide + H(2)O + 122-18

-i- CATALYTIC ACTIVITY: Nitric oxide + H(2)O + 122-18

-i- CATALYTIC ACTIVITY: Nitric oxide + H(2)O + 122-18

-i- CATALYTIC ACTIVITY: NITRIC OXIDER AND ONE ATOM OF TYI

-i- COPPER; FAD. TYPE 1 COPPER IS BOUND TO THE TYPE 2 COPPER SITE.

-- TYPE 1 SOUND TO THE TYPE 2 COPPER SITE.

-- TYPE 1 SOUND TO THE TYPE 2 COPPER SITE.
                                                                                                                                                                                                                                                                                                                                                                                                              Q60214;
Q60214;
Q60214;
Q1-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
DOMAIN
DOMAIN
METAL
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                                                                                                                                                                                                                                                   "Characterization of the gene encoding nitrite reductase and the physiological consequences of its expression in the nondenitrifying Rhizobium 'hedygari', strain HCNT1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PFU039%; CUNO2RDTASE.
PRINTS; PR00695; CUNO2RDTASE.
Oxidoreductase; Copper; Metal-binding; Flav
                                                                                                                                                                                                                                                                                                     MEDLINE=97055705; PubMed=8899992; Toffanin A., Wu Q., Maskus M., Ca
                                                                                                                                                                                                                                                                                           Shapleigh J.P.;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=50338;
                                                                                                                                                                                                                                                                                                                                                                                Rhizobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIR RHIHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001287; CuNO2_reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium hedysari.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S32112; S32112.
                                                     PATHWAY: Nitrate assimilation (denitrification).
SUBUNIT: Homotrimer (By similarity).
SUBCELULIAR LOCATION: Periplasmic (By similarity).
DOMAIN: THE TYPE I COPPER SITE IN NIR PLAYS A CRUCIAL ROLE FOR ELECTRON TRANSFER FROM PSEUDOAZURIN TO THE TYPE II COPPER SITE OF NIR, WHICH COMPRISES THE CATALYTIC CENTER OF NIR FOR THE REDUCTION OF NITRITE.
                                            SIMILARITY: Contains 2 plastocyanin-like domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 MPHNVDFHAATG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P38501; 1AS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MPHNVDFHAATG
                                                                                                                                                                                                                                                                                                                                                                              Proteobacteria; Alphaproteobacteria; Rhizobiales; 
eae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363
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194
113
113
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153
163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
363
193
363
113
113
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153
163
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                                                                                                                                                                                                                                             strain HCNT1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X
X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLASTOCYANIN-LIKE:
COPPER (TYPE 1) (B)
COPPER (TYPE 2) (B)
COPPER (TYPE 2) (B)
COPPER (TYPE 1) (B)
COPPER (TYPE 1) (B)
COPPER (TYPE 1) (B)
COPPER (TYPE 2) (B)
COPPER (TYPE 2) (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COPPER-CONTAINING PLASTOCYANIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                        Caselia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50DDB60CC4DC3E00
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Protein rcsF.
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STRAIN=K12 / MG1655;

MEDLINE=97426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                     Miyamoto K.;
Submitted (A
                                                                                                                                      Gervais F.G., Drapeau G.R.; "Identification of rcsF, a new "Identification, cloning, and characterization of rcsF, a new regulator gene for exopolysaccharide synthesis that suppresses division mutation ftsz84 in Escherichia coli K-12."; "O. Bacteriol. 174:8016-8022(1992).
                                                                                                                                                                                                                                   Escherichia coli, and
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Escherichia coli 06.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992;
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Oxidoreductase; Copper; Metal-binding; Flav
Nitrate assimilation; Repeat; Periplasmic;
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STRAIN=KI2 / W3110;

STRAIN=KI2 / W3110;

Takemoto K., Mori H., Miki T., Hatada E., Fukuda R.,

Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R.,

Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizc

"Systematic sequencing of the Escherichia coli genome: ar

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Davis K., Federsp
Lashkari D., Lew
                                                                                                                         METJA
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Bacterial capsule; Complete proteome.
CONFLICT 37 38 EP -> DA (IN REF. 1
CONFLICT 46 MISSING (IN REF. 1
SEQUIENCE 134 AA; 14163 MW; 824F82151C07BB41
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"Extensive mosaic structure revealed by the complete genome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
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nce 277:1453-1474(1997).
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D83536; BAA77873.1; -.
U70214; AAB08624.1; -.
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in D., Namath A., Oefner
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      MEDLINE-2192816; PubMed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Don Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
Genome Res. 12:689-700(2002).
-i- FUNCTION: Involved in protein export. Acts as maintaining the newly synthesized protein in a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                               SEQUENCE FROM N.A.
STRAIN=MB4 / JCM 11007;
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Oxidoreductase; Complete proteome.
SEQUENCE 389 AA; 42971 MW; 2CAA3DDE3EB0F5A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 273:1058-1073(1996).
-!- CATALYTIC ACTIVITY: Pyruvate + CoA + (COA + CO(2) + reduced ferredoxin.
-!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA,
                                                                                                                                                                                                        Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
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TIG OR TTE0624.
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Bult C.J., White O., Olsen G.J., Zhou
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BY THE SEQUENTIAL ACTION OF SPECIFIC TYDROLASES. SOME OF THESE
C ENZYMES REQUIRE SPECIFIC LOW-MOLECULAR MASS, NON-ENZYMIC PROTEINS:
THE SPHINGCLIPIDS ACTIVATOR PROTEINS (COPROTEINS) (BY SIMILARITY).

C -!- FUNCTION: SAPOSIN A AND SAPOSIN C STIMULATE THE HYDROLYSIS OF
GLUCOSYLCERAMIDE BY BETA-GALACTOSYLCERAMIDASE (EC 3.2.1.45). AND
GLACOTOSYLCERAMIDE BY BETA-GALACTOSYLCERAMIDASE (EC 3.2.1.46).

C GALACTOSYLCERAMIDE BY BETA-GALACTOSYLCERAMIDASE (EC 3.2.1.46).

C GALACTOSYLCERAMIDE BY BETA-GALACTOSYLCERAMIDASE (EC 3.2.1.46).

C GAPOSIN-C APPARENTLY ACTS BY COMBINING WITH THE ENZYME AND ACIDIC
LIPID TO FORM AN ACTIVATED COMPLEX, RATHER THAN BY SOLUBILIZING
THE SUBSTRATE BY SIMILARITY).

C CREBROSIDE SULFATE BY ARYLSULFATASE A (EC 3.1.6.8), GM1
GANGLIOSIDES BY BETA-GALACTOSIDASE A (EC 3.2.1.23) AND
GLOBOTRIAOSYLCERAMIDE BY ALPHA-GALACTOSIDASE A (EC 3.2.1.23)

C SAPOSIN-B FORMS A SOLUBILIZING COMPLEX WITH THE SUBSTRATES OF THE
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HAMMAP; MF 00303; -; 1.

InterPro; IPR001179; FKBP_PPlase.

InterPro; IPR005215; Trig_fac.

TIGRFAMs; TIGR00115; tig; 1.

PROSITE; PS00453; FKBP_PPIASE 1; FALSE_NEG.

PROSITE; PS00454; FKBP_PPIASE 2; FALSE_NEG.

PROSITE; PS00454; FKBP_PPIASE 3; 1.

Cell division; Chaperone; Isomerase; Rotamase; Complete proteome.

Cell division; Chaperone; Isomerase; FKBP_TYPE.

Cell division; Chaperone; FFDC7DC821072E15 CRC64;

A9762 MW; F7DC7DC821072E15 CRC64;
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EMBL; AF108656; AAF05899.1; -.
InterPro; IPR003119; SapA.
InterPro; IPR000004; SapB.
Pfam; PF05199; SAPA; 2.
Pfam; PF05194; SapB.; 4.
Pfam; PF05194; SapB.; 4.
ProDom; PD01732; SapB. sub; 3.
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FUNCTION: SAPOSIN D IS A SPECIFIC SPHINGOMYELIN PHOSPHODIESTERASE ACTIVATOR (EC 3.1.4.12) (BY SIMILARITY).

SUBUNIT: SAPOSIN B IS A HOMODIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: Lysosomal (By similarity).

PTM: THIS PRECURSOR IS PROTECLYTICALLY PROCESSED TO 4 SMALL PETTIDES, WHICH ARE SIMILAR TO EACH OTHER AND ARE SPHINGOLIPID HYDROLASE ACTIVATOR PROTEINS (BY SIMILARITY).

SIMILARITY: Contains 2 saposin A-type domains.

SIMILARITY: Contains 4 saposin B-type domains.
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RESULT 9
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AC P54719;
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A.M., Borchert S.,
RA Borriiss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connexton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ebrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parso V., Pohl T.M., Portetelle D., Porwollik S., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Seriguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Seriguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Waisarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Wasarotti A.,
"The complete genome sequence of the Gram-positive bacterium Bacillus Bubtilis.";
Br. Nature 190, 246,6(1997)
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Hypothetical
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or send a
                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
EMBL; D50543; BAA09107.1;
EMBL; Z99108; CAB12651.1;
PIR; F69802; F69802.
HSSP; P13569; INBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WAEDLINE=96262713; PubMed=8704981; Yamamoto H., Uchiyama S., Fajar A.N., Ogasawara N., Sekig "Determination of a 12 kb nucleotide sequence around the region of the Bacillus subtilis chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: Iftegral membrane protein (Potential).
-i- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MSBA SUBFAMILY.
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
ABC transporter ATP-binding protein yfic.
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IPR003593; AAA_ATPase.

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RESULT 10
C555_CHLLT
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                                  METAL
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01-NOV-1997 (Rel. 35, Last annotation update)
Cytochrome c-555 (C555).
Chlorobium limicola f.sp. thiosulfatophilum.
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
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InterPro; IPR003439; ABC_tran
Pfam; PF00064; ABC_membrane;
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transpc
                                                                                                                                                                                                  "Structure of cytochrome c555 of Chlorobium thiosulfatophilum: primitive low-potential cytochrome c.";
Proc. Natl. Acad. Sci. U.S.A. 74:5244-5247(1977).
-!- FUNCTION: This basic c-type monoheme cytochrome has been found
                                                                                                                                                                                                                                                                                               "The amino acid sequences of the cytochromes, sulphur bacteria of the genus Chlorobium."; Biochem. J. 159:757-774(1976).
                                                                                                                                                                                                                                                                                                                                         MEDLINE=77087088; PubMed=188412; van Beeumen J., Ambler R.P., Mey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
Hypothetical protein; ATP-binding; Transport; Transmembrane;
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SMART; SM00382; AAA;
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InterPro; IPR000345; CytC_heme_bind.
                                                                                                                                    with reductases. HSSP; P11732; 1CC5.
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RESULT 11
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STRAIN-TLS / ATCC 49652 / DSM 12025;

MEDLINE-22103685; PubMed=12093901;

MEDLINE-22103685; PubMed=12093901;

Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,

Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,

Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,

Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

"The complete genome sequence of Chlorobium tepidum TLS, a
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InterPro; IPR002323; Cyt_CIE.
InterPro; IPR000345; CytC_heme_bind
                                                                                                                                                                                                                                                                                                                                                                                                tosynthetic, anaerobic, green-sulfur bacterium.";

(Natl. Acad. Sci. U.S.A. 99:9509-9514(2002)

FUNCTION: This basic c-type monoheme cytochrome has been found exclusively in the green photosynthetic bacteria, although its role in bacterial photosynthesis is not established. It has an unusually low redox potential compared with mitochondrial cytochrome c. It is reactive with cytochrome c oxidases but not
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RESULT 13
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Best Local
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01-AUG-1992
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis and phylogenetic reconstruction of the genes encoding the large and small subunits of ribulose-1,5-bisphosphate carboxylase/oxygenase from the chlorophyll b-containing prokaryote prochlorothix hollandica.";

J. Mol. Evol. 32:379-395(1991).

-I- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of ribulose 1,5-bisphosphate, the primary event in photosynthetic.

- carbon dioxide fixation, as well as the oxidative fragmentation the pentose substrate in the photorespiration process. Both reactions occur simultaneously and in competition at the same
                                   RBS_SYNP2
Q44178;
15-DEC-1998
15-DEC-1998
15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prochlorothrix hollandica.
Bacteria; Cyanobacteria; Prochlorophytes;
Prochlorothrix.
                                                                                                                                                                                                        Lyase; Ox
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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MEDLINE=91251137; PubMed=1904095;
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Photosynthesis; Carbon dioxide fixation; Photorespiration;
Lyase; Oxidoreductase; Monoxygenase.
                                                                                                                                                                                                                                                 PIR; S16437; S16437.
InterPro; IPR000894; RuBisCO_small.
Pfam; PF00101; RuBisCO_small; 1.
PRINTS; PR00152; RUBISCOSMALL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    phospho-D-glycerate.
CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate
3-phospho-D-glycerate + 2-phosphoglycolate.
SUBUNIT: 8 large chains + 8 small chains.
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CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate
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license agreement (See http://www.isb-sib.ch/announce/
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O67284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKIYAMA H., KANAI S., Hiranc Submitted (JUN-1994) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Photosynthesis; Carbon dioxide fixation;
Lyase; Oxidoreductase; Monooxygenase.
SEQUENCE 111 AA; 13212 MW; 182FA0950;
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Pfam; PF00101; RuBisCO_small; 1.
PRINTS; PR00152; RUBISCOSMALL.
ProDom; PD000290; RuBisCO_small; 1.
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Graham D.E., Overbeek R., Spead M.A.,
Feldman R.A., Short J.M., OIson G.J.,
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                          Nature 392:353-358(1998).
                                           aeolicus
                                                                                                                     MEDLINE=98196666; PubMed=9537320;
                                                                                                                                   STRAIN-VFS
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Bacteria; Aquificae;
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                                                                                                                                                 EQUENCE
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SUBUNIT: 8 large chains + 8 small chains.
SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
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CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ribulose 1,5-bisphosphate, the primary event in photosynthetic carbon dioxide fixation, as well as the oxidative fragmentation the pentose substrate in the photorespiration process. Both reactions occur simultaneously and in competition at the same
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l protein )
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Chroococcales; Synechococcus
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                                                     Haasterland T., Young W.C
Spead M.A., Keller M., A
OIson G.J., Swanson R.V.
We hyperthermophilic bact
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SEQUENCE
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Pfam; PF00380; Ribosomal S9; 1.
ProDom; PD001627; Ribosomal S9; 1.
PROSITE; PS00380; RIBOSOMAL S9; 1.
Ribosomal protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of the lactic acid bacterium lactis ssp. lactis IL1403.", Genome Res. 11:731-753 (2001).
-!- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAT. PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat)
305 ribosomal protein S9.
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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Bolotin A., Wincker P., Mauger S., Jaillon O.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000730; AAC07249.1; -. PIR; A70407; A70407. Hypothetical protein; Complete
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HAMAP; MF_00532; -;
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                                           GKITVNG 453
GKITVNG 32
                                                                                                                                                                                   protein;
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                                                                                               DB
20;
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17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
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RESULT 16 GREA_BRUME

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Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
A Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
A Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
A Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,
The Brucella suis genome reveals fundamental similarities between
animal and plant pathogens and symbionts.";
Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
L. Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
L. Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
C. elongation past template-encoded arresting sites. The arresting
sites in DNA have the property of trapping a certain fraction of
celongating RNA polymerases that pass through, resulting in locked
ternary complexes. Cleavage of the nascent transcript by Cleavage
factors such as grea or greB allows the resumption of elongation
from the new 3'terminus. GreA releases sequences of 2 to 3
nucleotides (By similarity).
C. -i- SIMILARITY: BELONGS TO THE GREA/GREB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GREA BRUME
Q8YID6;
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., "The genome sequence of the ferrice R.;
                                                  Pfam; PF03449; GreA_GreB N; 1.
ProDom; PD004918; GreA GreB; 1.
TIGREAMS; TIGR01462; greA; 1.
PROSITE; PS00829; GREAB 1; 1.
PROSITE; PS00830; GREAB_2; 1.
                                                                                                                      InterPro; IPR006359; GreA.
InterPro; IPR001437; GreA GreB.
Pfam; PF01272; GreA GreB; 1.
Pfam; PF03449; GreA GreB N; 1.
                                                                                                                                                                                      HAMAP; MF-00105; -; 1.
                                                                                                                                                                                                                                     PIR;
                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isbor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                     This
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Transcription regulation; DNA-binding; Coiled coil; Complete DOMAIN 46 74 COILED COIL (POTENTIAL). SEQUENCE 157 AA; 17528 MW; 5651BAFED6942B3F CRC64;
                                                                                                                                                                                                                                                    EMBL; AE009493; AAL51689.1;
EMBL; AE014445; AAN30415.1;
                                                                                                                                                                                                                      TIGR;
                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                   between
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DelVecchio V.G., Kapatral V., Redkar R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=B.melitensis; STRAIN=16M /
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15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                     AF3315; AF3315.
                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                    BR1504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 41, Last sequence update)
(Rel. 42, Last annotation update
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greA (Transcript cleavage factor
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RESULT 17
KCH5_MOUSE
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SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
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28-FEB-2003 (Rel. 41, Last annotation update)
Voltage-gated potassium channel subfamily H m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                              InterPro; IPR001610; PAC.
InterPro; IPR000700; PAS-assoc_C.
InterPro; IPR000014; PAS_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          potassium channel
                                                                                                                                                    PROSITE; PS50113; PAC; 1.
PROSITE; PS50112; PAS; PARTIAL.
                                                                                                                                                                                                                               EMBL; AF309565; AAL09442.1; -.
                                                                                      DOMAIN
                                                                                                                                  Potassium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCNH5 OR EAG2
                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains SIMILARITY: Contains
                                                                                                                                                                                                                                                                                                                                                                                          subunit assembly.

SUBUNIT: The potassium channel is probably composed of a homo- or heterotetrameric complex of pore-forming alpha subunits that can associate with modulating beta subunits. Heteromultimer with KCNH1/EAG (By similarity).
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SIMILARITY: Belongs to
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7; Conserv
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172
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(Rel. 41,
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59
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172
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Rodentia;
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ium; Potassium transport; Multigene fa
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Pred. No. 24;
                                                                                    CYTOPLASMIC PAS.
                              Score 7; 1
Pred. No.
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Sciurognathi; Muridae;
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                     Mismatches
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                              DB 1;
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                                                                                                          SIMILARITY)
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008545; 055217;
01-NOV-1997 (Re
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"Characterization of the genes for mouse mouse LERK-4/Ephrin-A4 (Epl4), and human conservation of intron/exon structure.";
Genomics 47:131-135(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ephrin-A3 (EPH-related receptor tyrosine kina
(EHKI ligand) (EHKI-L) (Fragment).
EFNA3 OR EPLG3 OR LERK3 OR EPL3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D. "Distinct and overlapping expression patterns of ligands Eph-related receptor tyrosine kinases during mouse embryone transfer of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
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InterPro; IPR001799; Ephrin.
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                                                                                                                                                                                                                                                                                                               Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                      ProDom; PD002533; Ephrin; PROSITE; PS01299; EPHRIN;
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(EPLG6):
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MEDLINE-2338234; PubMed-12471157;
Melch R.A., Burland V., Plunkett G. III, Redford P., Roescl Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
Metansive mosaic structure revealed by the complete genome of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

-i- SUBCELLULAR LOCATION: Attached to the membrane by a lij
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Hypothetical lipoprotein year precursor.
YEAY OR B1806 OR C2210.
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EMBL; AE016761; AAN8
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EMBL; D90825; BAA15615.1; -.
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Itoh T. Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K. Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Mashimoto H., Nishio Y., Oshima T., Salto N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map."; DNA Res. 3:379-392(1996).
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Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I
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Science 277:1453-1474(1997).
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                                                                               ypothetical protein; Lipoprotein;
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PS00013; PROKAR_LIPOPROTEIN;
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Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Kerlavage A.R., Graham D.E., Kyrpides N.C., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
                                                                                                                Pfam; PF00827; Ribosomal L15e; 1. PROSITE; PS01194; RIBOSOMAL L15E; 1 Ribosomal protein; Complete proteom
                                                                                                                                                  HAMAP; MF 00256; -; 1.
InterPro; IPR000439; Ribosomal_L15e.
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                                                                                                                                                                                                                                                                                                                                                       reducing archaeon Archaeoglobus
Nature 390:364-370(1997)
                                                                                                     SEQUENCE
                                                                                                                                                                                  TIGR; AF2319;
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                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of the hyperthermophilic, reducing archaeon Archaeoglobus fulgidus.";
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134
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Q50712;
Q1-NOV-1997
01-NOV-1997
16-OCT-2001
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                                                                                                                 DNA BIND
                                                                                                                                                                           TubercuList; Rv3414c; ...
InterPro; IPR000838; Sigma70_ECF.
Pfam; PF04542; Sigma70_r2; 1.
Pfam; PF04545; Sigma70_r4; 1.
PROSITE; PS01063; SIGMA70_ECF; 1.
Transcription regulation; Sigma factor; DNA-directed
                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restrue by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laboratory strains.";
Submitteed (APR-2001) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT
-- ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION
THEN IS RELEASED (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY. ECF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN=CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Fleischai W., Utterback T., Weidman J., Khouri H., Gill J., Mikula,

Fleischai W., Utterback T., Weidman J., Khouri H., Gill J., Mikula,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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EMBL; AE007157; AAK47861.1;
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C70737; C7
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OR RV3414C OR MT3523 OR MTCY78.15.
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llarity 100.0%;
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    Last sequence update
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RESULT 22
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p31461; P76736;
01-JUL-1993 (Rel. 26, Created)
28-FEB-2003 (Rel. 41, Last sequence upda
28-FEB-2003 (Rel. 41, Last annotation up
Hypothetical protein yidX.
YIDX OR B3696 OR SF3768.
Escherichia coli, and
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Sher
Yang J., Yang F., Zhang X., Zhang J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu
Cheng H., Yao Z., He B., Chen R. Ms
Yu J.;
                                                                                                                                                                                                                                                                                                                                        through
Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=E.coli; STRAIN=K12 / MG1655; MEDLINE=97426617; PubMed=9278503; Bloch C.A., Per Blattner F.R., Plunkett G. III, Bloch C.A., Per Riley M., Collado-Vides J., Glasner J.D., Rode Gregor J., Davis N.W., Kirkpatrick H.A., Goeder
                                                                                                            EMBL;
                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fcentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome: organizational symmetry around the Genomics 16:551-561(1993).
                                                                                                                                                                                                                                                                         Rudd K.E.;
Unpublished observations
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                                                Hypothetical protein;
TRANSMEM 11 3
SEQUENCE 218 AA; 2
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                                                                                                                                                                                                                                                                                                                                        "Genome sequence of Shigella flexneri 2a: insi
through comparison with genomes of Escherichia
Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.; "DNA sequence and analysis of 136 kilobases of the Escherichia
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           Local
                        Match
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                                                                                             L10328; AAA62047.1; ALT FRAME.
AE000446; AAC76719.1; ALT_FRAME
AE015384; AAN45211.1; -.
Similarity 7; Conserv
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cein; Transmembrane; Co
potential.
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                                                31
24169
             100.0%;
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G., Wu H., Qu D.
n B., Ding K., C
ang B., Wen Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.
MBDLINE=96198612; PubMed=8925906;
Kohlhoff M., Dahm A., Hensel R.;
"Tetrameric triosephosphate isomerase from hyperthermophilic
                                                                                                                                                                                                                                                                     HAMAP; MF_00147; -; 1.
InterPro; IPR003009; FMN_enzyme.
InterPro; IPR00652; Triophos_ismrse.
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30-MAY-2000
                                                                                                                                                                                                                             ProDom; PD001005; Triophos ismrse; TIGRFAMs; TIGR00419; tim; I. PROSITE; PS00171; TIM; FALSE_NEG.
                                                                                                                                                                                                                                                                                                            EMBL; Y11302; CAA72160.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produ between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                      phosphate.
-!- PATHWAY: Plays an important role in several metabolic pathway-
-!- SIMUNIT: Homodimer.
-!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (
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TPIA OR TPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000
28-FEB-2003
                                                                                                                                                                                                                                                               Pfam; PF00121; TIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schramm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=DSM 862;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota;
Methanobacteriaceae; Me
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2161;
                                                                                                                                                                                                                    somerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 Lett. 383:245-250(1996).
CATALYTIC ACTIVITY: D-glyceraldehyde
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                                                                                                                                    Similarity
7; Conserve
                                                                                                                                                                                                         shunt
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                                                                                                               TGENALK 262
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                                                                                                                                                                                                                 S00171; TIM; FALSE_NEG.
Glycolysis; Gluconeogenesis;
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                                   STANDARD;
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                                                                                                                                    red. No. 32;
Mismatches
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   RESULT 25
EFA3_HUMAN
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Best Local
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H.,
Klausner R.D., Collins F.S., Wagner L., Shenr
                                                                                      MEDLINE=95063919; PubMed=7973638; Davis S., Gale N.W., Aldrich T.H., Maisonpierre P.C., Lhotak V., Pawson T., Goldfarb M., Yancopoulos G.D.; Pawson T., related receptor tyrosine kinases that require membrane attachment or clustering for activity."; Science 266:816-819(1994).
                                                                                                                                                                                                           Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III Cerretti D.P., Beckmann M.P.;
"Ligands for the receptor tyrosine kinases hek and elk: isolation cDNAs encoding a family of proteins.";
Oncogene 10:299-306(1995).
                                                                                                                                                                                                                                                                                                                                                                                                           Ephrin-A3 precursor (EPH-related (LERK-3) (EHK1 ligand) (EHK1-L). EFNA3 OR EPLG3 OR LERK3 OR EFL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFA3 HUMAN STANDARD; PRT; 238 AA
P52797;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; T15381; T15381.
WormPep; C03B1.9; CE03910.
Hypothetical protein.
SEQUENCE 230 AA; 26473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nemato Rhabditidae; Peloderinae; Rhabditidae; Peloderinae; Rhabi_TaxID=6239;
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                                            SEQUENCE FROM N.A. TISSUE=Duodenum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
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Altechul S.F.,

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Buetow K.H.,

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RESULT 26
YG1P_YEAST
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A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Erownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Chench A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A. 99:1699-16903 (2002).
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Best Local S
Matches
01-OCT-1996 |
01-OCT-1996 |
01-NOV-1997 |
Hypothetical
YGR036C.
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PIR; I38849; I38849.
Genew; HGNC:3223; EFNA3.
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CONFLICT
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P53223;
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SIGNAL
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-!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKELETAL MUSCLE, SPLEEN,
-!- THYMUS, PROGTATE, TESTIS, OVARY, SMALL INTESTINE, AND PERIPHERAL BLOOD LEUKOCYTES.
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$GD; $60:03268; CAX4.

GO; $G0:0030176; C:endoplasmic reticulum membrane, i
GO; $G0:0030176; C:endoplasmic reticulum membrane, i
GO; $G0:0030176; C:endoplasmic reticulum membrane, i
GO; $G0:0016462; F:pyrophosphatase activity; IDA.
GO; $G0:0016462; F:pyrophosphatase activity; IDA.
GO; $G0:0006487; P:lipid biosynthesis; IGI.
GO; $G0:0016462; F:pyrophosphatase activity; IDA.
GO; $G0:001646; F:pyrophosphatase activity; IDA.
GO; $G0:001646; F:pyrophosphatase activity; IDA.
GO; $G0:00
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30-MAY-2000
30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rieger M., Brueckner M., S
"Sequence analysis of 203
chromosome VII.";
                                                    MEDLINE=97435481; PubMed=9290212;
Rieger M., Brueckner M., Schaefer M., Mus
"Sequence analysis of 203 kilobases from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                           Methanococcus maripaludis.
Archaea; Euryarchaeota; Methanococci;
Methanococcaceae; Methanococcus.
                                                                                                                                                                                                                                           NCBI_TaxID=39152;
                                                                                                                                                                                                                                                                                                                                               Tungsten-containing (EC 1.2.99.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                               Yu J.-P., Whitman W.B.;
                                                                                                                                                                                STRAIN=JJ;
                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       St 13:1077-1090(1997).
SUBCELLULAR LOCATION: Integral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 SVGALTG
                methanofuran + reduced acceptor.
OFACTOR: TUNGSTEN (BY SIMILARITY).
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                                                                                                                                                                                                     FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVGALTG
                                                                                                                                                                                                                                                                                                         (Rel. 39, Createu,
(Rel. 39, Last sequence update,
, (Rel. 39, Last annotation update)
whtaining formylmethanofuran dehydrogenase II subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
Methanogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Pred. No.
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                                                                                                                                                                                                                                                                                       Methanococcales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
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                                                          + acceptor = CO(2)
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THIS
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                                                                                                    ENZYME
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RESULT 28
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Best Local S
Matches 7
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16-OCT-2001
16-OCT-2001
15-SEP-2003
                                                                                       STRAIN-Nine Mile phase I / RSA 493;
MEDLINE=22608657; PubMed=12704232;
Seshadri R., Paulsen I.T., Elsen J.A., Read T.D., Nelson K.E.,
Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J.,
DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
EMPOURI H.M., Lee K.H., Carty H.A., Scannlan D., Heinzen R.A.,
Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
"Complete genome sequence of the Q-fever pathogen, Coxiella
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-Nine Mile phase I / RSA 493;
Willems H., Jaeger C.;
Submitted (JAN-1997) to the EMBL/Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                SYGA
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contenting the statement is not removed.
                                                   burnetii.";
Proc. Natl. Acad. Sci. U.S.A.
-!- CATALYTIC ACTIVITY: ATP +
                                                                                                                                                                                                                                                                                                                                                                Glycyl-tRNA synthetase alpha alpha chain) (GlyRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COXBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (so or send an email to license@isb-sib.ch).
                         + glycyl-tRNA(Gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           Coxiellaceae;
                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                      Coxiella burnetii.
                                                                                                                                                                                                                                                                                                                                                  GLYQ OR CBU1913
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 similarity)
SUBCELLULAR
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7; Conserv
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(Rel. 40, Last sequence upd.
(Rel. 42, Last annotation u
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llarity 100.0%;
Conservative
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96
115
141
160
179
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108
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108
127
153
172
191
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7 X 13 AA REPEATS OF
G-X-[IL]-X-[IV]-X-G.
 Cytoplasmic
                                                                                                                                                                                                                                                                                                                        Gammaproteobacteria; Legionellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7; Pred. No
                          alpha and
                                                100:5455-5460(2003)
glycine + tRNA(Gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50912BD8B47A4BF0 CRC64;
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5. 38;
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5 6.1.1.14)
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                          beta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [GW] -X-X- [MLP] -X-X-
                                                  AMP + diphosphate
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Best Local
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EMBL; AE016966; AA091404.1; -.
TIGR; CBU1913; -.
HAMAB; MF 00254; --; 1.
InterPro; IPR006194; tRNA synt 2e.
InterPro; IPR006194; tRNA synt Gly.
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1 STRP3
HAM1 STRP3
Q8K8I7;
28-FEB-2003
28-FEB-2003
15-SEP-2003
                                                                                  STRAIN-SSI-1 / Serotype M3;
Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hayashi H., Hamada S.;
"The genome of invasive Streptococcus pyogenes; a of S. pyogenes SSI-1, SF370 and MGAS8232,";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ datal-i-SIMILARITY; BELONGS TO THE HAM1 NTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=MGAS315 / Serotype M3;
MEDLINE=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei I
Mammarella N.D., Liu M.-Y., Smoot J.C., Pol
Campbell D.S., Smith T.M., McCormick J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAM1 protein homolog.
SPYM3_0263 OR SPS1596.
Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IFACOU-
Pfam; PF02091; tRNA Synt Ze; 1.
PRINTS; PR01044; TRNASYNTHGA.
ProDom; PD006995; tRNA synt Ze; 1.
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                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of a serotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGREAMS; TIGR00388; gTyQ; T.
PROSITE; PS50861; AA TRNA LIGASE II GLYAB; 1.
AMINDACY1-TRNA SYNTHETASE; ProteIn biosynthesis; Ligase; ATP-binding.
DOMAIN 301 305 POLY-SER.
                                                                                                                                                                                                                                                   STRAIN=SSI-1
                                                                                                                                                                                                                                                                                                                                                 emergence.";
                                                                                                                                                                                                                                                                                                                                                                       phage-encoded toxins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
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                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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copyright. It is produced through a collaboration tute of Bioinformatics and the EMBL outstation - ics Institute. There are no restrictions on its
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., Porcella S.F., Parkins
J.K., Leung D.Y.M.,
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or send a
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MEDLINE=21927593; PubMed=11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP005146; BAC64691.1; -.
HAMAP; MP01405; fused; 1.
InterPro; IPR002637; Hamlp_like.
Pfam; PF01725; Hamlp_like; 1.
                                                                                                                                                                    EMBL; AE009983; AAL97155.1; -.
HAMAP; MF 01405; fused; 1.
InterPro; IPR002637; Ham1p_like; 1.
ProDom; PD004952; Ham1p_like; 1.
                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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SPYM18_0412.
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DOMAIN 1 129
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ProDom; PD004952; Hamlp_like; 1.
TIGRFAMs; TIGR00042; TIGR00042; 1.
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                                                    SEQUENCE
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STRAIN=MGAS8232 /
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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28-FEB-2003
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HAMAP, MF 01405; fused; 1.
InterPro; IPR002637; Hamip like.
Pfam; PF01725; Hamip like; 1.
ProDom; PD004952; Hamip like; 1.
TIGRPAMS; TIGR00042; TIGR00042; 1.
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                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
18-FEB-2003 (Rel. 41, Last annotation
Aspartate carbamoyltransferase (EC 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=SF370 / ATCC 700294 / Serotype MEDLINE=21192684; PubMed=11296296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9A1B6;
                        PYRB.
                                   transcarbamylase)
                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003
28-FEB-2003
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                      Hydrolase; Complete proteome.
             Lactobacillus leichmannii.
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                                                                                                                                                                                                             Similarity 7; Conserv
                                                                                                                                                                 AVYLPEG 111
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n homolog.
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                                                                                                        STANDARD;
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                                    (ATCase).
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2.1.3.2) {
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                                               (Aspartate
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Best Local S
Matches 7
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01-JAN-1990 ()
01-FEB-1991 ()
Avirulence C )
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              Tamaki S., Dahlbeck D., Staskawicz B., Keen N.T.;

"Characterization and expression of two avirulence genes cloned from the state of the structure of two avirulence genes cloned from the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the 
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EMBL; X78999; CAA55634.1; -.
PIR; T46956; T46956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Becker J., Brendel M.;
"Molecular cloning and characterization of the pyrB gene of Lactobacillus leichmannii encoding aspartate transcarbamylase.";
Biochimie 78:3-3(1996).
                                                                                                                                                                                                                                                                              Pseudomonas syringae (pv.
Bacteria; Proteobacteria;
Pseudomonadaceae; Pseudomo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGREAMS; TIGRO0670; asp carb tr; 1.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
Pyrimidine biosynthesis; Transferase.
SEQUENCE 351 AA; 39857 MW; 8C36C48B1AE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (s
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P13836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR006130; Asp/Orn_COtranf.
InterPro; IPR002082; Asp_carbmltransf.
InterPro; IPR006131; OTCace_O.
InterPro; IPR006132; OTCace_P.
Pfam; Pr00185; OTCace; 1.
Pfam; PF02729; OTCace, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
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MEDLINE=96285745; PubMed=8725005;
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NCBI_TaxID=28039;
                                                                                                                                                           MEDLINE=89008107; PubMed=3049552;
                                                                                                                                                                                      STRAIN=Race 0;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0100;
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                                                                                                                                                                                                                                                      CBI_TaxID=318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Pyrimidine biosynthesis; second step. SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
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CULTIVARS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the Entransmiss Through services Bioinformatics are no restricted.
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLSADDV 493
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                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 13, Created)
(Rel. 13, Last sequence update)
(Rel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                         protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
SOYBEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AOTCASE.
                                                                                                                                                                                                                                                                                   Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase.
7 MW; 8C36C48B1AEBD956 CRC64;
                                                                                                                                                                                                                                                                                                    glycinea).
Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7; DB 1, Pred. No. 47; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Best Local S
Matches 7
                           TIGRFAMs;
PROSITE; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gomez L., Carrasco P.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ datab
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ datab
I-FUNCTION: CATALYZES THE FORWATION OF S-ADENOSYL
METHIONINE AND ATP
-I- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O
diphosphate + S-adenosyl-L-methionine
-I- COFACTOR: Binds 2 divalent ions, such as magnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
5-adenosylmethionine synthetase 2 (EC 2.5.1.6)
adenosyltransferase 2) (AdoMet synthetase 2).
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P49613;
                                                                        InterPro; IPR002133; S-AdoMet_synt
pfam; pr00438; S-AdoMet_synt; 1.
pfam; pr02772; S-AdoMet_syntD2; 1.
pfam; pr02773; S-AdoMet_syntD3; 1.
                                                                                                                                                                         PIR; S
                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
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                                                                                                                                                                                                                    EMBL; X82077; CAA57581.1; -. EMBL; L36681; AAA58773.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pisum sativum (Garden pea)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 potassium ion per subunit (FPATHWAY: Activated methyl cycl
                                                                                                                                                                                                S66352; S66352.
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                                                                                                                                                                         P04384;
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PS00376; ADOMET_SYNTHETASE_PS00377; ADOMET_SYNTH
                                                                                                                                                                                                                                                                                          equires a license agreement email to license@isb-sib.cl
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                                                                                                                                                                                                                                                            "Characterization and regulation of the gene encoding nitrite reductase in Rhodobacter sphaetroides 2.4.3.";

J. Bacteriol. 179:1090-1095(1997).

-I- CATALYTIC ACTIVITY: Nitric oxide + H(2)O + ferricytochrome c = nitrite + ferrocytochrome c.

-I- COPACTOR: CONTAINS ONE ATOM OF TYPE I COPPER AND ONE ATOM OF TYPE II COPPER; FAD. TYPE 1 COPPER IS BOUND WITHIN A SINGLE MONOMER, WHILE TYPE 2 COPPER IS HELD BY RESIDUES FROM EACH OF TWO MONOMERS, OF THE TRIMER. NITRITE IS BOUND TO THE TYPE 2 COPPER SITE.

- PSEUDOAZURIN IS THE PHYSIOLOGICAL ELECTRON DONOR FOR THE CU-NIR IN VITRO (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Magnesium;
NP_BIND
METAL
                                                                                             or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Rhodoba, Rhodobacteraceae; Rhodobacter.
                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
PRINTS; PR00695; CUNO2RDTASE.
Oxidoreductase; Copper; Metal-binding; Flavoprotein;
Nitrate assimilation; Repeat; Periplasmic; Signal.
                              InterPro; IPR001117; Cu-oxidase
InterPro; IPR001287; CuNO2_reduc
Pfam; PP00394; Cu-oxidase; 2.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                      PATHWAY: Nitrate assimilation (denitrification).
SUBCUNIT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Periplasmic (By similarity).
DOMAIN: THE TYPE I COPPER SITE IN NIR PLAYS A CRUCIAL ROLE I ELECTRON TRANSFER FROM PSEUDOAZURIN TO THE TYPE II COPPER S. OF NIR, WHICH COMPRISES THE CATALYTIC CENTER OF NIR FOR THE REDUCTION OF NITRITE.
                                                                                                                                                                              SIMILARITY: Contains 2 plastocyanin-like domains.
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                                                              U62291; AAB05767.1;
P25006; INIF.
                                                                                             an email to license@isb-sib.ch).
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RESULT 36
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Sasaki H.,
                                                                              MEDLINE=98019216; PubMed=9353305; Murphy M.E., Turley S., Adman E.T
                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS). MEDLINE=96032602; PubMed=7547950;
                                                                                                                                                                                                                                                                                     MEDLINE=94227056; PubMed=8172899;
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15-SEP-2003
                                                        Murphy M.E., Turley S., Adman E.T.; "Structure of nitrite bound to copper-containing niform Alcaligenes faecalis. Mechanistic implications
                                                                                                                          Murphy M.E., Turley S., Kukimoto M., Nishiyama M., Sasaki H., Tanokura M., Adman E.T.; "Structure of Alcaligenes faecalis nitrite reductariste mutant, M150E, that contains zinc."; Biochemistry 34:12107-12117(1995).
                                                                                                                                      site mutant,
                                                                                                                                                                                                                      Biochemistry
                                                                                                                                                                                                                                                                 Kukimoto M., Ni
Horinouchi S.,
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COPPER-CONTAINING N
PLASTOCYANIN-LIKE 1
PLASTOCYANIN-LIKE 2
COPPER (TYPE 1) (B)
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                                   oxide + H(2)O + ferricytochrome
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               COPPER
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 COPPER AND ONE ATOM OF TY WITHIN A SINGLE MONOMER,
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                                                                     nitrite
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PRINTS; PR00695; CUNO2RDTASE.
TIGREAMS; TIGR01409; TAT_signal_seq; 1.
Oxidoreductase; Copper; Metal-binding; Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                            MAIN
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2AFN; 01;
1NTD; 00;
1AQ8; 21;
1AS6; 21;
1AS7; 22;
1AS7; 22;
1AS8; 2
3; 1ET5; 2
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SUBUNIT: Homotrimer.
SUBCELLULAR LOCATION: Periplasmic.
SUBCELLULAR LOCATION: Periplasmic.
INDUCTION: UNDER ANAEROBIC GROWTH CONDITIONS AND BY NITRITE.
DOMAIN: THE TYPE I COPPER SITE IN NIR PLAYS A CRUCIAL ROLE FOR
ELECTRON TRANSFER FROM PSEUDOAZURIN TO THE TYPE II COPPER SITE
DOFNIR, WHICH COMPRISES THE CATALYTIC CENTER OF NIR FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 2 plastocyanin-like domains.
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                                                                                                                                                                                                                                                                             assimilation;
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IPR001287; CuNO2_reductase
IPR006311; Tat.
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342
   Repeat; Periplasmic; Signal; 3D-structure;
                                                                                                                                                                                                                                                                     acid
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COPPER (TYPE 1).
COPPER (TYPE 2).
COPPER (TYPE 2).
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H-X: LOOSES NITRITE-REDUCING ACTIVITY.
M->E: CONTAINS ONLY A TYPE II COPPER ATOM
AND FAILS TO CATALYZE THE REDUCTION OF
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AC P25006;
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DT 01-NOV-1997 (
DT 15-SEP-2003 (
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OC ALCALIGENACE FROM
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STRAIN=IAM 1013;
MEDLINE=96193667; PubMed=8605003;
                                          Achromobacter cycloclastes.
Bacteria; Proteobacteria; Bet
Alcaligenaceae; Achromobacter
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(Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
aining nitrite reductase precursor
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100.0%; Fi
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                                                   Betaproteobacteria; Burkholderiales;
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%; Pred. No. 50;
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Length 376;

Indels

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Gaps

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1.7.2.1) (Cu-NIR).

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R EMBL; Z48635; CAA88564.1; -.

R PIR; JC4648; JC4648.

PDB; 2NRD; 07-DEC-95.

R PDB; 1NIA; 07-DEC-95.

R PDB; 1NIB; 07-DEC-95.

R PDB; 1NIC; 07-DEC-95.

R PDB; 1NIC; 07-DEC-95.

R PDB; 1NIC; 07-DEC-95.

R PDB; 1NIC; 07-DEC-95.

R PDB; 1NIF; 07-DEC-95.

R PDB; 1NIF; 07-DEC-95.

R InterPro; IPR001217; CunO2_reductase.

R InterPro; IPR001217; Tat.

R InterPro; IPR006311; Tat.

R InterPro; IPR006311; Tat.

R Pfam; PF00394; Cu-oxidase; 2.

R Pfam; PF00394; Cu-oxidase; 2.

R Pfam; PF00394; Cu-oxidase; 2.

R PINTS; PR00695; CUNO2RDTASE.

R TIGRRAMS; TIGR01409; TAT signal seq; 1.

Oxidoreductase; Copper; Metal-binding; Flavoprotein; FAD W Nitrate assimilation; Repeat; Periplasmic; Signal; 3D-st
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le Gall J.;
"Cloning, ch
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          copper J. Biol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96070866; PubMed=7499203;
Adman E.T., Godden J.W., Turley S.;
"The structure of copper-nitrite reductase from
cycloclastes at five pH values, with NO2-bound a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

MEDLINE=91320115; PubMed=1862344;

Godden J.W., Turley S., Teller D.C., Adman E.T.,

Payne W.J., le Gall J.;

"The 2.3-A X-ray structure of nitrite reductase
cycloclastes.";
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STRAIN-IAM 1013;
MEDLINE-91308101; PubMed-1830217;
Fenderson F.F., Kumar S., Adman E.T.,
le Gall J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       generating nitrite reductase and Achromobacter cycloclastes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science
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SUBCULTI.HOMOCITIMEY.
SUBCELLULAR LOCATION: Periplasmic.
DOMAIN: THE TYPE I COPPER SITE IN NIR PLAYS A CRUCELLORD THANSFER FROM PSEUDOAZURIN TO THE TYPE I:
OF NIR, WHICH COMPRISES THE CATALYTIC CENTER OF N:
REDUCTION OF NITRITE.
SIMILARITY: Contains 2 plastocyanin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             per depleted.";
Biol. Chem. 270:27458-27474(
CATALYTIC ACTIVITY: Nitric
nitrite + ferrocytochrome c
COPACTOR: CONTAINS ONE ATOM
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30:7180-7185(1991).
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COPPER-CONTAINING NITRITE REDUCTASE PLASTOCYANIN-LIKE 1. PLASTOCYANIN-LIKE 2.
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                                     . Similarity 7; Conserv
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Pred. No.
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                                                                               Length 378;
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RESULT YM12_MY

136

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142

Q10400; 01-OCT-1996

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STANDARD;

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                               Query Match
Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EWBI outsit the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
                                                                                                                                                                                                                                   EMBL, Z70283; CAA94255.1; -.
EMBL, ABO07072; AAK46554.1; ALT_INIT
PIR, E70786; E70786.
HSSP; P19754; 1AWK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Hypothetical protein Rv2212.
RV2212 OR MT2268 OR MTCY190.23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CDC 1551 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                       TubercuList; Rv2212; -.
InterPro; IPR001054; G_cyclase.
                                                                                                                                                                                                                      TIGR; MT2268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                cyclase family.
                             7; Conserv
                                                                                          al protein; Complete proteome.

208 317 GUANYLATE CYCLASE.

378 AA; 39775 MW; AF26A9CFC13C91DC CRC64;
                                              1.4%;
                            Score 7; DB 1
Pred. No. 50;
O; Mismatches
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                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
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Q01840; Q9CIK3;
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          Complete
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PIR; B86669; B86669.
                                                                                                                                             ProDom; PD000229; RecA; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00321; RECA_1; 1.
PROSITE; PS50162; RECA_2; 1.
PROSITE; PS50163; RECA_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21235186; PubMed=11337471;
Bolotin A., Wincker P., Mauger S., Jaillon O
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic
lactic ssp. lactis IL1403.";
Genome Res 11731-753(2001).
Genome Res 11731-753(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201840; (year),
01-APR-1993 (Rel. 25, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                 HSSP; P26345; 1G19.
HAMAP; MF_00268; -; 1.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR001553; RecA.
                                                                                                                                                                                                                                                                                                                                           EMBL; M88106; AAA25216.1; -.
                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duwat P., Ehrlich S.D., Gruss A.; "Use of degenerate primers for polymerase chain reaction cloning sequencing of the Lactococcus lactis subsp. lactis recA gene."; Appl. Environ. Microbiol. 58:2674-2678(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92384590; PubMed=1514816;
Duwat P., Ehrlich S.D., Gruss A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactococcus lactis (subsp. factis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECA protein, c
                                                                                                                                  DNA damage; DNA
                                                                                                                                                                                                                        PRINTS; PRO0142; RECA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAS. IT INTERACTS WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                      PF00154; recA;
                                                                                                                                                                                                                                                                                                                              AE006272; AAK04452.1;
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                                                                                                                                  recombination;
          87
288
298
333
343
351
387
         ATP (BY SIMILARITY).

R -> S (IN REF. 1).

D -> E (IN REF. 1).

EI -> DV (IN REF. 1).

T -> A (IN REF. 1).

EA -> DS (IN REF. 1).

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                                                                                                                               response; ATP-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387
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   Query Match
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Best Local
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HSSP; P04384; 1MXB.
InterPro; IPR002133; S-AdoMet_synt; 1.
Pfam; PF00438; S-AdoMet_syntD2; 1.
Pfam; PF02772; S-AdoMet_syntD3; 1.
Pfam; PF02773; S-AdoMet_syntD3; 1.
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15-JUL-1998
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                                                                      SEQUENCE
                                                                                     BINDING
                                                                                                  PROSITE; PS00376; ADOMET_SYNTHETASE 1; 1.

PROSITE; PS00377; ADOMET_SYNTHETASE 2; 1.

Transferase; One-carbon metabolism; Multigene family; AT

Magnesium; Potassium; Metal-binding.

MP_BIND 119 124 ATP (POTENTIAL).

METAL 17 17 MAGNESIUM (BY SIMILARITY).

METAL 43 POTASSIUM (BY SIMILARITY).

METAL 271 271 POTASSIUM (BY SIMILARITY).

METAL 279 279 MAGNESIUM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diphosphate + S-adenosyl-L-methionine.
-!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt,
- 1 potassium ion per subunit (By similarity).
-!- PATHWAY: Activated methyl cycle.
-!- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97188555; PubMed=9037140;
Schroeder G., Eichel J., Breinig S., Schroeder J.;
"Three differentially expressed S-adenosylmethionine synthetases from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-203 (Rel. 41, Last annotation update)
S-adenosylmethionine synthetase 1 (EC 2.5.1.6)
adenosyltransferase 1) (AdoMet synthetase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATRO
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-i- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)0 = phosphate +
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                                                                  ATP (POTENTIAL).
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Oy 439 SIVANGL 445
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Db 292 SIVANGL 298
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Search completed: August 27, 2003, 18:43:03 Job time : 46 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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2: sp_bacteria:*
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4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
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sp_rodent:*
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sp_vertebrate:*
sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	% Query Match Length DB	BB	ID	Description
_	1487.5	56.6	510	16	Q8XPY3	Q8xpy3 ralstonia s
2	1388	52.9	390	16	Q9JYE1	
ω	1386	52.8	386	16	Q9JTB8	Q9jtb8 neisseria m
4.	787	30.0	486	N	Q8KKH4	Q8kkh4 hyphomicrob
υı	751.5	28.6	361	<u>, , , , , , , , , , , , , , , , , , , </u>	Q9Р9Н9	Q9p9h9 haloarcula
ი	481	18.3	360	N	Q9AQQ7	Q9aqq7 alcaligenes
7	451	17.2	360	N	068601	O68601 alcaligenes
8	442	16.8	455	16	Q8U7R7	Q8u7r7 agrobacteri
9	439.5	16.7	376	16	Q92Z29	Q92z29 rhizobium m
10	431	16.4	376	16	Q8YBB2	Q8ybb2 brucella me
11	429.5	16.4	364	N	031380	O31380 bradyrhizob
12	429	16.3	376	16	Q8FX29	Q8fx29 brucella su
13	390.5	14.9	478	16	Q8FTV6	Q8ftv6 corynebacte
14	258	9.8	343	16	Q8F5W1	Q8f5w1 leptospira
15	253	9.6	179	N	Q93TN1	Q93tnl nitrosomona
16	250.5	9.5	379	17	Q9HQF4	Q9hqf4 halobacteri

45	44	43	42	41	40	39	3 8 8	37	36	35	34	33	32	<u>3</u> 1	30	29	28	27						21	20	19	18	17
209.5	210.5	210.5	210.5	211.5	211.5	211.5	211.5	213.5	215	$\vdash$	216.5	219	219	219.5	221	222	222	223	224.5	226.5	228	228.5	228.5	230.5	232 .	233	236	248.5
8.0	8.0	8.0	8.0	8.1	8.1	8.1	8.1					8.3		8.4				æ .5										9.5
172	172	172	172	172	172	172	172	172	179	179	172	180	179	180	178	163	138	179	172	180	179	180	180	180	179	179	179	338
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_	Q8kpm8 uncultured	Q8kpl3 uncultured	Q8kpj8 uncultured	Q8ki80 uncultured		Q8kpk9 uncultured		თ	N	Q8rlt0 ochrobactru	0	U	Q8rls8 ochrobactru	Q93tn5 nitrosomona	Q8rls9 ochrobactru		Q9k098 neisseria m	Q8rlt1 ochrobactru	Q8kpm7 uncultured			Q93tn4 nitrosomona	Q93tn3 nitrosomona	nitroso	ensifer	<u> </u> t4	mesorhizob	Q8yq92 anabaena sp

## ALIGNMENTS

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STRAIN-GMI1000;  MEDLINE-21681879; PubMed=11823852;  Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Woisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;  "Genome sequence of the plant pathogen Ralstonia solanacearum.";  Nature 415:497-502(2002).  EMBL; AL646085; CAD18654.1;  InterPro; IPR0011287; CuNO2_reductase.  InterPro; IPR0001287; CuNO2_reductase.  InterPro; IPR0001287; CuNO2_reductase.  InterPro; IPR0003045; CytC heme_bind.  InterPro; IPR003088; Cyt_CI.  Pfam; PP00394; Cu-oxidase; 1.  Pfam; PP00394; Cu-oxidase; 1.  Pfam; PP00394; CytCochrome C; 1.  PRINTS; PR00695; CUNO2RDTASE.  PROSITE; PS00190; CYTCCHROME C; 1.  Oxidoreductase; Plasmid; Complete proteome.  SEQUENCE 510 AA; 54600 MW; 8008105DD99459AC CRC64;	IDLT 1  (PY3  QBXPY3  QBXPY3  QBXPY3  QBXPY3  O1-MAR-2002 (TrEMBLrel. 20, Created)  O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)  O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)  Probable major ANAEROBICALLY induced outer membrane transmembrane  protein (EC 1.7.99.3).  RS91503 OR RS03038.  Ralstonia solanacearum (Pseudomonas solanacearum).  Plasmid megaplasmid.  Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  RALStoniaceae; Ralstonia.  NCBI TaxID=305;  [1]  SEQUENCE FROM N.A.

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Matches 277
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01-OCT-2000
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STRAIN-MCS8 / Serogroup B;

MEDILINE-20175755; PubMede=10710307;

MEDILINE-20175755; PubMede=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K. Tettelin H., Saunders N.J., Hood D.W., Pederson J.F., Dodson R.J., Lisen J.A., Ketchum K.A., Hood D.W., Peterson J.D., Hickey E.K., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Dougherty B.A Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B. Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.C.;

Gmith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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                                                                                                                                                                          Science 287:1809-1815(2000).
EMBL; AE002512; AAF41975.1;
HSSP; P25006; INIF.
     Complete
                                                        InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001287; CuNO2_reductase
Pfam; PF00394; Cu-oxidase; 2.
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Q9JTB8;
01-OCT-2000
                                                                                                                                                                                               Parkhill J., Achtman M., James K.D., Bentley S.D., Churche Klee S.R., Morelli G., Basham D., Brown D., Chillingworth Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseri meningitidis Z2491.",
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                                                                              InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001287; CuNO2 reductase.
Pfam; PF00394; Cu-oxidase; 2.
PRINTS; PR00695; CUNO2RDTASE.
                                                                                                                                                                                                                                                                                                                                    STRAIN=Z2491 / Serogroup A / Serotype 4A;
MEDLINE-20222556; PubMed=10761919;
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ANIA OR NMA1887.
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01-OCT-2002
                                                                                                                                                                  Nature 404:502-506(2000).
EMBL; AL162757; CAB85110.1; :-.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                 SEQUENCE
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(TrEMBLrel. 15, Last sequence update)
(TREMBLrel. 22, Last annotation update)
uctase, major outer membrane copper-containing
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68.7%;
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Pred. No. 1.1e-85;
 Score
Pred.
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 1386; DB 16;
No. 1.4e-85;
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ data EMBL; AB076606; BAC00912.1; -...
InterPro; IPR001187; CuNO2_reductase.
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Bacteria; Proteobacteria; Alphaproteobacteria;
Hyphomicrobiaceae; Hyphomicrobium.
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01-OCT-2002
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Matches 154;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Copper-containing dissimilatory nitrite reductase p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             archaeon, Haloarcula marismortui.";
J. Bacteriol. 183:4149-4156(2001)
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InterPro; IPR001287; CuNO2_reductase.
Pfam; PF00394; Cu-oxidase; 1.
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HSSP; P38501; 1AS8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ichiki H., Tanaka
Fujiwara T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haloarcula marismortui (Halobacterium Archaea; Euryarchaeota; Halobacteria;
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nilarity 42.5%;
Conservative 55
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Y., Mochizuki K.,
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Pred. No. 9.2e-43;
5; Mismatches 138
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POTENTIAL.

COPPER-CONTAINING DISSIMILATORY NITRITE REDUCTASE.

12829C586AA3F5D0 CRC64;
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Halobacteriales;
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Q9AQQ7;
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01-JUN-2001 (TYEMBLrel. 23, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
Dissimilatory nitrite reductase.
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PROSITE; PS00283; SOYBEAN_KUNITZ; 1.
SEQUENCE 360 AA; 39072 MW; CAF063CB38430380 CRC64;
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NCBI_TaxID=133923;
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InterPro, IPR001287, CuNO2 reductase.
InterPro, IPR002160, Kunitz legume.
Pfam; PP00394; Cu-oxidase; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPTYVLMNGEKYAITPDRHGSPSMQVGETARVYFVTGGPNLDSSFHPIGSVWDEVWQQGS
                                                                                                                                                                                                                                                                                               <del>.</del> Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAVAPVGM----HIANGMYGLILVEPKEGLP-----KVDKEYYVMQGDFY----TKGKY
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                                                          YLHLNHNLIEAFELGAAGHIKVEGKWNDDL 348
                                                                                                    YVLVDHAIFRAFNKGALGILKVEGEENHEI 358
                                                                                                                                                                                                                               GNGGPNLTSSFHVIGEIFDKVHFEGGKGEN---HNIQTTLIPAG--GAAITEFKVDVPGD
                                                                                                                                                                                                                                                                                                                                                GEQGLQPFDMEKAIRED------AEYVVFNGSVGALTGENALKAKVGETVRLFV
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                                                                                                                                                                           -HSQANRDTRPHLIGGHGDWV-WETGKFGNPPQKNLETWFIRGGSAGAALYTFK--QPGV
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                                                                                                                                                                                                                                                                                               KTLAESYGDTVEVMRKLTPSHIVFNGKVGALTGANALTAKVGETVLLI-
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Pred. No. 1.7e-24;
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Q8U7R7
Q8U7R7;
01-JUN-2002
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SEQUENCE
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Achromobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kataoka K., Furusawa H., Yamaguchi K., Suzuki "Cloning and Expression of Copper Nitrite Redu Alcaligenes xylosoxidans GIFU1051.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ EMBL; AF051831; AAC05831.1; -.
EMBL; AB013078; BAA33678.1; -.
HSSP, P25006; INIF.
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Submitted (MAR-1998)
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STRAIN=NCIMB11015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001287; CuNO2_reductase
Pfam; PF00394; Cu-oxidase; Z.
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                                                                                                                                                                                                             347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 VNPGEQATLRFKADRSGTFVYHC--APEGMVPWHVVSGMSGTLMVLPRDGLKDPQGKPLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 TAPGHTSTFSFKALQPGLYVYHCAVAPVGM---HIANGMYGLILVEPKEGLP-----K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGTAWAQDA-----DKLPHTKVTLVAPPQVHPHEQATKSGPKVVEFTMTIEEKKMVID
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                                                                                                                                                                                                                                                                    QAIDTQEAPKTPAP 388
                                                                                                                                                                                                                                                                                                                              GAALYTEK--QPGVYAYLNHNLIEAFELGAAGHIKVEGKWND
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      (TrEMBLrel.
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to the EMBL,
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the EMBL/GenBank/DDBJ databases
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Pred. No. 1.8e-22;
                                                             PRT;
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EMBL; AE008247; AAK89058.1; -.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001287; CuNO2_reductase.
InterPro; IPR006311; Tat.
Pfam; PF00394; Cu-oxidase; 2.
DETUTE: DETUTE: TROOGGE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
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Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mull
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Egp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markel
Golland C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
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[2]
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01-MAR-2003
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhiz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21608551;
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                            HFEGGKGENH----NIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVE
                                                                              LEVMRKLTPSHIVFNGAVGALTGEHALQAAVGE--KVLIVHSQANRDTRPHLIGGHGDYV
                                                                                                                EKAIRE-DAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNLTSSFHVIGEIFDKV
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(TrEMBLrel. 23, Last annotation update)
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Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P., Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J., Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L., Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.; "Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti pSymA megaplasmid.", Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
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PRINTS; PR00695; CUNCARDTASE.
TIGREAMS; TIGR01409; TAT_signal_seq; 1.
Oxidoreductase; Plasmid; Hypothetical p
SEQUENCE 376 AA; 40258 MW; 9B799927.
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NIRK OR RA0681 OR SMA1250.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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LPEG
                                                                                              TLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVY
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                                               WFIPGGTAGAAFYTFEQPGIYAYVNHNLIEAFELGAAAHFAVTGDWNDDLMT---
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IPR001287; CuNO2_reductase.
IPR006311; Tat.
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33.2%; Pred. No. 1.1e
tive 52; Mismatches
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STRAIN=16M / ATCC 23456 / Biotype 1;

MEDLINE=20020109; PubMed=11756688;

MEDLINE=20020109; PubMed=11756688;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brucella melitensis.";

Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

EMBL; AE009732; AAL54230.1; -.
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Brucellaceae; Brucella.
NCBI TaxID=29459;
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PRINTS; PR00695; CUNO2RDTASE.
TIGRPAMS; TIGR01409; TAT signal seq; 1.
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InterPro; IPR001287; CuNO2_reductase
InterPro; IPR006311; Tat.
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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Pred. No. 4.3e-21;
B; Mismatches 147;
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     sequence update)
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Best Local Similarity
Matches 126; Conserv
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01-MAR-2003
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SEQUENCE FROM N.A.

STRAIN=1330 / Biovar 1;
STRAINE=22247741; PubMed=12271122;
Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
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InterPro; IPRO01287; Cu-oxidase; 2.
Pfam; PF00394; Cu-oxidase; 2.
PRINTS; PR00695; CUNO2RDTASE.
SEQUENCE 364 AA; 39356 MW; D6C197
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Bacteria; Proteobacteria; Alphaproteobacteria;
Bradyrhizobiaceae; Bradyrhizobium.
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STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi
Usuda Y., Suzimoto S.;
Tho Paris Departs S.;
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  AAPAGGTNPAAVDVPGV-GARSVDHEGFTPVNPVL--
                                             AQPKSSTVDAAAKTANADNAASQEHQGELPVIDAIVTHAPEVPPPVDRDHPAKVVVKMET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVDVPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEG 372
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                                                                                                                            14.9%;
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34.5%; Pred. No. 5.
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. 23, Last sequ
. 23, Last anno
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Last annotation updat
                                                                                                                            Score 390.5; DB 1
Pred. No. 3.3e-18;
                                                                                                                                                                                                       282BD17175C02D4A CRC64;
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.9e-21;
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  -APAPTGTVHE---
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RESULT 15
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Hypothetical protein; Complete proteome.
SEQUENCE 343 AA; 38017 MW; 6D850CA0F12DB9D3 CRC64;
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Bacteria; Spirochaetes;
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Pred. No. 1.8e-09;
1; Mismatches 120
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Best Local S
Matches 74
                A Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
A Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
A Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
A Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
A Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
A Haddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
A Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H
A Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
A Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
A Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
T "Genome sequence of Halobacterium species NRC-1";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).
R EMBL, AE005046; AAC195611; -.
R InterPro; IPR001117; Cu-oxidase.
R InterPro; IPR001117; Cu-oxidase.
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SEQUENCE
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PANI OR VNG11873.
Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
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"Dissimilatory nitrite reductase oxidizing bacteria.";
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01-MAR-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=20504483; PubMed=11016950;
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AF339049; AAK53363.1; -
Pro; IPR001117; Cu-oxidase.
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23; Mismatches
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Q8YQ92;
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Complete proteome. *
SEQUENCE 379 AA; 4
                                                                                                                                          InterPro; IPR001287; CUNO2 reductase.
Pfam; PR00394; Cu-oxidase; 1.
PRINTS; PR00695; CUNO2RDTASE.
Hypothetical protein; Complete proteo;
SEQUENCE 338 AA; 38408 MW; AFBF1B
                                                                                                                                                                                                                                                                                                                 Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
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  94 VMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPDSKMPHNVDFHAATGPGGGA 153
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38 AA; 38408 MW; AFBF1BB9D01627F7 CRC64;
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Pred. No. 6.1
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Kawashima K., Kimura T.,
latsuno A., Muraki A.,
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                                                       12;
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RESULT 19
Q8RLT4
ID Q8RLT
AC Q8RLT
DT 01-JU
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Q8RLS7
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                                                                                                                                                                                                                        Query Match
Best Local S
Matches 70
  Q8RLT4;
Q8RLT4;
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBRLS7;
QBRLS7;
01-JUN-2002
01-JUN-2002
01-OCT-2002
                                                                                                                                                                                                                                                               NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               Mesorhizobium sp. 4FB11.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative dissimilatory nitrite reductase (Fragment).
                                                                                                                                                                                                                                                                                                    EMBL; AY078254; AAL82513.1; -.
InterPro; IPR001117; Cu-oxidase.
                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                           Pfam; PF00394; Cu-oxidase; 1.
                                                                                                                                                                                                                                                                                                                                   pacteria
                                                                                                                                                                                                                                                                                                                                        Nitrite reductase genes in halobenzoate degrading denitrifying
                                                                                                                                                                                                                                                                                                                                                   Song B., Ward B.B.;
                                                                                                                                                                                                                                                                                                                                                              STRAIN=4FB11
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=126151;
                                                                                      335
                                                                                                        116
                                                                                                                            278
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                                                                                                                                              88
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                                                                                                                                                                                                                                 Similarity
                                                                                      AIFRA
                                                                                                        ANRDSRPHLIGGHGDYV-WEEGKFANPPAKDLETWFIRGGSAGAALYTFLOPGVYAYVNH
                                                                                                                         PNLTSSFHVIGEIFDKVHFEGGKGEN---HNIQTTLIPAGGAAITEFKVDVPGDYVLVDH 334
                                                                                                                                            DGNFKKFDSLGESYEETMEVMRGLIPTHVVFNGRVGGLTGDNAMKSKVGETV-LFV-HSQ 115
                                                                                                                                                      VYHC--APEGMIPWHVVSGMHGTIMVLPRDGLKNEKGELVKSDTVYYIGDNEFYIP-RDE
                                                                                                                                                                                                   VYHCAVAPVGM---HIANGMYGLILVEPKEGLP-----KVDKEYYVMQGDFYTKGKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVLVMAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYYVMQGDFYTKGKYGEQGLQPFDMEKAIREDAEYVVFNGSVGALTGENALKAKVGETVR
                                                                    NLIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYVLNIIEYDPAVT--FHLHANFFDVYRY--GMSMKASEKTDVITMGVAERHILEFAFRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFVGN---GGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGGAA--ITEFKVDV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGKYMFHPHODAIAEN-GCMGQFEVVANNNONH 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGDYVLVDHAIFRAFNKGALGILKV--EGEENH 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMDGVRPVSNNSATIYEFDAEPYGVHLYHCHIEPVTRHIAKGLYGMFIIDPPTPRPPADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EASFTAP---GHTSTFSFKALQPGLYVYHCAVAPVGMHIANGMYGLILVEPKEGLPKVDK 210
                                                                                                                                                                                                                                                               179
179 AA;
                                                                                                                                                                                                                         Conservative
  (TrEMBLrel.
                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                       339
                                                                                                                                                                                                                                                               179
19893 MW;
                                                                                                                                                                                                                                  9.0%;
37.8%;
  21,
                                                                                                                                                                                                                        27;
  Created!
                                                                                                                                                                                                                      Score 236; DB 2;
Pred. No. 2.2e-08;
7; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---YDVDDNSHND--FYAFNGLPHHYM-DNPIQIYQNQLIR
                     PRT;
                                                                                                                                                                                                                                                               0060433CAD0A516C CRC64;
                     179
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                                                                                                                                                                                                                                         Length 179;
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                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                       Gaps
                                                                                                       174
                                                                                                                                                              277
                                                                                                                                                                                  57
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Q8RLT3
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Best Local Similarity
Matches 71; Conserv
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Query Match
Best Local Similarity
Matches 71; Conserv
                                                                       NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8RLT3;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative dissimilatory nitrite reductase (Fragment)
                                                                                                                                                 EMBL; AY078248; AAL82507.1; -. InterPro; IPR001117; Cu-oxidase.
                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiaceae; Ensifer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
                                                                                                                               Pfam; PF00394; Cu-oxidase;
                                                                                                                                                                                   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                         bacteria.
                                                                                                                                                                                                                                            Song B., Ward B.B.;
                                                                                                                                                                                                                                                             STRAIN=4FB6;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=126148;
                                                                                                                                                                                                                                                                                                                                                                         Ensifer sp. 4FB6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative dissimilatory nitrite reductase (Fragment)
                                                                                                                                                                                                                        "Nitrite reductase genes in halobenzoate degrading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AY078247; AAL82506.1; -. InterPro; IPR001117; Cu-oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=2FB8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobiaceae; Ensifer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ensifer sp. 2FB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nitrite reductase genes in halobenzoate degrading denitrifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Song B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TaxID=126147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 LIEA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 VYHCAVAPVGM---HIANGMYGLILVEPKEGLP-----KVDKEYYVMQGDFYTK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00394; Cu-oxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NRDTRPHLIGGHGDYV-WATGKFRNPPDLDQETWLIPGGTAGAAFYTFRQPGVYAYVNHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLTSSFHVIGEIFDKVHFEGGKGENH---NIQTTLIPAGGAAITEFKVDVPGDYVLVDHA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---GKYGEQGLQPFDMEKAIRE-DAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGP 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNYKKYETPGEAYEDAVKAMRTLTPTHIVFNGAVGALTGDHALTAAVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYHC--APEGMVPWHVTSGMNGAIMVLPRDGLKDEKGQPLTYDKIYYVGEQDFYVPKDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ward B.B.;
                                                                         179
179 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                         AA;
                                                                     179
19594 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19695 MW;
                 38.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.9%; Score 233; DB 2; 38.6%; Pred. No. 3.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alphaproteobacteria; Rhizobiales;
Score 232; DB 2;
Pred. No. 4.1e-08;
0; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last annotation
                                                                         B9EA63390E6ECF6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D94A75486978BD7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                                        Rhizobiales;
                                Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                      denitrifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --RVLVVHSQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116
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Conservative

20;

Indels

30;

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                                                                         RESULT 22
Q93TN3
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Best Local S
Matches 63
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Q93TN6,
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative dissimilatory nitrite reductase (Fragment)
   Q93TN3;
Q93TN3;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEAM; PF00394; Cu-oxidase; 1.
NON TER 1 1 1
NON TER 1A0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Casciotti K.L., Ward B.B.;
"Dissimilatory nitrite reductase genes oxidizing bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nitrosomonas marina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21218534; PubMed=11319103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nitrosomonadaceae; Nitrosomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Environ. Microbiol. 67:2213-2221(2001).
AF339044; AAK53358.1; -.
                                                                                                                                                                                                                                                                                                       59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity
63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLTSSFHVIGEIFDKVHFEGGKGENHN-----IQTTLIPAGGAAITEFKVDVPGDYVLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNYKKYETPGEAYEDAVKAMRTLTPTHIVFNGVVGALTGDHALTAAVGE--RVLVVHSQA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VYHC--APEGMVPWHVTSGMNGAIMVLPRDGLKDEKGQPLTYDKIYYVGEQDFYVPKDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYHCAVAPVGM---HIANGMYGLILVEPKEGLP-----KVDKEYYYMQGDFYTK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HNLIEA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAIFRA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRDTRPHLIGGHGDYV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GKYGEQGLQPFDMEKAIRE-DAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGP
                                                                                                                                                      NLIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                       VYHCAVAPVG----MHIANGMYGLILVEPKEGLP-----KVDKEYYVMQGDFY----T
                                                                                                                                                                                           AIFRA 339
                                                                                                                                                                                                                                                                                                     KGNFRKYDSPAAGMHEMLELSKGLIPTHVVFNGAVGAITGDNALSAKVGEKV-LFI-HSQ 116
                                                                                                                                                                                                                                                                                                                            KGKYGEQGLQPFDMEKAIRED----AEYYVFNGSVGALTGENALKAKVGETVRLFVGNGG
                                                                                                                                                                                                                                                                                                                                                                                VYHC--APGGTMIPFHVISGMNGAVMVLPRDGLKDAEGKPYRYDRTYYIGEQDYYLPQDD
                                                                                                                                                                                                                               ANRPSYPHLIGGHAD-LYWVGGSFSDTPLTSQETWFVPAGSAVAAAYEFHQPGLYVYLSH
                                                                                                                                                                                                                                                                  PNLTSSFHVIGEIFDKVHFEGGKGENHNI----QTTLIPAGGAAITEFKVDVPGDYVLVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
180 AA;
   (TrEMBLrel. 19, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19681 MW; 43E8D2BE098968FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 230.5;
Pred. No. 5.2e
33; Mismatches
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   Last
                       Created)
   sequence update)
                                                             180
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ches 62;
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Best Local Similarity
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       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nitrosomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIRK.
                                                             NON TER
NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oxidizing bacteria."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                       NIRK.
                                                                                                                                                                                                                                                                        STRAIN-URW;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=159352;
                                                                                                                       Pfam;
                                                                                                                                                                                                oxidizing bacteria."
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                                                                                                                                        nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
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                                                                                                                                                        Environ. Microbiol. 6' AF339046; AAK53360.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIFRA
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                                                           180
180 AA;
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Q93TN4 PRELIMINARY; PRT; 180 AA.
Q93TN4;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative dissimilatory nitrite reductase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Betapi
Nitrosomonadaceae; Nitrosomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative dissimilatory nitrite reductase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                Nitrosomonas sp. URW.
Bacteria; Proteobacteria; Betap
Nitrosomonadaceae; Nitrosomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21218534; PubMed=11319103;
Casciotti K.L., Ward B.B.;
"Dissimilatory nitrite reductase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appl. Environ. Microbiol. 67:2213-2221(2001)
EMBL; AF339047; AAK53361.1; -.
                                                                                                                                                                                                                                                    "Dissimilatory nitrite reductase
                                                                                                                                                                                                                                                                                                    MEDLINE=21218534; PubMed=11319103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 VYHCAVAPVG----MHIANGMYGLILVEPKEGLP-----KVDKEYYVMQGDFY----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00394; Cu-oxidase; 1.
                                                                                                                                   PF00394; Cu-oxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANRDSRPHLIGGHAD-LYWVGGSFSDTPLTSQETWWIPGGTAVAAAYEFHQPGLYVYLSH 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGKYGEQGLQPFDMEKAIRED----AEYVVFNGSVGALTGENALKAKVGETVRLFVGNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNLTSSFHVIGEIFDKVHFEGGKGENHNI----QTTLIFAGGAAITEFKVDVPGDYVLVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYHC--APGGTMIPFHVISGMNGAIMVLPRDGLKDAAGKPYQYDRAFYIGEQDFYLPQDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGNFKEYASPAAGMHEMLELSKGLVPTHVVFNGAVGAITGDNALSAKVGEKV-LFI-HSQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001117; Cu-oxidase
                                                                                                                                                              IPR001117; Cu-oxidase.
                                               180
19540 MW; BB7CA048F7CD6D29 CRC64:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.7%; Score 228.5; DB 2
35.1%; Pred. No. 7.1e-08;
8.7%;
35.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Betaproteobacteria; Nitrosomonadales;
                                                                                                                                                                                                           67:2213-2221 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Betaproteobacteria; Nitrosomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
  Score 228.5; DB 2
Pred. No. 7.1e-08;
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                                                                                                                                                                                                                                                       genes from autotrophic ammonia-
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                       Length 180;
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                                                                  RESULT 25
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Best Local Similarity
Matches 68; Conser
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    Q93TN2
Q93TN2;
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01-JUN-2002
01-MAR-2003
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative dissimilatory nitrite reductase (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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STRAIN=CH91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00283; SOYBEAN_KUNITZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002160; Kunitz legume.
Pfam; PF00394; Cu-oxidase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AY078255; AAL82514.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pacteria
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                                                                                                                                   172
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                                                                                                                                                                           VDHAIFRA 339
                                                                                                                                                                                                                                                           NGGPNLTSSFHVIGEIFDKVHFEGGKGEN---HNIQTTLIPAGGAAITEFKVDVPGDYVL 331
                                                                                                                                                                                                                                                                                                     GKYKDYA----DLGSSFQDSREAMRTLIPTHVVFNGKVGALTGDGALTAKVGETV-LFI-
                                                                                                                                                                                                                                                                                                                                             GKYGEQGLQPFDMEKAIREDAE-----YVVFNGSVGALTGENALKAKVGETVRLFVG
                                                                                                                                                                                                                                                                                                                                                                                       VYHC--APEGMVAWHVLAGMSGTLMVLPRDGLKDPEGKPLHYDRAYTIGEFDLYIPKDKD
                                                                                                                                                                                                                                                                                                                                                                                                                               VYHCAVAPVGM---HIANGMYGLILVEPKEGLP-----KVDKEYYVMQGDFY----TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIFRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNLTSSFHVIGEIFDKVHFEGGKGENHNI---QTTLIPAGGAAITEFKVDVPGDYVLVDH 334
                                                                                                                                                                                                                 HSQANRDTRPHLIGGHGDWV-WETGKFDNPPEKNLETWFIRGGSAGAALYTFQQPGVYAY 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANRDSRPHLIGGHAD-LYWVGGSFSDTPLTSQETWWIPGGTAVAAAYEFHQPGLYVYLSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYHC--APGGTMIPFHVISGMNGAIMVLPRDGLKDAAGKPYQYDRAFYIGEQDFYLPQDE
                                                                                                                                VNHNLIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339
                                                                                                                                   179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 .
19766 MW; 138BD941A73D835A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.7%; Score 228; DB 2; 36.2%; Pred. No. 7.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                        180 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 26
Q8KPM7
                                                                                                                                                                                             RRT RAX RRY OCCUR
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Best Local S
Matches 62
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8KPM7;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                                                                             MEDLINE=21914100; PubMed=11916709; Prieme A.. Braker G., Tiedje J.M.; Prieme A.. Braker G., Tiedje J.M.; Diversity of nitrite reductase (nirK and nirS) forested upland and wetland soils."; Appl. Environ. Microbiol. 68:1893-1900(2002). EMBL; AY121226; AAM94057.1; ...
                                                                SEQUENCE
                                                                                    Pfam; PF00394; Cu-oxidase; 1.
NON_TER 1 1
NON_TER 172 172
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                              NIRK
                                                                                                                                                                                                                                                                                                                                                                                                                             Nitrite reductase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8KPM7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=2121834; PubMed=11319103;
Casciotti K.L., Ward B.B.;
Clasciotti K.L., ward B.B.;
"Dissimilatory nitrite reductase genes from autotrophic ammonia-
oxidizing bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIRK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                     uncultured bacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nitrosomonas sp. C-113a.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative dissimilatory nitrite reductase
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=77133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00394; Cu-oxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF339048; AAK53362.1;
                                                                                                                                                  [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appl. Environ. Microbiol. 67:2213-2221(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=159354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nitrosomonadačeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 VYHCAVAPVG----MHIANGMYGLILVEPKEGLP-----KVDKEYYVMQGDFY----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity
62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIFRA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNLTSSFHVIGEIFDKVHFEGGKGENHNI----QTTLIPAGGAAITEFKVDVPGDYVLVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGKYGEQGLQPFDMEKAIRED----ABYVVFNGSVGALTGENALKAKVGETVRLFVGNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANRPSYPHLIGGHAD-LYWVGGSFSDTPLTSQETWFVPAGSAVAAAYEFHQPGLYVYLSH 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYHC--APGGTMIPFHVISGMNGAVMVLPRDGLKDAEGKPYRYDRAFYIGEQDYYLPQDD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGNFKKYDSPAAGMHEMLELSKGLIPTHVVFNGAVGAITGDNALSAKVGEKV-LFI-HSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001117; Cu-oxidase.
                                                                                                                                                                                                                                                                                                                                                                 environmental samples
                                                                                                                                                  IPR001117; Cu-oxidase.
                                                                172 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (TrEMBLrel. 22,
2 (TrEMBLrel. 22,
3 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nitrosomonas
                                                                19066 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19607 MW; 3720D1A6099B55DE CRC64;
8.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Betaproteobacteria; Nitrosomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
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Last annotation update)
ite reductase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 226.5; DB 2
Pred. No. 9.7e-08;
4; Mismatches 62
Score 224.5; DB 2
Pred. No. 1.2e-07;
                                                              F5C8F8FB7F83232B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
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                                                                                                                                                                                                                                  gene fragments
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                      Length 172;
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Best Local
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01-JUN-2002
01-OCT-2002
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                                                                                Cytochrome,
                                                                                                                                                                 01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                  Q9K098;
                                                                                                                                                                                                                                                                                          Q9K09B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY078250; AAL82509.1; -. InterPro; IPR001117; Cu-oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Song B., Ward B.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=3CB4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=126140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ochrobactrum sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative
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                                                                                                                                 01-MAR-2003
            Neisseria meningitidis (serogroup B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Nitrite reductase
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Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd
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meningitidis Z2491.";
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                                                                                            InterPro; IPR000345; CytC_heme_bind
InterPro; IPR003088; Cyt_CI.
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                                                            PF00034;
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            CYTOCHROME_C; 1.
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Pred. No. 1.3e-07;
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O1-DEC-2001 (TrEMBLrel. 19, Last sequence upco.

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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Ochrobactrum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8RLS9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Nîtrite reductase genes in halobenzoate degrading denitrifying bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Song B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=4FB13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=126138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
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163 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKY-----KKYDAPGDAYEDTVKVMRTLTPTHVVFNGAVGALTGDKAMTAEVGEKVLII-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKYGEQGLQPFDMEKAIREDA------EYVVFNGSVGALTGENALKAKVGETVRLFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYHC--APPGMVPWHVVSGMNGAIMVLPREGLHDGKGKALTYDKGYYVGEQDLYVPRDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYHCAVAPVGM---HIANGMYGLILVEPKEGLP-----KVDKEYYVMQGDFYT----K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ward B.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEMPATAISDADIAAVATYIMNAFDNGGGSVTEKDVKQAKNKK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVMPAIALSDQQIANVITYTLNSFGNKGGQLSADDVAKAKKTK 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQKVYESNCVACHGKKGEGRGTMFPPLYRSDFIMKKPQVLLHSMVKGINGTIKVNGKTYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKATYDSNCAACHQPDGKGVPNAFPPLANSDYLNADHARAASIVANGLSGKITVNGNQYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNHNLSR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDHAIFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -HSQANRDTRPHLIGGHGDYVWSTGKFNTPPDVDQETWFIPGGAAGAAFYTFQQPGIYAY 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178
178 AA;
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ilarity 42.7%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.4%; Score 221; DB 2;
35.3%; Pred. No. 2.2e-07;
tive 22; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 222; DB 16;
Pred. No. 1.7e-07;
4; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              867D313C8DF33COA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6A3864C883650E67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 163;
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RESULT 32
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Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                  Q8RLS8;
Q8RLS8;
01-JUN-2002
01-JUN-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PFO
NON_TER
NON_TER
SEQUENCE
                                                                                                                              Submitted (FEB-2002) to the EMBI EMBL; AY078253; AAL82512.1; -... InterPro; IPR001117; Cu-oxidase.
                                                                                                                                                                                                                                                      Ochrobactrum sp. 4FB14.
Bacteria; Proteobacteria; P
Brucellaceae; Ochrobactrum.
                                                                                    SEQUENCE
                                                                                                NON TER
                                                                                                                                                                                  "Nitrite reductase
                                                                                                                                                                                                       STRAIN-4FB14;
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          NCBI_TaxID=126139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=159351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF339045; AAK53359.1; -. InterPro; IPR001117; Cu-oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Casciotti K.L., Ward B.B., "Dissimilatory nitrite reductase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nitrosomonas sp. NO3W.
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
                                                                                                                       Pfam; PF00394; Cu-oxidase; 1.
                                                                                                                                                                      oacteria.
                                                                                                                                                                                                                                                                                                      Putative dissimilatory nitrite reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oxidizing bacteria."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21218534; PubMed=11319103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
177 VYHCAVAPVGM---HIANGMYGLILVEPKEGLP------KVDKEYYVMQGDFYTK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 VYHCAVAPVG----MHIANGMYGLILVEPKEGLP------KVDKEYYVMQGDFY----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00394; Cu-oxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Environ. Microbiol. 67:2213-2221(2001).
                                     65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _
                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGKYGEQGLQPFDMEKAIRED----AEYVVFNGSVGALTGENALKAKVGETVRLFVGNGG
                                                                                                                                                                               reductase
                                                                                                                                                                                                                                                                                                                                                                                                                            NLIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIFRA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYHC--APGGTMIPFHVISGMNGAIMVLPRDGLKDAAGKPYQYDRAFYIGEQDFYLPQDE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANRDSRPHLIGGHAD-LYWVGGSFSDTPLTSQETWWIPGGTAVAAAYEFHQPGLNVYLSH 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNLTSSFHVIGEIFDKVHFEGGKGENHNI---QTTLIPAGGAAITEFKVDVPGDYVLVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGNFKEYASPAAGMHEMLELSKGLVPTHVVFNGAVGAITGDNALSAKVGEKV-LFI-HSQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
180 AA;
                                                                                    179 AA;
                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 21, TrEMBLrel. 21, TrEMBLrel. 22,
                                                                                               179
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nitrosomonas.
                                                                                    19571 MW;
                                              8.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19491 MW;
                                                                                                                                                                                                                                                                 Alphaproteobacteria;
                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30;
                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                               halobenzoate
                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
ite reductase (Fragment).
                                                                                                                                                                                                                                                                                                                                          Created)
                                    Score 219; DB 2;
Pred. No. 3.1e-07;
9; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 219.5; DB 2;
Pred. No. 2.9e-07;
                                                                                    B3E82A9AB009F244 CRC64;
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                                     65;
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                                                                                                                                                         databases
                                                                                                                                                                                                                                                                   Rhizobiales;
                                                         Length 179;
                                     Indels
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                                                                                                                                                                                denitrifying
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                                    44;
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                                    Gaps
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Best Local
                                            01-OCT-2002
01-OCT-2002
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roesch C., Mergel A., "Biodiversity of deni acid forest soil.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel 21, Created)
01-JUN-2002 (TrEMBLrel 21, Last sequence update)
01-JCT-2002 (TrEMBLrel 22, Last annotation updat)
Copper-containing nitrite reductase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AY072263; AAL73092.1; - InterPro; IPR001117; Cu-oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Rhodospirillaceae; Azospirillum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8RT15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00394; Cu-oxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=GSF 71T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=92933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Azospirillum doebereinerae
     uncultured bacterium
                                                                                    Q8KPL0;
                                                                                                  Q8KPL0
                              Nitrite reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33
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                                                                                                                                                                                                                                                                                                     KGKYGE-----QGLQPFDMEKAIREDAEYVVFNGSVGALTGENALKAKVG 266
                                                                                                                                                                                                                                                                                                                                 FVYHC--APPGMIPWHVVSGMLRHIMVLPRDGLKDEKGKPIHYDRAYTIWEFDLYVPKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIYAYVNHNLIEA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLTSSFHVIGEIFDKVHFEGGKGE------NHNIQTTLIPAGGAAITEFKVDVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKFKKYDAPGDAYEDTVKVMRTLTPTHVVFNGAVGALTGDKAMTAAVGEKVLI--
                                                                                                                                                                                            DVPGDYVLVDHAIFRA 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- GKYGEQGLQPFDMEKAIRE-DAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VYHC--APPGMVPWHVVSGMNGAIMVLPREGLHDGKGKALTYDKIYYVGEQDFYVPRDED
                                                                                                                                                                  HQPGIYAYVNHNLIEA
                                                                                                                                                                                                                                                 ETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGEN---HNIQTTLIPAGGAAITEFKV 323
                                                                                                                                                                                                                        ETV-LFI-HSTANRDTRPHLIGGHGDYV-WERGKFVNAPEKGLETWFVAGGSAGVATYTF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                         180 AA;
                                            (TrEMBLrel. 22,
(TrEMBLrel. 22,
(TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l A., Bothe H.;
denitrifying and
                             (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                         180
19881 MW;
                                                                                                                                                                                                                                                                                                                                                                                                8.3%;
                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                     26;
                                            Last sequence update)
Last annotation update)
                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                  Score 219; DB 2;
Pred. No. 3.1e-07;
6; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                          9A4531553E7D6EFE CRC64;
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Q8BLTO OBRLT
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Best Local Similarity
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Best Local (
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QBRLT0;
01-JUN-2002
01-JUN-2002
01-OCT-2002
                                                                                                                                                                                               Pfam; PF00394; (
NON_TER 179
NON_TER 179
SEQUENCE 179
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21914100; PubMed=11916709; Prieme A., Braker G., Tiedje J.M.; Prieme A., Braker G., Tiedje J.M.; PubMersity of nitrite reductase (nirk and nirs) forested upland and wetland soils.";
                                                                                                                                                                                                                                                                                                                                                                                                  Ochrobactrum sp. 3CB5.
Bacteria, Proteobacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AY121544; AAM94075.1; -. InterPro; IPR001117; Cu-oxidase.
                                                                                                                                                                                                                                                                                                                                   STRAIN=3CB5;
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=126141;
                                                                                                                                                                                                                                                                                                                                                                                       Brucellaceae; Ochrobactrum
                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative dissimilatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; environmental
                                                                                                                                                                                                                                                                 EMBL; AY078251; AAL82510.1;
                                                                                                                                                                                                                                                                             Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                             bacteria.
                                                                                                                                                                                                                                                                                                                    Song B., Ward B.B.;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        "Nitrite reductase genes in halobenzoate degrading denitrifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CBI_TaxID=77133;
                                                                                                                                                                                                                                                  nterPro; IPR001117; Cu-oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287 IGEIFDKVHFEGGKGEN---HNIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 VGMHIANGMYGLILVEPKEGLP------KVDKEYYVMQGDEYT----KKKY-----GE
        279
                                                         223 GKYGE----QGLQPFDMEKAIRE-DAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGP
                                                                                                                177 VYHCAVAPVGM---HIANGMYGLILVEPKEGLP-----KVDKEYYVMQGDFYT----K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00394; Cu-oxidase; 1.
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                                                                                                                                           66;
                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGLQPFD-MEKAIREDAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNLTSSFHV
       NLTSSFHVIGEIFDKVHFEGGKGENHNI--QTTLIPAGGAAITEFKVDVPGDYVLVDHAI
                                 GKYKKYEAPGDADEDTVKVMRTLTPTHVVFNGAVGALTGDKAMTAAVGE--KVLIVHSQA 116
                                                                                       VYXC--APPGMVPWHVVSGMNGAIMVLPREGLHDGKGKALTYDKIYYVGEQDFYVPRDEN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPWHVVSGMHGTVMVLPRDGLKNREGKPLRYDRLYY I GENDLYVPKDEKGKYKSYETVGE
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172 AA;
                                                                                                                                                                                               179 AA;
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                                                                                                                                            Conservative
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19273 MW;
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35.2%;
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Pred. No. 4.3e-07;
                                                                                                                                                       Score 216; DB 2;
Pred. No. 4.9e-07;
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(Fragment)
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Best Local
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01-OCT-2002
01-OCT-2002
01-MAR-2003
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01-JUN-2002
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NON_TER
SEQUENCE
SEQUENCE FROM N.A.

MEDLINE=21914100; PubMed=11916709;
Prieme A., Braker G., Tiedje J.M.;
"Diversity of nitrite reductase (n
                                                                                                                    NCBI_TaxID=77133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AY078249; AAL82508.1; -.
InterPro; IPR001117; Cu-oxidase.
Pfam; PF00394; Cu-oxidase; 1.
                                                                                                                                                                                                                                                                                                                                         Q8KPM6
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Brucellaceae; Ochrobactrum.
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                                                                                                                                                                     uncultured bacterium
                                                                                                                                                                                                                  Nitrite reductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYHC--APPGMVPWHVVSGWNGAIMVLPREGLHDGKGKALTYDKIYYVGEQDFYVPRDEN
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                                                                                                                                               environmental
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179 AA;
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(TrEMBLrel.
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BLrel. 22,
BLrel. 23,
(Fragment)
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Last annotation updat
                                                                                                                                                                                                                                                                                          Created)
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3; Mismatches
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Pred. No. 5.8e-07;
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Q8KPK9
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Q8KPM5
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                                     RESULT 39
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Best Local Similarity 34.7
Matches 61; Conservative
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 Q8KPK9;
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08KPM5;
01-OCT-2002
01-OCT-2002
01-MAR-2003
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NON_TER
NON_TER
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                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; environmental samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIRK
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EMBL; AY121527; AAM94058.1;
                                                                                                                                                                                                                                                                                                                             Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uncultured bacterium
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                                                                                                                              63
                                                                                                                                                                                                                                                                                                                          PF00394; Cu-oxidase; 1.
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                                                                                                                                                   QGLQPFD-MEKAIREDABYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNLTSSFHV
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                                                                                                                              SYADTTEVMRKLI---PTHVVFNGRVGSLTGKNAMTSKVGETVMLV--HSQANRDTRPHL
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                                                                            IGGHGDYV-WEAGKFNNPPQKDLETWFVRGGSAGAALYTFREPGIYAYVNHNLIEA
                                                                                                    IGEIFDKVHFEGGKGEN---HNIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRA
                                                                                                                                                                                 VPWHVVSGMHGTVMVLPRDGLKNREGKPLRYDRLYYVGENDLYVPKDENGKYKSYETIGE
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                                                                                                                                                                                                                                                                                                                                      IPR001117; Cu-oxidase.
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172 AA;
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! (TrEMBLrel. 22, La
! (TrEMBLrel. 23, La
! (TrEMBLrel. 23, La
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              PRELIMINARY;
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y 35.1%; Pred. No. 6

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                                                                                                                                                                                                                                             Score 211.5; DB : Pred. No. 9.4e-07
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             172
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SEQUENCE
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MEDLINE=21914100; PubMed=11916709;
Prieme A., Braker G., Tiedje J.M.;
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01-MAR-2003 (TrEMBLrel. 23, L
Nitrite reductase (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00394; Cu-oxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Diversity of nitrite reductase (nirK and nirS) forested upland and wetland soils.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; environmental
NCBI_TaxID=77133;
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AY121545; AAM94076.1;
Pro; IPR001117; Cu-oxio
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172 AA;
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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                                                                                                 Score 211.5; DB 2;
Pred. No. 9.4e-07;
B; Mismatches 61;
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01-OCT-2002 (TrEMBLrel. 20, Last annotat)
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MEDLINE=2022556; PubMedca10761919;
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Klee S.R., Mozelli G., Basham D., Brown D., Chillingworth T.,
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EMBL; AL162757; CAB85110:1; -.
HSSP; P38501; 1AS8.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001287; CuNO2_reductase.
Pfam; PF00394; Cu-oxidase; 2.
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Bacteria; Proteobacteria; Betaproteobacteria;
Neisseriaceae; Neisseria.
NCBI_TaxID=65699;
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Q93w69 zea mays su
Q93w60 zea mays su
Q9pnw0 campylobact
Q8zgg3 yersinia pe
Q9zz4 rhizobium m
Q99rv1 staphylococ
Q8ckm3 yersinia pe
Q9x690 mercury res
Q9x690 mercury res
Q9x690 hesperantha
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Q8rt04 uncultured
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Q8rt07 uncultured
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QBrCx6 thermoanner
QBq4m9 bifidobacte
QBqdk4 chimpanzee
QBqdk3 chimpanzee
QBqdk1 chimpanzee
QBqdk6 chimpanzee
QBqdk6 escherichia
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Q8r189 ochrobactru
Q9fz87 bacteriopha
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STRAIN=MC58 / Serogroup B;
MEDLINE=20175755; PubMed=10710307;
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InterPro; IPR001287; CuNO2_reductase
Pfam; PF00394; Cu-oxidase; 2.
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EMBL; AE002512; AAF41975.1; -.
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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A Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
A Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
A Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
A Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
A Weissenbach J., Boucher C.A.;
T "Genome sequence of the plant pathogen Ralstonia solanacearum.";
L Nature 415,497-502(2002).
R EMBL; AL646085; CAD18654.1; -.
R InterPro; IPR000145; CuNO2 reductase.
R InterPro; IPR000345; CytC heme_bind.
R InterPro; IPR0003088; Cyt_CI.
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Pfam; PF00034; cytochrome c; 1.
PRINTS; PR00695; CUNO2RDTASE.
PROSITE; PS00190; CYTOCHROME C; 1.
Oxidoreductase; Plasmid; Complete proteome.
Oxidoreductase; Plasmid; Complete proteome.
SEQUENCE 510 AA; 54600 MW; 8008105DD99459AC CRC64;
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Avrahami S., Conrad R., Braker G.;
"Effect of Soil Ammonium Concentration on N(2)O Release and Community Structure of Ammonia Oxidizers and Denitrifiers.";
Appl. Environ. Microbiol. 68:5685-5692(2002).
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Fields M.W., Yan T., Wu L.
"Molecular diversity and of
fragments (nirK and nirS)
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                                        SEQUENCE FROM N.A.
                                                                                NCBI_TaxID=155900;
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STRAIN=B06-16-18;
Fields M.W., Yan T., W
"Molecular diversity a
fragments (nirk and ni
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                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                     252 VGALTGENALKA 263
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AF548919; AAN59843.1; -.
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characterization of nitrite reductase gene
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SEQUENCE FROM N.A.
STRAIN=B02-05-26;
Fields M.W., Yan T., W
"Molecular diversity a
             fragments (nirK and groundwater.";
Environ. Microbiol.
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STRAIN-E01-03-40;
Fields M.W., Yan T., Wu L., Zu Y., Tiedje J.M., Zhou J.;
"Molecular diversity and characterization of nitrite reductase
"molecular diversity and nirs) from nitrate and uranium-contaminated
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unclassified;
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                                     SEQUENCE
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                                                                                                                                                                                                                                                                                 uncultured organism.
unclassified; environmental samples
                                                                                                                                                                                                                                                                                                                                             Nitrite reductase (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=155900;
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                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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STRAIN=D02-05-81;
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                                                                                            AF548932; AAN59856.1;
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Q8BFK9;
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Q8BFL4;
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                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-HOI-03-137;

Fields M.W., Yan T., Wu L., Zu Y., Tiedje J.M., Zhou J.;

"Molecular diversity and characterization of nitrite reductase (
fragments (nirK and nirS) from nitrate and uranium-contaminated
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Fields M.W., Yan T., Wu I
"Molecular diversity and
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                                                                                                                                                                                                                   groundwater.";
Environ. Microbiol, 0:0-0(2002).
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NCBI_TaxID=155900;
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Environ. Microbiol.
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d characterization of nitrite reductase gene
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unclassified; enviro
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                                                                                                                                                                                                      SEQUENCE
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AF548931; AAN59855.1; -...
AF548949; AAN59876.1; -...
AF548953; AAN59876.1; -...
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Prieme A., Braker G., Tiedje J.M.;
"Diversity of nitrite reductase (nirK and nirS)
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Hyphomicrobiaceae; Hyphomicrobium.
NCBI_TaxID=48292;
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EMBL; AY121543; AAM94074.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ224902; CAA12205.1;
                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reductase
                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                  upland and wetland soils."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGALTGENALKA 83
                                                                                                                                                                                                                                                                            IPR001117;
                                                                                                                                                                          172
172 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 22, (TrEMBLrel. 23,
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                             AΑ;
                                                                                                                                                                                                                                                  Cu-oxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cu-oxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Fragment).
                                                                                                                                                                          18832 MW;
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                                                                                                  2.4%;
100.0%;
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                                                                                                                                                                                                                                                                            Cu-oxidase.
                                                                                                                                                                                                                                                                                                                        68:1893-1900(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64:3769-3775(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                    Score 12;
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Pred. No
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                                                                                                                                                                          8A7D4E22E814B686 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F76814D01D4FD1BA CRC64;
                                                                          Mismatches
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0.0013;
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                                                                                                                      Length 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 12
  Query Match
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Matches 12
                                                                                                                                                                                                                                                          Kataoka K., Fukui A., Kabayashi M., Yamaguchi K., Suzuki S., "Cloning and expression of copper-containing nitrite reductase Hyphomicrobium denitrificans.", Suzuki Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AB076606; BAC00912.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shoun H., Takaya N.;
"Alcaligenes sp. STC1 nitrite reductase gene.";
"Alcaligenes sp. STC1 nitrite reductase gene.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB046603; BAB21510.1; -.
HSSP; P25006; INIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hyphomicrobium denitrificans.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Hyphomicrobiaceae; Hyphomicrobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0695; CUNO2RDTASE.
PRINTS; PRO0695; CUNO2RDTASE.
PROSITE; PS00283; SOYBEAN_KUNITZ; 1.
SEQUENCE 360 AA; 39072 MW; CAF063CB38430380 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIRK.
Alcaligenes sp. Sitt.
Bacteria; Proteobacteria; Be
Bacteria; Alcaligenes.
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=A3151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8KKH4;
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPRO01117; Cu-oxidase.
InterPro; IPR001287; CuNO2 reductase.
InterPro; IPR002160; Kunitz legume.
Pfam; PF00394; Cu-oxidase; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001
01-MAR-2003
                                                                                                  SEQUENCE
                                                                                                                                                                    PROSITE; PS00079; MULTICOPPER_OXIDASE1;
                                                                                                                                                                                                PRINTS; PR00695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nitrite reductase precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=STC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                             InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001287; CuNO2_reductase.
PRINTS; PR00695; CUNO2RDTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=53399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
12; Conserv
  Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPHNVDFHAATG 148
                                                                                                486 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. (TrEMBLrel.
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.4%;
                                                                                           39
52238 MW; 6984E02ECEF791AF CRC64;
                         2.4%; Score 12;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17, Created)17, Last sequence update)23, Last annotation update)
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Pred. No.
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  Mismatches
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o. 0.003;
0;
                                             DB 2; Length 486;
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                           0.004;
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  Indels
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Best Local S
Matches 11
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01-MAR-2003
01-MAR-2003
01-MAR-2003
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Q8BFL0;
01-MAR-2003
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SEQUENCE
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                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                    groundwater."
                                                                                                                                                                                                                                                                                                                                                                                                                                  NIRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              groundwater.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fields M.W., Yan T., "Molecular diversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=H02-05-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uncultured
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nitrite
                                                                                                                                                                                                                        Environ.
                                                                                                                                                                                                                                                         "Molecular diversity and characterization of nitrite reductase fragments (nirK and nirS) from nitrate and uranium-contaminated
                                                                                                                                                                                                                                                                             "Molecular diversity
                                                                                                                                                                                                                                                                                                                STRAIN=G02-05-110;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             unclassified;
                                                                                                                                                                                                                                                                                                                                                                                                           uncultured organism
                                                                                                                                                                                                                                                                                                                                                                                                                                               Nitrite reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Environ.
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                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=155900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eragments (nirK and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity
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                                                                                                                                                                                                     AF548950; AAN59873.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF548945; AAN59868.1; -.
 64
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                                                                                           Similarity
                                                                                                                                                                                                                          Microbiol.
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                             GALTGENALKA
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                                                                                                                                               102
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ed; environmental
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                                                                                                                                               102 :
11264 MW;
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 74
                                  263
                                                                     2.2%; Score 11; DB
100.0%; Pred. No. 0.
Live 0; Mismatches
                                                                                                                                                                                                                                                                             Wu L., Zu Y., Tiedje J.M., Zhou J.; and characterization of nitrite reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73
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Pred. No.
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Best Local S
Matches 10
  Query Match
Best Local Similarity
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01-OCT-2002
01-OCT-2002
01-MAR-2003
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Copper-containing dissimilatory nitrite reductase precursor
(EC 1.7.99.3).
                                                                                                                    NON_TER
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=21914100; PubMed=11916709;
Prieme A., Braker G., Tiedje J.M.;
"Diversity of nitrite reductase (nirK and nirS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             archaeon, Haloarcula marismortui.";
J. Bacteriol. 183:4149-4156(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Purification, characterization, and dissimilatory nitrite reductase from
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Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Haloarcula.
                                                                                      SEQUENCE
                                                                                                                                                                                Pfam;
                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uncultured
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nitrite
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Pfam; PF00394; Cu-oxidase; 1.
PRINTS; PR00695; CUNO2RDTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P38501; 1AS8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujiwara T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ichiki H.,
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                                                                                                                                                                                                                                                                                               forested
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _TaxID=77133;
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                                                                                                                                                                                                     Environ. Microbiol. 6
AY121559; AAM94090.1;
Pro; IPR001117; Cu-oxio
                                                                                                                                                                             PF00394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AJ278286; CAB93142.1;
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10; Conserv
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172
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Y., Mochizuki K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361
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                                                                                      18829 MW;
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  Score 9;
Pred. No.
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COPPER-CONTAINING DISSIMILATORY
REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                      995E2A402D3DA095 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                annotation update)
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MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

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MEDLINE=21156231; PubMed=11258796; MEDLINE=21156231; PubMed=11258796; Hayashi M., Makino K., Ohnishi M., Ihan C.-G., Ohtsubo E., Nakayama K.,
                                                  SEQUENCE FROM N.A. STRAIN=0157:H7 / R
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EMBL; AP004600; BAC14034.1; -.
Isomerase; Complete proteome.
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Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from
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                                                                                                                                                                                                                                                                                                   QBKPM6;
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MEDLINE-21914100; PubMed=11916709;
MEDELINE-21914100; PubMed=11916709;
Prieme A., Braker G., Tiedje J.M.;
"Diversity of nitrite reductase (nirK and forested upland and wetland soils.";
forested upland and wetland soils.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; environmental samples.
NCBI_TaxID=77133;
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SEQUENCE FROM N.A.
MEDLINE=21914100; PubMed=11916709;
Prieme A., Braker G., Tiedje J.M.;
"Diversity of nitrite reductase (nirK and
                                                                                                                                                                                       NIRK.
                                                                                                                                                                                                                               01-MAR-2003
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EMBL; AY121567; AAM94098.1;
                                                                                                                                          Bacteria;
                                                                                                                                                           uncultured bacterium
                                                                                                                                                                                                          Nitrite reductase
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                                                                                                              NCBI_TaxID=77133;
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InterPro; IPR002160; Kunitz_legu
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171 AA;
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RESULT 31
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Matches
QBPVI5 PRELIMINARY;
QBPVI5;
QBPVI5;
Q1-OCT-2002 (TrEMBLrel. 22, C
Q1-OCT-2002 (TrEMBLrel. 22, L
Q1-MAR-2003 (TrEMBLrel. 23, L
Tungsten formylmethanofuran d
1.2.99.5).
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01-JUN-2002
01-JUN-2002
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF
NON_TER
NON_TER
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MEDLINE=21929760; PubMed=11932238;
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Pfam; PF01493; GXGXG; 1.
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EMBL; AE010745; AAM04271.1; -.
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Pfam; PF00394; Cu-oxidase; 1.
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172 AA;
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
------ Aehvdrogenase, subunit C.
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Conservative
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Last annotation update)
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Pred. No.
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5. 27;
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RESULT 32
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J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
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[1]
[1]
SEQUENCE FROM N.A.
STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / MEDLINE=22120827; PubMed=12125824;
MEDLINE=22120827; PubMed=12125824;
MEDLINE=22120827; PubMed=12125824;
MEDLINE=22120827; PubMed=12125824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97471969; PubMed=9330910; Sato S., Kotani H., Nakamura Y., Kaneko T., A Miyajima N., Tabata S.; "Structural analysis of Arabidopsis thaliana features of the 1.6 Mb regions covered by twe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
ABC transporter-like protein (Fragment)
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EMBL; AE01345; AAW31674.1; -.
InterPro; IPRO02489; DUF14.
Pfam; PF01493; GXGXG; 1.
Oxidoreductase; Complete proteome.
SEQUENCE 252 AA; 26742 MW; 59CA399B11BBEIAC CRC64;
                                                                                                                                                                                                                                                                          ProDom; PD000006; ABC_transporter; SMART; SM00382; AAA; I.
PROSITE; PS00211; ABC_TRANSPORTER;
                                                                                                                                                                                                                                                                                                                                                                                   -i- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY EMBL; AB005235; BAB17024.1; -. Interpro; IPR003593; AAA ATPase. Interpro; IPR003593; AAA Transporter. Pfam: PF00005. ABC transporter.
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ProDom; PD000006; ABC transporter; 1.
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Arabidopsis thaliana (Mouse-ear cress).
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Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                     ATP-binding; Transport.
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01-MAR-2003
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"Cloning and Expression of Copper Nitrite Reductase Gene
Alcaligenes xylosoxidans GIFU1051.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB013078; BAA33678.1; -.
EMBL; AB013078; BAA33678.1; -.
HSSP; P25006; 1NIF.
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EMBL; AP004173; BAC44653:1; -. Complete proteome
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Suzuki E., Horikoshi
Submitted (MAR-1998)
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NCBI_TaxID=515;
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                                                                                                                                         InterPro; IPR001287; CuNO2_reductase
Pfam; PF00394; Cu-oxidase; 2.
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Sasaki Y., Ishikawa J., Yamashita A.,
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NCBI_TaxID=28227;
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STRAIN=Z2491 / Serogroup A / Serotype 4A;

MEDLINE=20222556; PubMed=10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd

Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
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MEDLINE=20175755; PubMed=10710307;

MEDLINE=20175755; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E. Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Dougherty B.A., Nelson T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
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InterPro; IPR000051; !
Hypothetical protein;
SEQUENCE 483 AA; 5:
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Bacteria; Proteobacteria; Betaproteo
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EMBL; AE002381; AAF40694.1; -.
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NCBI_TaxID=491;
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SORBERRA
Oryza sativa (Rice).
Eukaryota, Viridiplantae; Strep
Epermatophyta; Magnoliophyta; L
Ehrhartoideae; Oryzeae; Oryza.
NCBI TaxID=4530;
[1]
                                                                                               Q9AV50 PRELIMINAKI; ....,
Q9AV50;
Q9AV50;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation updat
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Q98I12;
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasawatanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimot Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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Nature 404:502-506(2000).
EMBL; AL162752; CAB83340.1; -.
                                                                                        OSJNBA0093B11.1
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InterPro; IPR006094; Oxid_FAD_bind
Pfam; PF01565; FAD_binding_4; 1.
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01-OCT-2002
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"Complete DNA sequence of a
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100.0%; Pred.
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100.0%; Pred. No.
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                                            Streptophyta; Embryophyta; Tracheophyta; yta; Liliopsida; Poales; Poaceae;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr P.C. Halao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S. Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V. Quackenbush J., White O., Salzberg S.L., Fraser C.M.; "Ofrya sativa chromosome 10 BAC OSJNBa0093B11 genomic sequence."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; ACO24594; AAK21352.1; -.
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,

Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,

Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,

Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,

Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki

Davis R.W., Ecker J.R., Theologis A.,
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"Full Length CDNA of gene At5903910 (GI:15237574).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABC transporter-like protein (Putative ABC transporter protein F8F6, 120 OR ATSG03910.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magmoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Gramens, Q9Av50; ...
InterPro; IPR001159; DS_RBD.
InterPro; IPR002965; P_rich_extensn.
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EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                           gene At5g03910 (GI:15237574).";
to the EMBL/GenBank/DDBJ databases.
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C.Y., VanAken S.E.,
Feldblyum T.V.,
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Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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InterPro; IPR001140; ABC_TM_transpt.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00664; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
Propom; PD00006; ABC_transporter; 1.
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PROSITE; PS00211; ABC_TRANSPORTER;

ATP-binding; Transport.
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Science 282:2012-2018(1998).
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503
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ep; F20D1.6; CE09499.
NCE 915 AA; 104585
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nitrite reductase (EC 1.7.99.3) NMB1623 [similarity] - Neisseria meningitidis (stra N,Alternate names: outer membrane protein Panl homolog c;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: E81062 R;Tetteslin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eiser Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, ri, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000 Science 287, 1809-1815, 2000 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, F. A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, F. A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, F. A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, F. A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, F. A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, F. A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, F. A;Authors: Grandi, G.; Sun, L.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
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A;Residues: 1-392 <HOE>
A;Note: sequence extracted
C;Keywords: oxidoreductase
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C;Keywords: oxidoreductase
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A; Residues: 1-363 < ZI
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nitrite reductase (EC 1.7.99.3) Pan1 [similarity] N;Alternate names: outer membrane protein Pan1 (C;Species: Neisseria gonorrheeae C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 C;Accession: A49208 R;Hoehn, G.T.; Clark, V.L. Infect. Immun. 60, 4704-4708, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Nolecule type: DNA
A;Molecule type: DNA
A;Residues: 1-390 <TET>
A;Cross-references: GB:AE002512; GB:AE002098; NID:g7226866; PIDN:AAF41975.1; PID:g72268
A;Cross-references: GB:AE002512; GB:AE002098; NID:g7226866; PIDN:AAF41975.1; PID:g72268
                                                                                                                                                                                                                                                                                           (EC 1.7.2.1) (EC 1.7.2.1) - Pseudomonas aureofaciens C;Species: Pseudomonas aureofaciens C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #t
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                                                                                                                              :Keywords: copper; oxidoreductase
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A;Status: preiimin, A;Status: preiimin, A;Status: preiimin, A;Nolecule type: nucleic acid A;Nolecule type: nucleic acid A;Nolecule type: nucleic acid A;Nolecule type: nucleic acid A;Cross-references: GB:L04474; NID:g147530; PIDN:AAA24508.1; PID:g147532 A;Cross-references: GB:L04474; NID:g147530; PIDN:AAA24508.1; PID:g147532 A;Cross-references: GB:L04474; NID:g147530; PIDN:AAA24508.1; PID:g147532 A;Cross-references: GB:L04474; NID:g147530; PIDN:AAA24508.1; PID:g147532
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Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: D64744
                                                                                                                                                               A;Gene: ECs0198
C;Superfamily: Escherichia coli exopolysaccharide
                                                                                                                                                                                                                                                                                                                                                           A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
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C;Accession:
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A; Residues: 1-134 <HAY>
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A;Accession: F90653
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;Accession: D64744; B47040
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Kasunaga, T.; Kuhara, S.;
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C;Accession: JE0215
R;Vandenberghe, I.H.M.; Meyer, T.E.; Cusanovich, M.A.; Van Beeumen, J.J.
Biochem. Biophys. Res. Commun. 247, 734-740, 1998
Biochem. Biophys. Res. Commun. 247, 734-740, 1998
A;Title: The covalent structure of the blue copper-containing nitrite reductase
A;Reference number: JE0215; MUID:98321197; PMID:9847763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 1-336 < VAN>
C; Comment: This enzyme is 1
C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: F85504
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Maviller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Nature 409, 529-533, 2001
  A;Cross-references: GB:AF051831
C;Keywords: copper; oxidoreduct
                                                                                              Biochem. Biophys. Res. Commun. 255, 427-431, 1999
A;Title: Cloning, sequencing, and transcriptional studies
A;Reference number: JG0170; MUID:99160880; PMID:10049725
A;Accession: JG0170
                                                                                                                                                                                                     nitrite reductase (BC 1.7.99.3) - Alcaligenes denitrificans subsp. xylosoxydans C;Species: Alcaligenes denitrificans subsp. xylosoxydans C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000 C;Accession: JG0170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Achromobacter xylosoxidans
C;Date: 21-Aug-1998 #sequence_revisio;
C;Accession: JE0215
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C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: rcsF
C;Superfamily: Escherichia coli exopolysaccharide synthesis regulator
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                                          A;Molecule type: DNA
A;Residues: 1-360 <SUZ>
                                                                                 A;Status: preliminary
                                                                                                                                                                                    R;Suzuki, E.; Horikoshi, N.; Kohzuma,
                                                                                                                                                                                                                                                                                                                 RESULT 9
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copper; oxidoreductase
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R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A. rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschin A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: D64333
A;Status: preliminarv. m.cl.:
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C;Species: Methano
C;Date: 13-Sep-1996
C;Accession: D64333
R;Bult, C.J; White
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A;Start codon: GTG
C;Superfamily: pyruvate synthase
C;Keywords: coenzyme A; oxidored
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-389 <BUL>
                                                                                                                                                                                                                                                                                                                            A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, A; Title: Complete genome sequence of Neisseria meningitidis serog. A; Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                              R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eiser Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein NMB0240 [imported] - Neisseria meningitidis (strain MC C;Species: Neisseria meningitidis C;pate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
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C;Genetics:
                                                                                                                                                                                                              Residues: 1-483 <TET>
Cross-references: GB:AE002381;
Experimental source: serogroup
                                                                                                                                                                                                                                                                       Status: preliminary Molecule type: DNA
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B, strain MC58
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A; Experimental source: strain 1
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A; Residues: 1-494 < PAR>
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                                    AAAKTANA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Achtman, M.; James, Jagels, K.; Leather,
                                                                    Conservative
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte. C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch. A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle. iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinose, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sakowska, A.; Sero akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, I., Althors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Roference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable integral membrane protein NMA0020 [importe C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 C;Accession: H81992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: אייאיטיבי
C;Superfamily: Neisseria meningitidis probable integral membrane
                                                                                                                                                                                      A; Gene: yfic C; Superfamily: Escherichia coli ABC transporter mdlA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABC transporter (ATP-binding protein) homolog yfic - Bacillus subtilis C_iSpecies: Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                         ;Keywords: ATP; nucleotide binding; P-loop;382-576/Domain: ATP-binding cassette homology <ABC>;399-406/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Date: 05-Dec-1997 #sequence_revision 05-Dec-1997
                                                                                                                                                                                                                                                                               ; GB:AL009126; NID:g2633055; 168
Score 8; DB 2; Pred. No. 20; 0; Mismatches
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S.; Moule, S.;
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              DB 20;
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17;
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Mungall,
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  0
                                                      Length 604;
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    Neisseria meningitidis

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ll, K.; Quail,
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                                                                                                                                                                                                                                                                                                         PIDN: CAB12651.1;
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M.A.;
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Rajandream,
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cytochrome c555 - (C;Species: Chlorobi
C;Date: 13-Jul-1981
C;Accession: A00116
R; Van Beeumen, J.; Ambler, R.P.; Meyer, T.E.; Kamen, M.D.; Blochem. J. 159, 757-774, 1976
A;Title: The amino acid sequences of the cytochromes c-555 A;Reference number: A00116; MUID:77087088; PMID:188412
A;Accession: A00116
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: X
A;Introns: 45/3; 75/3; 126/3; 166/2; 196/3; 243/3; 271/2; 321/1; C;Superfamily: Caenorhabditis elegans hypothetical protein F20D1
                                                                                                                                                                                                RESULT 16
CCCF55
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A;Experimental source: clone F20D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, August 1996
A;Reference number: Z19382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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A; Residues: 1-634 <BEV>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-915 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F20D1.6 - Caenorhabditis elegans
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                                                                                                                     ;Species: Chlorobium sp.
;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 03-Mar-2000
;Accession: A00116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: T21147
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Best Local
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8; Conserv
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Pred. No.
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                                                                                                  T.E.; Kamen, M.D.; Olson, J.M.; Shaw,
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o. 28;
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21;
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                                                             two green sulphur bacte
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A;Note: the source is designated as Chlorobium thiosulfatophilum
R;Korszun, Z.R.; Salemme, F.R.
Proc. Natl. Acad. Sci. U.S.A. 74, 5244-5247, 1977
A;Title: Structure of cytochrome c555 of Chlorobium thiosulfatophilum: primitive low-po-
A;Reference number: A38043; MUID:78094383; PMID:202947
A;Contents: annotation; X-ray crystallography, 2.7 angstroms
C;Comment: This basic c-type monoheme cytochrome has been found exclusively in the gree-
low redox potential compared with mitochondrial cytochrome c. It is reactive with cyto-
C;Superfamily: cytochrome c6; cytochrome c6 homology
C;Superfamily: cytochrome c6; cytochrome c6 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; photosynthesi
F;14.81/Domain: cytochrome c6 homology cYCc>
F;14,17/Binding site: heme (Cys) (covalent) #status experimental
F;18,60/Binding site: heme iron (His, Met) (axial ligands) #status experimental
                                                                                                                                                                                          R;Cohen, J.H.M.; Guetard, D.; Philbert, F.; Chamaret, submitted to the EMBL Data Library, January 1995
A;Description: A novel HIVI-O strain illustrates the
                                                         A; Molecule type: genomic RNA
A; Residues: 1-104 < COH>
                                                                                                                                                                                                                                                                                                  GP41 ENV protein - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-98 <KUR>
A;Cross-references: GB;AE008689; PIDN:AAL44933.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner, I.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Atu4133 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
A; Cross-references: C; Superfamily: type
                                                                                                                                       A; Reference number: S52929
A; Accession: S52930
                                                                                                                                                                                                                                                                           C; Accession:
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                                                                                                             A;Status: preliminary
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A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Authors: Yoo, H.; Tao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: AG3064
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Best Local (
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Gene: Atu4133
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  nces: EMBL:X84328; NID:g695526; PIDN:CAA59066.1; PID:g695527
type E retrovirus env polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.4%;
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39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PID:g17742587; GSPDB:GN00187
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                                                                                                                                                                                                diversity of the O group
                                                                                                                                                                                                                                                 S.; Tabary, T.; Montagnier,
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A; Molecule type: DNA A; Residues: 1-109 < MON A; Residues: 1-109 < MON A; Residues: 1-109 < MON A; Residues: PIDN: CAA40633.1; A; Cross-references: EMBL: X57359; NID: 945542; PIDN: CAA40633.1; C; Superfamily: ribulose-bisphosphate carboxylase small chain C; Keywords: carbon-carbon lyase; carboxy-lyase
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                                                                                                                                                                                                                                                                                 A;Residues: 1-111 <AQF>
A;Cross-references: GB:AE000730; NID:g2983674;
A;Experimental source: strain VF5
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A;Accession: A70407
                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein aq_1239 - Aquifex aeolicus C;Species: Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jun-2000 C;Accession: A70407
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A; Title: Sequence analysis and phylogenetic reconstruction
aryote Prochlorothrix hollandica.
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ribosomal protein S9 [similarity] - Lactococcus lactis subsp. lactis (strain C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-May-2002
                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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                                                 E86906
                                                                RESULT 21
                                                                                                                                                                                                                                    ;Gene: aq_1239;
;Superfamily:
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                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                        R;Ogata, H.; Audic, S.;
Science 293, 2093-2098,
A;Title: Mechanisms of
                                                                                                                                                                                                                                     RESULT
B97802
                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: transcription C; Keywords: transcription
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AF3315
                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-161 <KUR>
                                 A; Cross-references:
                                                                                           A; Accession: B97802
                                                                                                           A; Reference number: A97700;
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A;Residues: 1-157 <KUR>
A;Cross-references: GB:
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les 7; Conserv
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hypothetical protein RC0818 [imported] - Rickettsia conorii (strain Malish C;Species: Rickettsia conorii C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001 C;Accession: B97802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten A;Reference number: AD3252; PMID:11756688
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A;Residues: 1-130 <STO>
A;Cross-references: GB:AE005176; PID:g12725323; PIDN:AAK06351.1;
A;Experimental source: strain IL1403
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C;Superfamily: transcription elongation factor
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                                                                                                                                                                                                                                                                                                                                                                                                    EGDTIEV 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                 S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:AE008917; PIDN:AAL51689.1;
GB:AE006914;
                                                                                                                     Evolution
                                                                                                                                                2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4%; 5c-
100.0%; Pr/
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                                                                                                      ution in Rickettsia conorii and MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 2; Pred. No. 56; 0; Mismatches
PIDN: AAL03356.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7; DB 2; Pred. No. 65; 0; Mismatches
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PMID:11337471
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PID:g15619918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:g17982422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89
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                                                                                                                            Rickettsia
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                                                                                                                                                                                                               22-Oct-2001
  GSPDB:GN00173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weissenbach,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: membrane-bound cytochrome cycM; cytochrome c homology C;Keywords: chromoprotein; heme; iron; metalloprotein #544,87/Binding site: heme (Cys) (covalent) #status predicted F;88/Binding site: heme iron (His) (axial ligand) #status predicted F;150/Binding site: heme iron (Met) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: A97742
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A;Molecule type: DNA
A;Residues: 1-175 <KUR>
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                                                                                                                                                                                                                                                                                                                                      A;Title: Genome sequence of Yersinia pestis, the causative agent of plague A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                           A;Gene: YPO1613
                                                                                                                                                                                                                                               A;Cross-references:
                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-191 < KUR>
                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                     A; Accession: AH0196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable lipoprotein YPO1613 [imported] - Yersinia pestis (strain CO92)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A97742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;Cross-references: GB:AE006914; PIDN:AAL02875.1; PID:g15619399; GSPDB:GN00173
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Best Local S
Matches 7
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Best Local
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                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [imported] - Rickettsia conorii (strain Malish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                              EVPPPVD 77
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                                                           EVPPPVD
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                                                                                                                                                                                                                                            GB:AL590842; PIDN:CAC90435.1;
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100.0%; Pred. No.
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Pred. No.
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77;
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o. 72;
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probable outer membrane protein ECs2515 [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli
C;Bare: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: C90943
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                                                                           C90943
                                                                                          RESULT 28
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RESULT

26

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R;Fulda, M.; Heinz, E.; Wolter, F.P.

Mol. Gen. Genet. 242, 241-249, 1994
A;Title: The fadD gene of Escherichia coli Kl2 is located close
A;Reference number: $41588; MUID:94150456; PMID:8107670
A;Accession: $41588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: F64941; S41588
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Ct. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 5
A;Introns: 7/3; 101/3
C;Superfamily: beta-galactoside-binding lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: Î-192 <BLA>
A;Cross-references: EMBL:U64852; PIDN:AAB04967.1; GSPDB:GN00023; CESP;W01A11.4
A:Experimental source: strain Bristol N2; clone W01A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Blanchard, M.; Bradshaw, H. submitted to the EMBL Data Library, July 1996 A;Description: The sequence of C. elegans cosmid WOIA11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein WOLA11.4 - C;
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_rev
C;Accession: T29645
                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 121-123,'P',125-193 < FUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: The complete genome sequence of Escherichia coli K-12
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE000275; GB:U00096; NID:g1788106; A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-193 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: CESP:W01A11.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: F64941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rnd protein - Escherichia coli (strain K-12)
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Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
Accession: F64941; S41588
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                                      ALMLSGC 23
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                                                                               Score 7; DB; Pred. No. 78
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5. 78;
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C.G.

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R;Hayashi, T.; Makino, A., J., Shiba, T.; Hattur, ..., Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattur, ..., DNA, Res. 8, 11-22, 2001

DNA, Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7

A;Trance number: A99629; MUID:21156231; PMID:11258796
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A; Molecule type: DNA
A; Residues: 1-193 <HAY>
A; Residues: 1-193 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB35938.1; PID:g13361982;
A; Cross-references: Strain O157:H7, substrain RIMD 0509952
                                                                                                                              , S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AD0725
                                                                                                                                                                                                                                                                                                                                                                                                                                probable lipoprotein STY1949 [imported] - Salmonella enterica subsp. enterica (;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AD0725
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C;Genetics:
C;Superfamily: rnd protein
                                     A; Molecule type: DNA
A; Residues: 1-193 <P
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th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd,
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AD0725
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A; Residues: 1-193 <S'
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GB:AL513382; PIDN:CAD05502.1; PID:g16503006; GSPDB:GN00176
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l, L.; White, N.; Farrar,
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PEGAPQA 83

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C;Genetics:
A;Gene: STY1949
C;Superfamily:
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A;Cross-references: GB.AE000944; GB:AE000782; NID:g2668267; PIDN:AAB88937.1; PID:g26482
C;Superfamily: rat ribosomal protein L15
C;Keywords: cytosol; nucleotide binding; P-loop; protein biosynthesis; ribosome
F;160-168/Region: nucleotide-binding motif A (P-loop)
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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, Smith, H.O.; Woese, C.R.; Venter, J.C.
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C;Accession: G69539
                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-202 <SEE>
A;Cross-references: EMBL:AL096852;
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                    R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, submitted to the EMBL Data Library, July 1999 A;Reference number: Z21598
A;Accession: T36138
                                                                                                                                                                                                                                                                                                                                 hypothetical protein SCE19A.15c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 08-Sep-2000
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                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-194 <K
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probable sigD protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C;Accession: C70737

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, (Connor, R.) Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genomular number: A70500; MUID:98295987; PMID:9834230

A;Accession: C70737
                                                                                                                                                                                                                                                                                                          RESULT 35
C70737
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Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant

noference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable harpin-induced protein (imported) - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #semiance recipies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-211 <STO>
A;Cross-references: GB:
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R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
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Best Local S
Matches 7
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Best Local
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Gene: AT4g09590
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preliminary; nucleic acid sequence not
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84;
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shown; translation not shown
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R;Wu, X.; Le, T.T. submitted to the EMBL Data Library, November 1996 submitted to the EMBL Data Library, November 1996
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A;Experimental source: strain H37Rv
C;Genetics:
                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-215 <POG>
A;Cross-references: EMBL: Z47
C;Superfamily: proline-rich
                                                                                                                                                                                                   A;Reference number:
                                                                                                                                                                                                                                                                                          probable arabinogalactan protein precursor - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
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A; Introns: 12/1; 43/3; 78/3; 108/3; 155/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U80448; PIDN:AAB37817.1; GSPDB:GN00019; A;Experimental source: strain Bristol N2; clone F59A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F59A3.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
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A; Residues: 1-212 < COL>
A; Cross-references: GB:
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                                                                                                                                                                                                                A; Title: Characterization of a cDNA encoding the protein A; Reference number: S55925; MUID:95322597; PMID:7599320
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A;Gene: CESP:F59A3.5
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7; Conserv
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PKTPAPA 51
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                                                                                                                                       EMBL: Z47980; NID: g872126; PIDN: CAA88023.1;
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100.0%; Pred. No. 84
tive 0; Mismatches
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100.0%; Pred. No.
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84;
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RESULT 38

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C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999
C;Accession: 138849
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; I Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of A;Reference number: 138849; MUID:95140419; PMID:7838529
A;Accession: 138849
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G91207
                                            A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-238 <RES>
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A;Gene: CESP: CO3B1.9
A;Introns: 29/1; 116/1; 134/3; 192/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid CO3B1
A;Reference number: Z18340
A;Accession: T15381
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C;Accession: G91207
                                                                                                                                                                                                                                                                                                               LERK-3 - human
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;Residues: 1-230 <MAR>
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Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999;Accession: T15381
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;Cross-references: GB:BA000007; PIDN:BAB38054.1; PID:g13364106; GSPDB:GN00154
;Experimental source: strain O157:H7, substrain RIMD 0509952
Genetics:
                      Cross-references: EMBL:U14187; NID:g642832; PIDN:AAC50078.1; PID:g642833
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Best Local Similarity
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Search completed: August 27, 2003, 18:45:53
Job time : 72 secs

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
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September 5, 2003, 08:38:48 ; Search time 5500 Seconds (without alignments) 3733.933 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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Moraxella catarrhalis
Bacteria; Proteobacteria;
Moraxellaceae; Moraxella.
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           GlyHisThrSerThrPheSerPheLysAlaLeuGlnProGlyLeuTyrValTyrHisCys
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 Moraxella catarrhalis
Moraxella catarrhalis
                                               1509 bp
from Patent W00119996
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RESULT 2 AX098866 LOCUS DEFINITION	B	γO	DЬ	γQ	90	γQ	рь	Qy	ф	Ş	Db	γQ	дь	γQ	Вb	γ	Db	Qy	Дb	Ş	DЬ	δ	Дb	δ	В	Ş	Db	8	ф	γQ	DЪ	γQ
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                                                                         GlyHisThrSerThrPheSerPheLysAlaLeuGlnProGlyLeuTyrValTyrHisCys
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/mol_type="genomic DNA/db_xref="taxon:480"
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ANADNAASQEHQEELPVIDAIVTHAPBVPPPVDRDHPAKVVVLOMETVEKVMRLADGVE
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GHTSTTESFKALQPGLYVYLCAVAPVGHIANGMYGLLLVEPKEGLPKVDKEYYVMQGD
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VNGNQYESVMPAIALSDQIANVITYTLNSFGNKGGQLSADDVAKAKKTKPN"

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Qy 221 ThrLysGlyLysTyrGlyGluGlnGlyLeuGlnProPheAspMetGluLysAlaIleArg 240 	201 ProLysGluGlyLeuProLysValAspLysGluTyrTyrValMetGlnGlyAspPheTyr	Qy 181 AlaValAlaProValGlyMetHisIleAlaAsnGlyMetTyrGlyLeuIleLeuValGlu 200	Qy 161 GlyHisThrSerThrPheSerPheLysAlaLeuGlnProGlyLeuTyrValTyrHisCys 180	Oy 141 ValAspPheHisalaAlaThrGlyProGlyGlyGlyAlaGluAlaSerPheThrAlaPro 160	Qy 121 GluGlyAspThrIleGluValGlnPheSerAsnHisProAspSerLysMetProHisAsn 140	Qy 101 ValGluTyrGlnPheTrpThrPheGlyGlyGlnValProGlyGlnMetIleArgValArg 120	Qy 81 ProAlaLysValValValLysMetGluThrValGluLysValMetArgLeuAlaAspGly 100	Oy 61 ValileAspAlaileValThrHisAlaProGluValProProValAspArgAspHis 80	Oy 41 AlaAlaLyeThrAlaAsnAlaAspAsnAlaAlaSerGlnGluHisGlnGlyGluLeuPro 60	Qy 21 SerGlyCysSerAsnGlnAlaAspLysAlaAlaGlnProLysSerSerThrValAspAla 40	Qy 1 MetSerLysBroThrLeuIleLysThrThrLeuIleCysAlaLeuSerAlaLeuMetLeu 20	Indels: 6 Gaps: 2) x AX067454 (1-66986)	: imilar imilar	NT 18889	Bource	TITLE Nucleotide sequences of moraxella catarrhalis genome JOURNAL Patent: WO 0078968-A 29 28-DEC-2000; Incyte Genomics, Inc. (US) FEATURES Incertion/Onalifiers	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  Moraxellaceae; Moraxella.  REFERENCE 1  AUTHORS Lagace R.E. Patterson C. and Berg K.L.	
AUTHORS Salanoubat,M. AUTHORS Arlat,M., Bil Chandler,M., Gaspin,C., La	Ralstonia Ralstonia Bacteria; Burkholder	ACCESSION AL646085 AL646 VERSION AL646085.1 GI KEYMORDS	AL646085/c LOCUS AL646085 DEFINITION Ralstonia	501 FIGASII         5242 CCAAAC	5182 5182	5122	5062	Qy 421 PREPROPE            Db 5002 TICCCACC	4942	4882	4822	341 4762	Qy 321 PheLysVa           Db 4702 TTTAAGGT	Qy 301 GlyGluAs          Db 4642 GTGAAAA	Qy 281 ThrserSe                     Db 4582 ACATCATC	Qy 261 LeuLysAl           Db 4522 CTAAAAGC	Qy 241 Gluaspal          Db 4462 GAAGATGC	
.,M., Genin,S., Artiguenave,F., Gouzy,J., Mangenot,S., Billault,A., Brottier,P., Camus,J.C., Cattolico,L., M., Choisne,N., Claudel-Renard,C., Cunnac,S., Demange,N., Lavie,M., Moisan,A., Robert,C., Saurin,W., Schiex,T.,	solanacearum solanacearum Proteobacteria; Betaproteobacteria; Burkholderiales; ciaceae; Ralstonia.	10/11. ALG46053 .1 GI:17431932	166050 bp DNA linear BCT 11-APR-2003 golanacearum GMI1000 megaplasmid, complete sequence;	5247	PREGLYASHLYSGLYGLYGLTGLUSEKALAASPASDVALALALYSKALALYSKITKLYS 500			ValalaasnSerrSplyLeuAsnAcgalaAspH184.AASgAlaAlaserL1e 440					PheLysvalAspvalProGlyAspTyrvalLeuvalAspHisAlaIlePheArgAlaPhe 340 	GlyGluAsnHisAsnIleGlnThrThrLeuIleProAlaGlyGlyAlaAlaIleThrGlu 320 	ThrSerSerPheHisVallleGlyGlullePheAspLysValHisPheGluGlyGlyLys 300	LeuLysAlaLysValGlyGluThrValArgLeuPheValGlyAsnGlyGlyProAsnLeu 280	GluaspalaGluTyrValWalPheAsnGlySerValGlyAlaLeuThrGlyGluAsnAla 260 	

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Genome sequence of the plant pathogen Ralstonia solanacearum Nature 415 (6871), 497-502 (2002)

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http://sequence.toulouse.inra.fr/R.solanacearum.html.
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Gene name confidence : hypothetical
predicted by Codon usage
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                                                                                                                                                                                                                                                                    /note="Product confidence: putative 
Gene name confidence: hypothetical 
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Gene name confidence : hypothetical
predicted by Codon_usage
predicted by FrameD"
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Best Local Similarity:
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                    ValValValLysMetGluThrValGluLysValMetArgLeuAlaAspGlyValGluTyr
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GTCATCGTGGAGCTGGAAGTGATCGAGAAGGGAAATGCCGATCTCCGAAGGGGTCAGCTAC
                                                                GCGGTGCTCACGAGTCCGCCCAACGTGCCGCCGATCCACCGCAACTATCCGGCCAAG
                                                                                              AlaIleValThrHisAlaProGluValProProProValAspArgAspHisProAlaL
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Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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AGTVQRVSSQARAADGRGQGSRGTAEFEMQILFKPPTDAGRSSLRVGSAVNMSLAPEPG
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                                                                                                                                                                                                                                                                                                         ThrAspAlaValTyrLeuProGluGlyAla---ProGlnAlaIleAspThrGlnGluAla
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               GTGCTGCACGGCCTGAACGCCAAGATCAAGGTGAATGGCCAGGAATACGATTCCGTGATG
                                        ValAlaAsnGlyLeuSerGlyLysIleThrValAsnGlyAsnGlnTyrGluSerValMet
                                                                                                 ProLysThrProAlaProAlaAsnLeu-----GlnGluGlnIleLysAlaGlyLysAla
                                                                                                                                                                                                                                                                                  CTCGATGCGGTGTACCTGGGCGACCGTGCCGGCCCCAACCTGTCGGCCGTCACCCGGGCG
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gene	TITLE JOURNAL COMMENT FEATURES FEATURES	TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	AEO02512 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	Qy 461 Db 48585 Qy 480 Db 48525 Qy 500 Db 48468
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/product="major anaerobically
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (30-MAR-2000)
sequencing team, Sanger
Hinxton, Cambridge CB10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL162757 AL157959
AL162757.2 GI:736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Details of N. meningitidis sequencing at the Sanger Centre available on the World Wide Web.
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Details of N.
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Parkhill, J.
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Neisseria meningitidis Z2491
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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AL162757 AL1
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Neisseria meningitidis serogroup
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             /note="NMA1730, dapE, succinyl-diaminopimelate desuccinylase, len: 381aa; similar to many eg. SW:P24176 (DAPE_ECOLI) dapE, succinyl-diaminopimelate desuccinylase from Escherichia coli (375 aa) fasta scores; E(): 0, 56.39 identity in 371 aa overlap. Contains Pfam match to entry
                                                                                                                                         complement (668. .1813)
                                                                                                                                                                             complement (668. .1813)
                                                                                                                                                                                                                                  /label=Correia
complement(667.
                                                                                                         /gene="dapE"
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                                                                                                                                                              /gene="dapE"
                                                                                                                                                                                                                                                                                                                                                /note="Correia element;
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l56), score: 51.92"
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                                                                                                                                                                                                                                                                                                                             label=Correia
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Peptidase_M20
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complement (3185.
/gene="NMA1733"
/note="NNA1733, H.8 outer membrane protein, len: 183aa; /note="NNA1733, H.8 outer membrane protein, len: 183aa; strongly similar to SW:P07212 (H8_NEIME) H.8 outer membrane protein from Neisseria meningitidis (183 aa) fasta scores; E(): 0, 96.7% identity in 183 aa overlap. Contains Pfam match to entry PF00127 copper-bind, Copper binding proteins, plastocyanin/azurin family and Prosite match to PS00196 Type-1 copper (blue) proteins signature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="NMA1732, conserved hypothetical protein, 169aa; similar to SW:P43971 (Y243_HAEIN) hypothe protein from Haemophilus influenzãe (172 aa) fai E(): 0, 49.7% identity in 169 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="NMA1732"
complement(2581.
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SLDWHCYKADVSPIALPDYNRWLDNFDTEKYASFDMWHGAESEYDDYRTVAQQNESDR
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                                                                                                                                                                                                                                                                                                                                                               EIMAARRRR"
                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SPTREMBL:Q9JTK9"
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NQLVLQTIRQITRYENVAAPLHHEDEEENFFPLLLQYAPQAQESVDELLRQHVSLHGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="conserved hypothetical protein"
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/db_xref="GI:7380374"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (2581.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (1927./gene="NMA1731"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="NMA1731"
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/transl_table=11
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db_xref="GI:7380373"
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transl_table=
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                        US-10-088-045-2 (1-502) x NMA6Z2491 (1-326301)
                                                                                                                                                                                                            Alignment Scores:
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TGRLMSGRRWSEGLHQAVEAKEGVEIKRENQTLASITFQNYFRLYTKLSGMTGTADTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="NMA1735, secA, preprotein translocase SecA subunit, len: 916aa; similar to many eg. SW:P10408 (SECA ECOLI) preprotein translocase SecA subunit from Escherichia coli (901 aa) fasta scores; E(): 0, 58.0% identity in 920 aa overlap. Contains Pfam match to entry PF01043 SecA protein, SecA protein, amino terminal region and Prosite match to PS01312 Protein secA signatures."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MMLEQLEGREDALLSGLLKQAGGWRRLDAAVKKLLPANLHPHFQT
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4306. .4315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Pfam match to entry PF00127 copper-bind, Copper binding proteins, plastocyanin/azurin family, score 218.60, E-value 9.1e-62" complement (3212. .3259) /gene="NWA1733" /gene="NWA1733" complement (4017. .4439) /gene="NWA1734" .4439)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Core DNA uptake
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/protein_id="CAB84962.1"
/db xref="GI:7380376"
/db_xref="SPTREMBL:09.7™KR"
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/gene="NMA1733"
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/transl_table=
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1570. .7320
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/protein id="CAB84961.1"
/db_xref="Gi:7380375"
/db_xref="SWISS-PROT:P57025"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="secA"
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                                 HisLysGlnThrAspAlaValTyrLeuProGluGlyAlaProGlnAlaIleAspThrGln 380
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                                                                                                                                                                            PheLysValAspValProGlyAspTyrValLeuValAspHisAlaIlePheArgAlaPhe 340
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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                                                      GlyValGluTyrGlnPheTrpThrPheGlyGlyGlnValProGlyGlnMetIleArgVal 119
                                                                                                                                                                  ProVallleAspAlaIleValThrHisAlaProGluValProProProValAspArgAsp
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/note="sequence too long, cut in 8 pieces.~seq 1: 1 to
349980 349980 bases~seq 108: 300001 to 649980 349980
bases-seq 109: 600001 to 949980 349980 bases-seq 110:
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349980 bases-seq 112: 1500001 to 1849980 349980 bases-seq
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188260 CGCGAAGGCGATACGGTTGAAGTGGAATTTTCCAACAATCCTTCTTCTACCGTTCCGCAC
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1 (bases 1 to 2069)
Hoehn,G.T. and Clark,V.L.
Isolation and nucleotide sequence
major anaerobically induced outer
                                                                                                                                                                                                                                                                                                                                             NGOPANI 2069 bp DNA Neisseria gonorrheae major anaerobically protein (Pani) gene, complete cds.
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Neisseria gonorrhoeae
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                                                              Kataoka, K., Fukui, A., Kabayashi, M., Cloning and expression of copper-cor
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Submitted (19-DEC-2001) Kunishige Kataoka, Kanazawa Depatment of Chemistry, Faculty of Science; Kakuma, Ishikawa 920-1192, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (31-MAY-2000) Fujiwara T., Department of Biology and Geosciences, Faculty of Science, Shizuoka University, 836 Ohya Shizuoka 422-8529, JAPAN
Location/Qualifiers
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J. Bacteriol. 183 (14), 4149-4156 (2001)
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Direct Submission
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DSSFHFIGSVWDEVWQQGSIAGPPNRYYQTTPVKPGSCAIATLHAEVPGPIKLVDHAL
                                                                                                                                                                                                 /gene="nirK"
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269. .1449
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                                                                                                                                                                                                                                                     SRVARKATMAI INREGAANPDVFEPEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                   reductase"
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                                                                                          /evidence=experimental
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269. .281
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                                                       /gene="pcn"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="copper-containing dissimilatory nitrite
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IALGVDATDELFYVDAEGDTDDVHLELTRDDLIDLTPGDAHSLFSLDYLKNMNKAIPK
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Nagashima, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGCCGAGCATGCAGGTGGGTGAGACAGCCCGGGTGTACTTCGTGACCGGCGGCCCGAAC 1188
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EC_number="
                                                                                                                                                                                                                                                           /gene="nirK"
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422-8529, 836 (
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Ohya, Shizuoka,
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                          В
                            GTCGACGGTGGCCCGAACCTCTCCAGTAGCTTCCACCCCATCGGAAGCGTCTGGGAGACA
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BASE COUNT ORIGIN	KGCMAVVRAEGPEDPETFDPDPDPQ" T 265 a 503 c 470 g 201 t
Alignment Pred. No. Score: Percent S Best Loca Query Mat. DB:	jnment Scores:       1.2e-41       Length:       1439         d: No.:       754.50       Matches:       152         re:       754.59       Conservative:       56         cent Similarity:       41.64%       Mismatches:       128         c Local Similarity:       41.64%       Mismatches:       29         ry Match:       28.73%       Indels:       29         ry Gaps:       5
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Qy	77 AspArgAspHisProAlaLysValValValLysMetGluThrValGluLysValMetArg 96
Дb	533 GACCGGAGCCAGCCCGCGGAGGTCGACGTCACGCCCGGACGAGGTGACCGCGGAG 592
Q	97 LeuAlaAspGlyValGluTyrGlnPheTrpThrPheGlyGlyGlnValProGlyGlnMet 116
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9	137 MetProHisAsnValAspPheHisAlaAlaThrGlyProGlyGlyGlyAlaGluAlaSer 156
Db	713 ATGCCGCACAACGTCGACGCCGTCGCCGGCCCCGGCGGGGGCGCGAGGCGACG 772
8	157 PheThrAlaProGlyHisThrSerThrPheSerPheLysAlaLeuGlnProGlyLeuTyr 176
Db	773 ATGACGAACCCCGGCGCGAGACGCGCACCTGCGGTTCAAGGCGACCTACCCCGGCGCGTAC 832
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В	1073 CCCAACGGCCGGGGACCGCGACCGTCGGCACCGGCGAGACGGTCCGGGTGTACTTC 1132
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Pred. No.:  3.7e-24 Length: Score: 494.50 Matches: Percent Similarity: 43.57% Conservative: 53 Best Local Similarity: 32.57% Mismatches: 146	// Gene="hirk" // Codon starte1 // Codon starte1 // trans_table=11 // trans_table=11 // product="dissimilatory nitrite reductase" // protein_id="Bab21510.1" // protein_id="Bab21510.1" // db_xref="GI:12597209" // translation="MKALRPTLLAAALIVTLPASLAHAQNADQLPRAKVALVAPPQVH PHEQVAK/GEPKVVETMTIEEKKMVIDDKGTTLQAMTEDGSMPGPTLVVHEGDYVELT LVNPATNAMPHNUDFHAATGALGGAKLTNVNPGEQATLRFKADRSGTFVYHCAPEGMV PMHVVSGMSGTLMVLPROGLKDPDGKFLRVDRVTTIGEFDLYIPKDDKGKKXDYKTLA ESYGDTYEVMRKLTPSHIVFNGKYGALTGANALTARVGETVLLHSQANKDTRPHLG ESYGDTYEVMRETGKFGNPQKNLETWFIRGGSAGAALYTFKQPGVYLHLNHNLIEAFELGA GHGDWVWETGKFGNPQKNLETWFIRGGSAGAALYTFKQPGVYLHLNHNLIEAFELGA AGHIKVEGKWNDDLMKQIKAPGPIPR" BASE COUNT 359 a 649 c 569 g 246 t  ORIGIN Alignment Scores:	rce	2 (bases 1 to 1823) 2 (bases 1 to 1823) 3 (bases 1 to 1823) Shoun, H. and Takaya, N. Direct Submission Submitted (27-JUL-2000) Hirofumi Shoun, University Institute of Applied Biochemistry; Tennodai 1-1-1, 305-8572, Japan (B-mail:p450nor@sakura.cc.tsukuba.a Tel:81-298-53-4603, Fax:81-298-53-4605) Location/Qualifiers	SOURCE Alcaligenes sp. STC1 ORGANISM Alcaligenes sp. STC1 Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales Alcaligenaceae; Alcaligenes.  REFERENCE 1 (sites) AUTHORS Shoun, H. and Takaya, N. TITLE Alcaligenes sp. STC1 nitrite reductase gene JOURNAL Published Only in DataBase (2001)	RESULT 13 AB046603 AB046603 AB046603 AB046603 AB046603 AB046603 VERSION AB046603 AB046603 AB046603 AB046603 AB046603 AB046603 AB046603 AB046603 AB046603 AB046603 AB046603 AB046603 AB046603 AB046603 AB046603 AB046603 AB046603 AB046603	Qy 351 GluGlyGluGluAsnHisGluIleTyrSerHisLysGlnThrAspAlaValTyrLeuPro	Qy 294 ValHisPheCiuGlyGly
Qy 294 ValHisPhe 	9 9 11 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		, , , , , , , , , , , , , , , , , , ,	D Q D Q	reductase, Db 6	370 Oy 1402 Db 5	1249 US-10-088-0 330 Qy 1309 Db 5 350 Qy 1369 Db 5
94 ValHisPheGluGlyGlyLySGlyGluAsnHisAsnIleGlnThrThrLeu 310     ::	226 GlyGluGlnGlyLeuGlnProPheAspMetGluLysAlaIleArgGluAsp 242  1158 AAGGACTAC	197 IleLeuValGluProLysGluGlyLeuPro	60 ProGlyHisThrSerThrPheSerPheLysAlaLeuGlnProGlyLeuTyrValTyrHis 179		81 ProAlaLysValValLysMetGluThrValGluLysValMetArgLeuAlaAsp 99	43 LysThrAlaAsnAlaAspAsnAlaAlaSerGlhGluHisGlnGlyGluLeuProValIle 62	Indels: 127 Gaps: 20  45-2 (1-502) x AB046603 (1-1823)  3 LysProThrLeuIleLysThrThrLeuIleCysAlaLeuSerAlaLeuMetLeuSerGly 22 3::       :::

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-APR-1998) Shinnichiro Suzuki, Osaka University, Department of Chemistry, Graduate School of Science; Machikaneyama 1-16, Toyonaka, Osaka 560-0043, Japan (E-mail:bic@ch.wani.osaka-u.ac.jp, Tel:+81-6-850-5768, Fax:+81-6-850-5785)
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Unpublished
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Suzuki,S. and Kataoka,K.
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                                  Glu---AspAlaGluTyrValValPheAsnGlySerValGlyAlaLeuThrGlyGluAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATACCAAGGTCACGCTGGTCGCTCCGCCCCAGGTGCATCCGCACGAGCAGGCGACCAAG
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     ACGCTGACGCCGTCGCACATCGTCTTCAATGGCAAGGTCGGCGCCGCCTGACCGGCGCCAAC
                                                                                                                                                                                                          TACGACCGCGCCTACACCATCGGCGAGTTCGACCTGTACATCCCCAAGGGCCCGGACGGC
                                                                                                                                                                                                                                                                                                            GCACGCTGATGGTGCTGCCGCGCGACGCCTGAAGGATCCGCAGGGCAAGCCGCTGCAT 1388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACAAGGGCACGACGCTGCAGGCCATGACGTTCAACGGCTCCATGCCCGGCCCCACGCTG
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                                                                                                       AAGTACAAGGACTACGCCACGCTGGCCGAAAGCTATGGCGACACGGTGCAGGTGATGCGC
                                                                                                                                                       LysTyrGlyGluGlnGlyLeu-----GlnProPheAspMetGluLysAlaIleArg
                                                                                                                                                                                                                                                         ValAspLysGluTyrTyrValMetGlnGlyAspPheTyr----
                                                                                                                                                                                                                                                                                                                                                              GlyLeuIleLeuValGluProLysGluGlyLeuPro-----
                                                                                                                                                                                                                                                                                                                                                                                                              TACCACTGC-----GCGCCCGAAGGCATGGTGCCCTGGCACGTGGTGTCGGGCATGAGC 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrHisCysAlaValAlaProValGlyMet------HisIleAlaAsnGlyMetTyr 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCAACCCTGGCGAGCAGGCCACGCTGCGCTTCAAGGCCGATCGCAGCGGCACCTTCGTC
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/translation="MMALRFTLAAALAFTMAAGTAWAQDADKLPHTKVTLVAPPQVH/translation="MMALRFTLAAALAFTMAAGTAWAQDADKLPHTKVTLVAPPQVHPDATKSGPKVVEFMTIEEKKMVIDDKGTTLQAMTENGSMPGPTLVVHEGDYVQLTLVHDATNAMPHNVDEHGATGALGGAKLTNVNPGEQATLRFKADRSGTEVYHCAPEGMVPMHVVSGMSGTLMVLPRDGLKDPQGKPLHYDRAYTIGEFDLYIPKGPDGKYKDYATLAESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSQANRDTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSQANRDTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSQANRDTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSQANRDTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSQANRDTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSQANRDTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSQANRDTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSQANRDTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSQANRDTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSQANRDTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSQANRDTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSQANRDTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSQANRDTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSQANRDTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSQANRDTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANALTAKKGETVLLIHSGANALTAKKGETVLLIHSGANALTAKTGANATTRPHLIGESYGDTVQVMRTLTPBHIVFNGKVGALTGANATTAKTGANATTRPHLIGESYGDTVATAGANATTRPHLIGESYGDTVATATTRPHLIGESYGDTVATATTRPHLIGESYGDTVATAGANATTRPHLIGESYGDTVATAGANATTRPHLIGESYGDTVATAGANATTRPHLIGESTURGANATTRPHLIGESYGDTVATAGANATTRPHLIGESYGDTVATAGANATTRPHLIGESYGDTVATAGANATTRPHLIGESYGDTVATAGANATTRPHLIGESYGDTVATAGANATTRPHLIGESYGDTVATAGANATTRPHLIGESYGDTVATAGANATTRPHLIGESYGDTVATAGANATTRPHLIGESYGDTVATAGANATTRPHLIGESYGDTVATAGANATTRPHLIGESYGDTVATAGANATTRPHLIGESYGDTVATAGANATTRPHLIGESYGDTVATAGANATTRPHLIGESTURGANATTRPHLIGESYGDTVATAGANATTRPHLIGESTURGANATTRPHLIGESTURGANATTRPHLIGESTURGANATTRPHLIGESTURGANATTRPHLIGESTURGANATTRPHLIGESTURGANATTRPHLIGESTURGANATTRPHLIGESTURGANATTRPHLIGESTURGANATTRPHLIGESTURGANATTRPHLIGESTURGANATTRPHLIGESTURGANATTRPHLIGESTURGANATTRPHLIGESTURGANATTRPHLIGESTURGANATTRPHLIGESTURGANATTRPH
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ORGANISM
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                                                                     Submitted (26-JUN-1996) Microbiology,
Hall, Ithaca, NY 14853-8101, USA
Location/Qualifiers
                                                                                                                                                                                                   1 (bases 1 to 1307)
Tosques, I.E., Kwiatkowski, A.V., Shi, J. and Shapleigh, J.P.
Characterization and regulation of the gene encoding nitrite
reductase in Rhodobacter sphaeroides
                                                                                                                                                                                                                                                                                                                                                                                                                     Rhodobacter sphaeroides gene, complete cds.
                                                                                                                                              2 (bases 1 to 1307)
Tosques, I.E., Shi, J. and Shapleigh, J
                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                   complete
               /organism="Rhodobacter sphaeroides"
/mol_type="genomic DNA"
/mol_type="genomic
/strain="2.4.3"
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                                                                                             SerPheLysAlaLeuGlnProGlyLeuTyrValTyrHisCysAlaValAlaProValGly 186
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CCGATGATCCCCTGGCÁCGTCGTCTCGGGCÁTGGCGGGCTGCATCATGGTGCTGCCGCGC
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                               ------MetHisIleAlaAsnGlyMetTyrGlyLeuIleLeuValGluProLys
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prvkiturpeppahaiequalasgpu/inefemriiekevquldea/lqawtfdgsipgp
lmivhegdyveltilinpeenmiphidphaafgalgggtilinpeevyvylgesdhyipa
Gafvyhcapggmiphidvesgmagcimvlproglkdiegkpvrydtvyvylgesdhyip
KDedgtymrfstpsegyedmvavmdtlipshivfngavgaltgegalkakvgdnvlfv
HSQPKRDSRPHLIGGHGDLVWETGKFHNAPERDLETWFIRGGTAGAALYKFLQPGVYA
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/trans1_table=11
product="copper containing nitrite reductase"
/protein_id="AAB05767.1"
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                                                                   Submitted (Chemistry,
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Achromobacter cycloclastes
Bacteria, Proteobacteria; Betaproteobacteria;
Alcaligenaceae; Achromobacter.
1 (bases 1 to 1903)
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A.cycloclastes gene for nitrite
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organism="Achromobacter/mol_type="genomic DNA"
                                                                    (09-MAR-1995) Wen-Chang (
, Academia Sinica, PO Box
                                                  Location/Qualifiers
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                                                                                                                                                                                            Commun.
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                  CACGTCACCTCGGGCATGAACGGCGCCATCATGGTGCTGCCGCGCGACGGACTGAAGGAC 1080
                                               HisIleAlaAsnGlyMetTyrGlyLeuIleLeuValGluProLysGluGlyLeuPro---
                                                                                                                                                                                         GlyGlyAlaGluAlaSerPheThrAlaProGlyHisThrSerThrPheSerPheLysAla 170
                                                                                                                                                                                                                                                                                                  TCGGTGCCTGGTCCGCTGATGGTGGTGCATGAGAACGACTATGTTGAACTGCGGCTGATC
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/trans1_table=11
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/protein id="CAA88564.1"
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QDFYVPKDEAGNYKKKETPGEAXYEDAVKAMRTLTFTHIVENGAVGALTGDHALTAAVG
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                                          Sinorhizobium meliloti (Rhizobium meliloti)
Sinorhizobium meliloti
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                        complete plasmid sequence.
AE007256 AE006469
AE007256.1 GI:14523793
                      Rhizobiaceae; Sinorhizobium/Ensifer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (29-MAR-2001) Biological Sciences,
371 Serra Mall, Stanford, CA 94305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barnett, M.J., Fisher, R.F., Jones, T., Komp, C., Abola, A.P., Barloy-Hubler, F., Bowser, L., Capela, D., Galibert, F., Gouzy, J., Gurjal, M., Hong, A., Huizar, L., Hyman, R.W., Kahn, D., Kahn, M.L., Kalman, S., Keating, D.H., Palm, C., Peck, M.C., Surzycki, R., Kalman, S., Keating, D.H., Palm, C., Peck, M.C., Surzycki, R., Wells, D.H., Yeh, K.-C., Davis, R.W., Federspiel, N.A. and Long, S.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 10587)
Barnett, M.J., Fisher,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="Miscellaneous; Not classified regulator" /note="glimmer prediction picked ORF start at codon 61; ATG picked further upstream based on BLASTX of upstream region, found homology to Pseudomonas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Azul pseudoazurin (blue copper protein)"
(protein id="AAK65336.1"
(db xref="GI:14523794"
(translation="MRIJAKGMAVAAVLAAFTGSAFAADFEVRMLNKGSEGVMVFEPA
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PHVGMGMVAAVVVGDAPANVEKVKAVKLPKKARERLDAALAVALQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-"glimmer prediction; pseudoazurin, also called blu copper protein, a soluble electron transfer protein associated with periplasmic nitrite reductase; Cu-binding/plastocyanin domain; Cu-binding/plastocyanin
                                                                  precursor of Pseudomonas,
                                                                                                                                                              /note="synonym:
complement(1987.
                                                                                                                                                                                                                                   complement (1987.
                                                                                                                                                                                                                                                       TQVTEDGQQIIVRVVHPGDLFGFAKALQRSDYPGTATAATESLALSWPTDLWPQFVEQ
NPHLAVSTMQTIGQRLEEAHTRIREMSTQEVERRVAHAVLRLSRQAGKQEKGGVRIDF
PISRQDIAEMTGTTLHTVSRILSAWEQKGLVEGGRQKLIICDLSGLAALADGGRD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SMal245"
complement (715. .1362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="synonym: SMa1243"
complement(161. .604)
                                            denitrification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (715. .1362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domaın"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (161.
                                               "gene="nirV"
function="Small molecule metabolism"
/function="Small molecule metabolism"
/note="glimmer prediction; global length homology to NirV
/note="glimmer prediction; global length step in
                                                                                                                                                                                                                                                                                                                                                     db_xref="GI:14523795"
                                                                                                                                                                                                                                                                                                                                                                           'producT="putative crp/fnr-like transcriptional regulator"
protein_id="AAK65337.1"
                                                                                                                                                                                                                                                                                                                                                                                                                               transl/
                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="SMa1245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function="Small molecule metabolism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="azul"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /plasmid="pSymA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 translation="MSDADLDRMLAHATARRVPQGDAVFEQGQRATSFFLLLHGRLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Sinorhizobium meliloti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _type="genomic DNA"
                      _start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                               table=11
                                                                                                                                                              SMa1247"
. .2901)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .604)
                                                                                                                                                                                                                                   .2901)
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blue

product="NirV periplasmic nitrate reductase"

gene

CDS

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/transl tartal
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/db_xref="701:1452797"
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5701. .5970
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TLWIAALVGHLEVAGSYGAHAWHAHEMLFGFAPAVLAGFLLTAVPNWTGRLPVSGWPL
AGLFTLWLAGRAALLSDDVIGIPDAAALDGLFLPALLLIGARTVJKFVLKVLGG
LLALSLANACFEHFAVVTGDHYHIAMRLGISAYVALVTIIGGRILPSFTRWALNKAGRT
LLALSLANACFEHFAVVTGDHYHIAMRLGISAYVALVTIIGGRILPSFTRWALNKAGRT
EFFPVFYNHFDTVAILAGIAALGAWTLAPDHPVTAVPAFAAALLLHTVRLARWRGWRTWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SMa1252"
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/function="Miscellaneous; By global identity to ORF 396
/note="glimmer prediction; 30% global identity to ORF 396
in the denitrification gene cluster of Pseudomonas
stutzein; 46% global identity to NnrS which is found
divergently transcribed from NnrR, a transcription factor
that regulates denitification in R. sphaeroides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SMa1252"
4376. .5587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVPGPLMVVHQDDYVELTLINPDTNTLQHNIDFHSATGALGGGALTVVNPGDTTVLRF
KASKAGVFVYHCAPPGMVPMHVTSGMNGAIMVLPREGLTDGKGNSITYDKVYYVGEQD
FYVPRDANGKFKKYESVGEAYADTLEVMRTLTPSHIVFNGAVGALTGDSALKAAVGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carbon; anaerobic respiration"
/note="glimmer prediction. Global full length homology of
/nirk-like Cu-containing nitrite reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEEPPVVTVAPRDFRYRVAGEFFKNGYAVDGPVETVHMSAPLTIMKYQVTAADYARCV
AEDACLPAEPEHVPVDPARMPATGVSFDDAQAYAAWLSRRTGAIWVLPTDEQLAFAAG
SRFPDDALGVEDDASNPALRWLADYYRETARKASRESEPQRLGHFGESETGLSDFAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILVRKRRAVQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMLLVILHVAYAFVPLGFAATGIGALGFVEELSVMHVLTVGAIAAMMLAVMTRASRGH
TGYPLTASRLTAASYAAVVLSALLRPLAEMLPEIAPTLYAVSGSAWILAFALFCIEYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIYAYVNHNLIEAFELGAAAHFAVTGDWNDDLMTSVRAPSGT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (5643. .6278)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (5643.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (3000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="conserved hypothetical protein"
/protein_id="AAK65340.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="SMa1254"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SMa1254"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MAALSKSREVAPVALAIPSALILILAGLLALETGLLGSAPSGSA/
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/db_xref="GI:14523796"
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                                                                                                                 3881
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gene

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US-10-088-045-2 (1-502) x AE007256 (1-10587)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                         AAGAAGATCGTCATCGACGAGCAGGGTACGGAGCTTCATGCCATGACCTTCAACGGTTCG 3822
GTCCCCGGTCCGCTGATGGTCGTGCACCAGGACGACTATGTCGAGCTGACGCTCATCAAT 3762
                                                                                                                                        ---LysValMetArgLeuAlaAspGlyValGluTyrGlnPheTrpThrPheGlyGlyGln 111
                                                                                                                                                                                      CATACGCAGAAGGCGGAAGGTCGCCCAAGGTCGAGGTTCACGCTGACGATCGAGGAG 3882
                                                                                                                                                                                                                                                                                  AACGTCGCATCGCTGCCCCGTGTCAAGGTCGACCTGGTGAAACCGCCCTTCGTCCACGCC 3942
                                         ValProGlyGlnMetIleArgValArgGluGlyAspThrIleGluValGlnPheSerAsn 131
                                                                                                                                                                                                                                    HisPro-
                                                                                                                                                                                                                                                                                                                                                                            CCGCTGATCGGCGCTGTCTCTGCGCATGCGGAAGAGGCGGTCGCCAAGACCGCCCACATC 4002
                                                                                                                                                                                                                                                                                                                                                                                                                        ProValIleAspAlaIleValThrHisAlaProGlu-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (6948..7478)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="Miscellaneous; Hypothetical/Global homology" /note="glimmer prediction; global similarity to putative dTDP-4-keto-L-rhamnose reductase from S. mutans (GI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (7482.
/gene="SMa1259"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SMal255"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mtietqnpaprefdvrpilksggepfqaimeavnglrpgqalrl
Lapfrpqplfkvmggrgfsheaqeiqggdwevlfkpnaagapvevsadadnaaswpdp
VENLDLTELDppepmvrilaaverlqpgevlfallsrepiflfpelskrghqwagnfd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SMa1256"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVEDGGIAHVTMTTTTKGCPASEYLKEAVRNCVWYVPGVEYAEVRLTYEPAWTPDMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SMa1255"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MGAESNVRLLRELCLHGRHISATQLAERSGLVRNSTRNALNSLR
QHGLVVEEGTDGARLFRFNSEHPLGDSIGQLFGAESEGFKISSKG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETRTTFRIFVRVGDKG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAK65344.../db_xref="GI:14523802"
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/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="Hypothetical
protein_id="AAK65342.
/db_xref="GI:14523800"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="glimmer prediction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SMa1253"
/function="Miscellaneous; Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                514804)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MIRAEAMSEPENATVCDSIRDALRMIIDPELGRNIVDLGLIYDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="glimmer prediction"
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456.00
46.81%
31.44%
17.36%;
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                                                                                GGGACTCCT
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Submitted (26-APR-1993) Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Characterization of the structural gene encoding copper-containing nitrite reductase and homology DNA of other denitrifiers Appl. Environ. Microbiol. 59 (1), 250-254 (1993)
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M97294
M97294.1 GI:151396
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Tiedje,J.M.
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Ye,R.W., Fries,M.R.,
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              /translation="MSEQFRLTRRSMLAGAAVAGALAPVVTSVAHAEGGGIKTNSAAT AANIATLERVKVELVKPPFVHAHTQKAEGEPKVVEFKMTIQEKKI VVDDKGTEVHAMT POGSVPGFMMI VHQDDYVELTLVNPDTNELQHNID FHSA TGALGGGALTVVNPGDTAV LRFKATKAGVFYYHCA PEGMVPHMYTSGMMGA HWLLPRDLKDHKGHELVDKVY YVG EQDFYVPKDENGKFKKYESAGEAY PDVLEAMKTLTPTHVVFNGAVGALTGDNALQAKV GDRVLILHSQANBDTR PHLIGGHGDYVWATGKFANPPELDQETWF I PGGAAGAAYYTF QQPGILAYVNHNLI EAFELGAAGHFKVTGDMNDDLMTAVVSPTSG" 668. 763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="nirU"
289. .303
                                                                                                                                        /codon_start=1
/trans1_table=11
/product="nitrite reductase
/protein_id="AAC79132.1"
/db_xref="G1:151397"
                                                                                                                                                                                                                                           668. .1807
                                                                                                                                                                                                                                                                                    the promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:71238"
/note="similar to Rhizobium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Pseudomonas
/mol type="genomic DNA"
 gene="nirU"
                                                                                                                                                                                                                                                                                                   standard_name="NtrA box (sigma-54) standard_name="NtrA box (sigma-54) function="facilitates recognition"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard_name="FNR
note="putative"
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es recognition of RNA polymera
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                                                                              CTGATCGGGGGGCATGGCGATTATGTC---TGGGCTACCGGCAAGTTCGCCAACCCGCCG
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/product="nitrite reductase"
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/function="nitrite reduction"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ye,R.W. and Laura,B.* Characterization of the DNA region responsible for nitrite reduction in Pseudomonas sp. G-179 containing a Cu-type nitrite
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Ye,R.W. and Laura,B.
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1803. .2699
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/product="nitrite reductase"
/product="nitrite reductase"
/protein id="AAB96769.1"
/db_xref="GI:2773328"
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GDRVLILHSQAARDTRPHLIGGHGDYVMATGKFANPBELLDGETWFIPGAAGAAYYTF
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582. .1721
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/db_xref="GI:2773329"
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/mol_type="genomic DNA"
/strain="G-179"
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G-179 nitrite reductase (nirU), NirV precursor
R (nnrR) genes, complete cds.
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TQVTEDGQQIIVRVHHGDLFGFARALGRTDYBGTAVAAESVTLAMPTELMPSEVEH
NPRLANTAMOTIGERLEBAHVBIREMSTEEVERRVAHTVIRLARKAGKOEKOGIRIDE
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               Submitted (14-AUG-2001) Bioinformatics, Cereon Gene Street, Cambridge, MA 02139, USA Approximately 800 bp of telomeric sequence missing end of the chromosome and 200 bp missing from the r
                                                                                                                                                             1 (bases 1 to 10484)
Hinkle,G., Slater,S.C. and Goodner,B.
Complete Genome Sequence of Agrobacterium tumefaciens
(Rhizobium radiobacter C58), the Causative Agent of Cr
Disease in Plants
                                                                                      2 (bases 1 to 10484)
Hinkle,G., Slater,S.C.
Direct Submission
                                                                                                                                                                                                                                                                   Agrobacterium tumefaciens str. C58 (Cereon)
Agrobacterium tumefaciens str. C58 (Cereon)
Agrobacteria, Proteobacteria, Alphaproteobacteria;
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FEKILAMAEMVNVDRPGDDSDDADGSAADELDDLTLGERKGRPSARFRFDLDLPPEAL
NHTALTAELTY PEMYKRSTTYLADHCRVISGPAKDAETAPEDDDTKULIRRVERQFE
VLRPRHELLRAQLDGNDLDLDAVVRARSDIAAGGQGSDRIHVASRPQAHDLAVTILVD
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DRRLNRDLYLMLAAAMALMPLEPVAAADPLRNDLARLHRAAELAEIVTRAFPGMKTRY
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ICAREVLAGRKMKDLKVLGGLLALSVANIVFHVAAIGGDHSQMATRLAVSAYTVLVII
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EPMGHTIERRIAALKPGFYTRIGPAIRHASAKLHERPERRKLLLLLTDGKPNDVDHYE
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transl_table=
                                                                                                               note="hypothetical
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note="CYTOCHROME C2"
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1354. .572
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. I RSGADTRAAMTA PQVVTVPAGRFTYRA EGEYFRDGYAVDGPMVDL TMRQNLTI MKY
)VSSANYARCVA EGGCQQPEPGFAA PVGGEI PATGI SQDDAHAYAKMLSERTGA VMRL
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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             ProGlyLeuTyrValTyrHisCysAlaValAlaProValGlyMet------HisIle 189
                                                                                     AlaGluAlaSerPheThrAlaProGlyHisThrSerThrPheSerPheLysAlaLeuGln
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DYQNADKEAMDY PHRNRATQENKAKYPVLSRDYLLEBATLGWWADEQETPYVEEKRFD
WFRGYHVGGRSLLMGRQTYRWSQDFBANAKGIJAVDW IEDVSPWDYVERFAGI
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RTPCQFRNKCRLGCPFGGYFSTQASTLPAAVATGNLTLRPFSIVKEILYDKDKKKARG
VGIIDAETNLTYEYTADIIFLANASTLNSTWVLMNSGNDYUSGGSSSGELGHNVNDH
HFRWGATGQVDGFEDFYFKGRRPAGFYIPRFRNTGDDKRCXLRGFGYQGSASRSRWER
EIAELNIGADYKDTLTEFGGWTIGMTAFGEMLFYHDNRVKLDHDKKDKMGLPVLSMNV
ENKQNBLLDMREDMVNNDAVEMFEAVGIKNVKPSRGTYAPGMGIHEMGTARMGRDPKTSV
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/gene="AGR_L_980
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/translat.ton="MMNRELLKLIATATGLPLIGADVLTAAENAAKPAGGGHVFSPE
EIRFLDEVABTIIPRTSTPGAKDAEVGAFMAVYAADCYTDEGRALFLSAIPEIEKRSQ
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/product="AGR_L_980p"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-SEP-2001) Department of Microbiology, University of Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA 98195-7242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agrobacterium tumefaciens str. C58 (U. Washington)
Agrobacterium tumefaciens str. C58 (U. Washington)
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE009367.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Nester, E.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 294 (5550), 2317-2323 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumefaciens C58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 10753)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nester, \mathbf{E}.\mathbf{W}. genome of the natural genetic engineer Agrobacterium
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                                                                                                                                                                                                     complement (1132.
                                                                                                                                                                                                                                                                                           complement
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Washington)"
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ocated using Blastx/Glimmer"
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                                                                                                                                                                                                                                                                                        (1132. .2367)
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complement (3827. .4360)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (4439. .4888)
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located using Blastx/Glimmer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           putative; ORF
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•	gene		FEATURES source	REFERENCE AUTHORS TITLE JOURNAL	TITLE JOURNAL MEDLINE	REFERENCE	VERSION VERSION KEYWORDS SOURCE ORGANISM		RESULT 22 AF083948/c LOCUS DEFINITION	B 8	р <b>Q</b>	Db 1	Ş	Db
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                                                                                                                                                                                                                                                              function="anaerobic
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CD.

Alignment Scores:

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SdC

D Qy	\$ &	β δ	d Q	D Qy	Qy db	9 6	Db .	Оу	dg Qy	B 8	dd dd		B &	Db Qy	Db Qy	US-10-088	Pred. No.: Score: Percent Sir Best Local Query Match DB:
343 ĠİYAlaLeuGİYİleL            2389 GGCGCGGCCGCCACT	323 ValAspValProGlyA        2449 TTCCAGCAGCCCGGTA	305AsmIleGlnThr ::: :::    2509 GAACTCGATCAGGAAACC	286 ValileGlyGluilePh :::      2566 CTGATCGGGGGGCATGG	266 GlyGluThrValArgLeu    :::    ::: 2620 GGCGATCGTGTC	246 ValValPheAsnGlyS	227 GluGlnGlyLeuGlnPr     2740 AGCGCCGGCGAGGCCTA	214 ValMetGlnGlyAspP     :::      2800 GTCGGCGAGCAGGACT	201 ProLysGluGlyLeuP    :::::       2860 CCGCGTGACGGTCTCA	184 ProValGlyMet	164 SerThrPheSerPheI :::      2974 GCGGTGCTGCGTTTCI	144 HisAlaAlaThrGlyP    :::         3034 CATTCGGCGACGGGTG	124 ThrIleGluValGlnPheS :::   ::: 3094 TATGTCGAACTGACCCTCG	104 GlnPheTrpThrPheGl        3154 CATGCGATGACGTTCGA	85 ValValLysmetGlu7        3214 GAGTTCAAGATGACCA	72 ValProProProVali	-045-2 (1-502) x AF0	: 3.5e-2 453.00 imilarity: 45.93% 1 Similarity: 32.35% ch: 17.25%
euLysValGluGlyGluGluAsnHisGluIle           :::   :::::  CAAGGTGACGGGGACTGGAACGACGACCTG	spTyrValLeuValAspHisAlaIlePheAr 	hrThrLeuIleProAlaGlyGlyAla 	PheAspLysValHisPheGluGlyGlyLysGlyGlu 	PheValGlyAsnGlyGlyProAsn ::: ::     CTGATTCTTCATTCGCAAGCCAAC	snGlySerValGlyAlaLeuThrGlyGluAsnAlaLeuLysAlaLysV      :::                ACGGGGCGGTCGGCGCCTGACGGCGATAACGCCTTGCAGGCAAAGG	oPheAspMetGluLysAlaIleArgGlu    ::: 	heTyrThrLys      TTTATGTCCCGAAGGATGAGAACGGCAAG	rolysValasp       AGGATCACAAGGGCCACGAGCTTGTTTACGAC	HisileAlaAsnGlyMetTyrGlyi    ::: :1:       cgrggcArgrcAcTrcgggcArgAarggrc	LysAlaLeuGlnProGlyLeuTyrValTyrHisCy         adgccaccaaggcgggggggggggggggggggggggggg	roGlyGlyGlyAlaGluAlaSerPheThrAla 	erAsnHisProAspSerLysMetProHis 	yGlyGlnValProGlyGlnMetIleArgVa 	UThrValGluLysValMetArgLeuAlaAsp		83948 (1-20761)	Length: 20761 Matches: 143 Conservative: 60 Mismatches: 176 Indels: 64 Gaps: 15
TyrSerHisLys 362 ::: ATGACA 2336	gAlaPheAsnLys 342        GGCGTTCGAACTC 2390	AlaIleThrGluPheLys 322 ::: GGGGCGGCTTACTACACG 2450	GluAsnHis 304     GCCAACCCGCCG 2510	LeuThrSerSerPheHis 285 :::     AGGGATACGCGCCCGCAC 2567	LysAlaLysVal 265 :::         CAGGCAAAGGTG 2621	AspAlaGluTyr 245 ::: ACCCCGACGCAT 2681	GlyLysTyrGly 226       TTCAAGAAATACGAA 2741	LYSGluTYrTYr 213 	JeuIleLeuValGlu 200    :::    CGATCATGGTCCTG 2861	CysAlaValAla 183        TGTGCC 2921	ProGlyHisThr 163         CCCGGTGACACG 2975	AsnValAspPhe 143    :::        AATATCGACTTC 3035	lArgGluGlyAsp 123   :::     TCACCAGGATGAT 3095	GlyValGluTyr 103          GGGACCGAGGTC 3155	ProAlaLysVal 84      CCCAAGGTTGTC 3215		

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suzuki,E., Horikoshi,N. and Kohzuma,T. Cloning, sequencing, and transcriptional studies of the gene encoding copper-containing nitrite reductase from Alcaligenes xylosoxidans NCIMB_11015
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Glu---AspAlaGluTyrValValPheAsnGlySerValGlyAlaLeuThrGlyGluAsn
                                                                                             ĻγsTγrGlyGluGlnGlyLeu--
                                                                                                                                                                                               ValAspLysGluTyrTyrValMetGlnGlyAspPheTyr-----ThrLysGly
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                                                 AAGTACAAGGACTACGCCACGCTGGCCGAAAGCTATGGCGACACGGTGCAGGTGATGCGC
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/product="dissimilatory copper-containing
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Pseudomonas chlororaphis
Bacteria; Proteobacteria; Gammaproteobacteria;
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/gene="nirK"
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                                                                                    citation=[1]
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ValMetGlnGlyAspPheTyr---ThrLysGlyLysTyrGlyGluGlnGlyLeuGlnPro
                                                                                                                   ProLysGluGlyLeu----ProLys----
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nitrite reductase. The gene product has both type I s
type II copper-binding sites"
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13. .84
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39.12%
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Matches:
Conservative:
Mismatches:
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•	JOURNAL FEATURES FEATURES	PUBMED REFERENCE AUTHORS TITLE	TITLE JOURNAL MEDLINE	AUTHORS	MEDLINE PUBMED REFERENCE	TITLE	AUTHORS	SOURCE	ACCESSION VERSION KEYWORDS	RESULT 25 AP005961 LOCUS DEFINITION	<i>Оу</i>	B 4			•		ob Oy	B &		8	Db
!	Submitted (20-NOV-2002) Takakazu Kaneko, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:kaneko@kazusa.or.jp, URL:http://www.kazusa.or.jp/rhizobase/, Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)  Location/Qualifiers  1. 298550	bmission	Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110 (supplement) DNA Res. 9 (6), 225-256 (2002) 22485002	Kaneko,T., Nakamura,Y., Sato,S., Minamisawa,K., Uchiumi,T., Sasamoto,S., Watanabe,A., Idesawa,K., Iriguchi,M., Kawashima,K., Kohara,M., Matsumoto,M., Shimpo,S., Tsuruoka,H., Wada,T., Yamada,M. and Tabata,S.	22484998 12597275	genomic sequence of nit zobium japonicum USDA110	Kaneko, T., Nakamura, Y., Sato, S., Minamisawa, K., Uchiumi, T., Sasamoto, S., Watanabe, A., Idesawa, K., Iriguchi, M., Kawashima, K., Kohara, M., Matsumoto, M., Shimpo, S., Tsuruoka, H., Wada, T., Yamada, M.	Bradyrhizobium japonicum USDA 110 Bradyrhizobium japonicum USDA 110 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium.	AP005961 BA000040 AP005961.1 GI:27355365	AP005961 Bradyrhizobium japonicum USDA 110 DNA, complete genome, section 27/31.	342 LysGlyAlaLeuGlyIleLeuLysValGluGlyGluGluAsnHisGluIle 358	946 ACCTTCAAGCAGCCGGGGACCTACGTGTACCTCAGCCATAACCTGATCGAGGCCATGGAA 1005	CCCCANCATCACATION TO THE LATE OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT	HisAsnIleGlnThrThrLeuIleProAlaGlyGlyAlaAlaIleThrGluPhe		HisVallleGlvGluIlePheAspLvsValHisPheGluGlvGlvLvsGlvGluAsn	265 ValGlyGluThrValArgLeuPheValGlyAsnGlyGlyProAsnLeuThrSerSerPhe 284	245 TyrValValPheAsnGlySerValGlyAlaLeuThrGlyGluAsnAlaLeuLysAlaLys 264	658GACCTGGCGTCCAGTTACCAGGACACCCGCGCGCGTCATGCGCACCCTGACCCCGAGC 714	233 PheAspMetGluLysAlaIleArgGlu	598 ATCGGCGAGTCCGACCTGTATATCCCCCAAGGACAAGGACGGCCACTACAAGGACTACCCCG 657
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FRRATISFLIGNVPAERAYAKAGFVFAEEKRDPAFEAIIGAPGFRMFTRAI"
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DSPGEAFTDTEEMMKKLIPSHVVFNGKVGALTGKNALTANVGENVLIVHSQANRDSRP
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QIVKLAPGGGHLMFIGLDAPLRVGDOVPVTLSFEHAGEVKVTLDVQAIGAQAPEKTER
TEIAQPAHHPEPAAAAPPAMVSEADESFFTHLHAEKAMANVTVLPGRAGPVEIAIQLE
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RDVAIATDRPAVQVSWHDAQAYAGWLSHRTGKTWRLPSDAEWAFAAGSRFKDDGAPVD
ADNPSKRWISRYERBSERDLSDTTAYAPGKFGANEHGIEDLAGNVWEWTSTCFVRSRT
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probable periplasmic nitrate reductase"
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5226. .6104
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                                                                            complement (7525. .8232)
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/protein_id="BAC52354.1"
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                           /gene="pcal"
/note="ORF_ID:bll7093"
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234 AspMetGluLysAlaIleArgGlu---AspAlaGluTyrValValPheAsnGlySerVal 252
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VKGLTVVSNNAGVDGIGLSRLLETRQIKKMISSYVGENKLFAQQFLAGELELEFNPQG
TLAERIRAGGAGIPAFYTKTGVGTLIAEGKEVKEFDGEKYLMERGLFADLAIVHAWKG
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/protein_id="BAC52358.1"
/db_xref="GI:27355375"
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Characterization of the gene encoding nitrite reductase physiological consequences of its expression in the non-denitrifying Rhizobium hedysari HCNT1
                                                                                                                                                                                                            Rhizobium hedysari copper contai complete cds
                                                     Shapleigh, J.P.
                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
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Hall, Ithaca, NY 14853, USA
Location/Qualifiers
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Toffanin, A. and Shapleigh, J.P.
Direct Submission
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      GTTCCTGGTCCGCTCATCGTTGTGCATCAGGACGACTACGTCGAGGTCACACTCGTCAAT
                             ValProGlyGlnMetIleArgValArgGluGlyAspThrIleGluValGlnPheSerAsn
                                                                  AAGAAGCTCGTGATCGATGGCAAGGGCACCGAAGTCAATGCCATGACCTTTGACGGATCG
                                                                                                                                                                                                                                                                                   AlaAlaAlaLysThrAlaAsnAlaAspAsnAlaAlaSerGlnGluHisGlnGlyGluLeu
                                                                                                                                                                                                                                                                                                                     ACCTCGGGGGGGGGGAATGCCTCCCCCACTCCTGTCAGAAAGCTCAGCGCCACTGAAATC
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EIAALFRYLDIKRPFVHNHTQKAEGGFKVVEVTLTIEEKKLJU DGKGTEVNAMTED

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DFYIFNDEKGEFKKYDSPGEAYEDTVANMRTLIFTHIVENGAVGLTGSNALTAAVGE

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PGIYAYVNHNLIEAFELGAAAHFKVTGDWNDDLMTTVRSPSGS"
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/codon start=1
/transI_table=11
/transI_table=11
/product="copper containing nitrite reductase"
/protein_id="AAB05880.1"
/db_xrefe"GI:|488172"
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/strain="HCNT1"
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Bradyrhizobium japonicum nirK g
AJ002516
AJ0025161 GI:2597837
nirK gene; respiratory nitrite
Bradyrhizobium japonicum
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Bacteria; Proteobacteria; Alphaproteobacteria;
Bradyrhizobiaceae; Bradyrhizobium.
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Direct Submission
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GGHGDYVMETGKFGNAPEVGLETWFIRGGSAGAAMYKFMQPGIYAYVTHNLIEAADLC
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/db_xref="GI:2597838"
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/transl_table=11
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/mol_type="genomic DNA"
/strain="USDA110"
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                             HisGlnProAspGlyLysGlyValProAsnAlaPheProProLeuAlaAsnSerAspTyr 429
                                                                                                                                                                                                                                                                                      ValLeuValAspHisAlaIlePheArgAlaPheAsnLysGlyAlaLeuGlyIleLeuLys 349
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                                                                                           AspLeuGlnGluGlnIleLysAlaGlyLysAlaThrTyrAspSerAsnCysAlaAlaCys 409
                                                                                                                                                        ProGluGlyAlaProGlnAlaIleAspThrGlnGluAlaProLysThrProAlaProAla 389
                                                                                                                                                                                                                       ValGluGlyGluGluAsnHisGluIleTyrSerHisLysGlnThrAspAlaValTyrLeu 369
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GGAATCACCGGCCCCTTC---TTCCTTTCGGGGGACGACATG 2049
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Los, T., Ivanova, N., Anderson, I., Bhattacharyya, A., Lykidis, A.,
Reznik, G., Jablonski, L., Larsen, N., D'Souza, M., Bernal, A.,
Mazur, M., Goltsman, E., Selkov, E., Elzer, P.H., Hagius, S.,
O'Callaghan, D., Letesson, J.-J., Haselkorn, R., Kyrpides, N. and
Overheaber
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Brucella
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Kapatral, V., Los, T., Ivanova, N., Anderson, I., Bh Lykidis, A., Reznik, G., Jablonski, L., Larsen, N., Bernal, A., Mazur, M., Goltsman, E., Selkov, E., Has Kyrpides, N., and Overbeek, R.
                                                                                                                                                                                                                                                                                                   O'Callaghan, D.
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Direct Submission
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                              Submitted (13-NOV-2001) Faculte
                                                                                                                                                                                                                                                                                     Direct Submission
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Brucella melitensis
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Delvecchio, V.G., Kapatral, V.,
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complement (132. .1262)
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, Universite of Namur,
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GHLENNDFSNAKDVGHRNIEKQRPLQAEVVRDVLAVVNAD"
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FYRIEHEEAMMREAFGSAYDEYSSRIGRIIPKPW"
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TVGGFLMVVHQDDYLELTLIRETNTLLHUIDFHAATCALGGGCLTEINFGEKTVLRF
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/codon pro----
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/codon stari
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'Codon stari
                                                                                 codon_start=1/transl_table=
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5.33e-19 431.00 48.43% 34.76% 16.41%

> Length: Matches:

Conservative: Mismatches: Indels:

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                                                                                                                                                                                                                                                                                                                                                                                                  complement (8791. .9603)
/gene="BMEII0997"
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/gene="BMEII0995"
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/gene="BMEII0995"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluTyrValValPheAsnGlySerValGlyAlaLeuThrGlyGluAsnAlaLeuLysAla
                                                     LysGlnThrAspAlaValTyrLeuProGluGly
                                                                                          CTGGGCGCGCAGCCCACTTCAAGGTGACGGGCGAATGGAATGACGACTTGATGACA---
                                                                                                                               LysGlyAlaLeuGlyIleLeuLysValGluGlyGluGluAsnHisGluIleTyrSerHis
                                                                                                                                                                           ACGTTCCGGCAGCCGGCATCTACGCCTATGTCAATCATAACCTGATCGAAGCCTTTGAG
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                                                                                                                                                                                                                                                     CCAGATGTCGACCAGGANACCTGGTTCATTCCGGGCGGTGCGGCAGCGGCAGCCTTCTAC
                                                                                                                                                                                                                                                                                                                                   CCGCACCTGATCGGCGGCATGGCGATTATGTCTGGGCGACCGGCAAGTTCAATACGCCG
                                                                                                                                                                                                                                                                                                                                                                      PheHisValIleGlyGluIlePheAspLysValHisPheGluGlyGlyLysGlyGluAsn
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                TCGATACTGGCGCCGTCGGGG
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Read,T.D., Dodson,R.J., Umayam,L.A., Brinkac,L.M., Beanan,M.J., Daugherty,S.C., Deboy,R., Durkin,A.S., Kolonay,J.F., Madupu,R., Nelson,W.C., Ayodeji,B., Kraul,M., Shetty,J., Malek,J.A., Van Aken,S.E., Riedmuller,S., Tettelin,H., Gill,S., White,O., Salzberg,S.L., Hoover,D.L., Lindler,L., Halling,S.M., Boyle,S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (14-AUG-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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Brucella suis 1330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE014526
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lsen,I., Seshadri,R.,.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ed (14-AUG-2002) The Institute for Genomic Center Dr., Rockville, MD 20850, USA Location/Qualifiers
                              /translation="mfgatlsrwtlsyfasslafliagvglmvegfgypfhgirapet
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Flggiftlafsgmsrmdmlmiaglsapfihalglggmmtftamgvyrlltwfflsp
DDERRTTRLVmwagaaaltvlgagvaafafgodradvyllaallpgvasvylyafdmr
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                avyrorkrkaielnsaasipafaamvlaillalalpwtgpsdpmigalvylfvfgwlt
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/db_xref="GI:23463595"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity; putative"
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                                                                                                                                                                                                                                by sequence similarity;
                                                                                                                                                                                                                                                   locus_tag="BRA0253"
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                                                                                                                                                                                                                                                                                                                                                                                                                  /product="conserved hypothetical
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transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:204722"
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                                                                                                                                                                                                                                                                                                               tag="BRA0253"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tag="BRA0252"
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Brinkac, L.M., Beanan, M.J.,
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Research,

Boyle, S.M.

(2002)

Boyle, S.M.

GP:14523803;

identified

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sequence

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/transI_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /locus_tag="BRA0256"
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by sequence similarity; putative"
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WSVSLDIRREHKLVTDGLYRTVRHPWYLLSFWLWAIAQFFLLPNWIAGLAGLLGVAILY
FYRIEHEEAMMREAFGSAYDEYSSRIGRIIPKPW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3961. .4545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIYRRIKRNFFRVHYQYVFGNTKAYWYDFFQICCGPASLSERMRDMLVGTAKESAQQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVQRLVDEPALEWCEMQCLTDVINFYKTDPVAEMKLKRPADRAFPLVRQVRIKDMLQF
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2789. .3964
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MVHVKMTTTTRGCPAAGFLTQAVQACIEEIEGVTGARVELTYEPEMKPEMAIPEVQAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /locus_1
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                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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protein_id="AAN33457.1"
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                                                                                                                                          locus_tag="BRA0258"
496. .5194
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58.1"
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                                                                                                                                                                US-10-088-045-2 (1-502) x AE014526 (1-11302)
                                                                                                                                                                                                                                           Query Match:
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                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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                                                       5661 AGGAAGGCCAGCGCAGAGGAAATTGCTGCGCTGCCGAGACAG---AAAGTGGAGCTGGTC
                                                                                                                                                                                                                                                                         Similarity:
  63 AspAlaIleValThrHisAlaProGluValProProProValAspArgAspHisProAla 82
                                                                                                         LysThrAlaAsnAlaAspAsnAlaAlaSerGlnGluHisGlnGlyGluLeuProValIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVPPDNLGFRLVRDGRWYAPVLMRLKDFTS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus_tag="BRA0261"
/note="similar to GP:14523796, and GP:2773329;
by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KATKROVFVYHCAPOMVPWHVVSGMNGAVMVLPREGLHDGKGNKLTYDKVYYVGEOD
FYVPRDENGNYKTYEAPGDAYEDTVKVMFUVVPKNGAVALTGDKALTAKSGEK
VLITHSQANROTRPHLIGGHGDYVWATGKENTPPDVDQETWFIPGGAAAAAFYTFRQP
GIYAYVNHNLIEAFELGAVAHFKVTGEWNDDLMTSILAPSGM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:J05016, SP:P13667, GB:J05016, SP:P13667, and PID:181508; iv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVALPQTVTIKPRTMTYRADGDFQKNNYPVDAPLTTRKLRRSFEIMKYQVTGAEYRRC
VDDGACQPPEDLPHNRNWASADKPVVGVSYTDAEDYAAWLSKKTGSVWHLPTDERWAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="BRA0260"
5550. .6680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGTRFADDAVGIEGDESKNPALRWLRDYEQQSARKQDRNQTVRPLGAFGENEYGLAD
IGGNVWEWTQTCHRRVNIDAYGKVASETTVCGVYVVNGKHRAAMSSFIRNPKTGGCSV
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SLPABAKTQQAAMPPNATSHQADVYLLEGRADIFSTGIDEICAELQAAGVNAHVQGH
AAMRLVLANGIVADQQKUGHLPVVLIGHSLGANAATYIABELBERGGIAVDYMATFAATB
PDPLPGNVRRVVNFYFKQHGWGLPLVPGPRSHGHLENRDFSNAKDVGHFNIEKQRPLQ
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5813. .7733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon start=1
/trans1 table=11
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/protein_id="AAN33462.1"
/protein_id="AAN33462.1"
/db_xref="GI:33463602"
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/translation="MADGIQVNRTTILAGAALAGALGPVLSATSAWGQGTMRKASAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence similarity; putative"
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/note="similar to GB
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/protein_id="AAN33461.1"
/db_xref="GI:23463601"
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note="identified by Glimmer2; putative"
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/protein_id="AAN33460.1"
/db_xref="GI:23463600"
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270. .5419
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316050 bp
Nitrosomonas europaea ATCC 19718,
BX321859 AL954747
BX321859.1 GI:30138466
                                                                                                                                                                                                                                CTGGGCGCGGTAGCCCACTTCAAGGTGACGGGCGAATGGAATGACGACTTGATGACA---
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                                                                                                                                                                                                                                                                                                                                                    LysValAspValProGlyAspTyrValLeuValAspHisAlaIlePheArgAlaPheAsn 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGCACCTGATCGGCGGCATGGCCGATTATGTCTGGGCGACCGGCAAGTTCAATACGCCG 6476
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                                                                                                                                                                                        LysGlnThrAspAlaValTyrLeuProGluGly
                                                                                                                                                                                                                                                                        LysGlyAlaLeuGlyIleLeuLysValGluGluGluAsnHisGluIleTyrSerHis 361
                                                                                                                                                                                                                                                                                                                                                                                                 CCAGATGTCGACCAGGAAACCTGGTTCATTCCGGGCGGTGCGGCAGCGGCAGCCTTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                       HisAsnIle-----GlnThrThrLeuIleProAlaGlyGlyAlaAlaIleThrGluPhe 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAATCCGGCGAAAAGGTGCTGATCATC-----CACTCGCAAGCCAACCGCGATACCCGT
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                                                                                                                                               TCGATACTGGCGCCGTCGGGA
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                                                                   DNA
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                                            genome; segment 4/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome consortium, the DOE Joint Genome Institute, Production
Genomics Facility, 2800 Mitchell Drive, Walnut Creek, CA 94598,
USA, and the Genome Analysis Group, Oak Ridge National Laboratory,
1060 Commerce Park Drive, Oak Ridge, TN 37831, USA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hommes, N., Whittaker, M. and Arp, D. Complete Genome Sequence of the Ammonia-Oxidizing Bacterium and Obligate Chemolithoautotroph Nitrosomonas europaea J. Bacteriol. 185 (9), 2759-2773 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chain, P., Lamerdin, J., Larimer, F., Regala, W., Land
Hooper, A., Klotz, M., Norton, J., Sayavedra-Soto, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nitrosomonas europaea ATCC 19718
Nitrosomonas europaea ATCC 19718
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-NOV-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 316050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /locus_tag="NE0847"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           order(complement(1038. .1094),complement(951. .1007))/locus_tag="NEO846"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Nitrosomonas"
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        'product="Phosphoglycerate
                                                                                                                                                                                                                                                                                                                                                      product="conserved hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                           locus tag="NEO847"
function """
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                                                                     codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                         function="COGs COG0726"
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                                                                                                                                 .2873)
                                                                                        IPR001345
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                                                                                           COG2062"
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4378. .4458
/note="Signal predicted by SignalP 2.0 HMM (Signal peptide
probabilty 1.000) with cleavage site probability 0.844 at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 order(complement(3496. .3561),complement(3418. .3483),complement(3112. .3177),complement(3034. .3099),complement(2935. .2997))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="similar to nodulin 21"
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                                                                                                                                                                                                                                                                                                                                                                                   GYPYAEIDGRLQDSLEPESFSYKITSAVLVGTGAKL"
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VĀRVMĀĀESLSHNHDSISQLREKLFGSWEMNWVĀFNERENVDLGTTKVSĀĀISKLPFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /locus_tag="NE0851"
4390. .5502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Phospholipase/Carboxylesterase"
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/trānslation="mpDN
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/locus_tag="NE0850"
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                                                                                                                                                                                                   complement (5615. .7336)
                                                                                                                                                                                                                                                                                                                                    complement (5615. .7336)
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/db_xref="GI:30138472"
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transl_table=11
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omplement(2627
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Percent Similarity:
Best Local Similarity:
Query Match:
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87890 TCCATGGATTTCCATGCTGCCAGGCTGGATGTGGTGGAGGATTTCGAGTCG---
                                                                                                                                                                                                                               01088
                                    140 AsnValAspPheHisAlaAla--ThrGlyProGlyGlyGly-AlaGluAlaSerPheThr 158
                                                                                                                                                       120 ArgGluGlyAspThrIleGluValGlnPheSerAsnHisProAspSerLysMetProHis 139
                                                                                                                                                                                                                                                                                100 GlyValGluTyrGlnPheTrpThrPheGlyGlyGlnValProGlyGlnMetIleArgVal
                                                                                                               ACTGAAGGGGATACGGTGGAATTTACCCTCATCAATGACAAAAATAGTAAGAACTCCCAT
                                                                                                                                                                                                                            GGAAGTACTTATCGTGCCTGGACGTTCGACGGTAAGGTTCCCGGTCCGGTCCGTACGGGTC
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complement(9708. .10664)
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Ilaigdmsyehfcgagkriderfealgakriqprvdcdvdyedpaavwstgiiallaa
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SERYLPDLITKIEGILTRYNLQNEPITLRMTGCPNGCSRPFIAEIGLTGRAPGKYNLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="cysB"
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/protein_id="CAD84764.1"
/db_xref="GI:30138474"
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/transl_table=1
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/function="InterPro
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                                   Direct Submission
Submitted (01-SEP-1992) Makoto Nishiyama, The University
Department of Biotechnology; 1-1-1 Yayoi, Bunkyo-ku, Toky
Depan (Tel:03-3812-2111(ex.5126), Fax:03-3812-0544)
Submitted (01-SEP-1992) to DDBJ by:
Makoto Nishiyama
                                                                                                                                                                                                                                            Cloning and characterization of a nitrite reductase ger Alcaligenes faecalis and its expression in Escherichia J. Gen. Microbiol. 139 (Pt 4), 725-733 (1993)
                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Betaproteobacteria; Alcaligenaceae; Alcaligenes.
1 (bases 1 to 2351)
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Alcaligenes faecalis
Alcaligenes faecalis
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A.faecalis gene for nitrite reductase,
D13155
D13155.1 GI:398121
  Faculty of Agriculture
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGATAGGAGCGGGAGATGCGGCAACGCTGGATCTGATTTCTCCGGTTGAAGGTGCCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGGATCGGGTTTACCCCAGCGGCAACCCCCAAAAACGTCCAGTATGCCCTGCAATCCTAT
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                  of Agricultural Chemistry
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1-1-1 Yayoi, Bunkyo-ku
  GlyGlyGlyAlaGluAlaSerPheThrAlaProGlyHisThrSerThrPheSerPheLys 169
                                         ATCAACCCTGAAACCAACACGCTGATGCACAATATCGATTTCCATGCGGCAACCGGTGCA
                                                                           SerAsnHisProAspSerLysMetProHisAsnValAspPheHisAlaAlaThrGlyPro 149
                                                                                                                                                                                                                                            ValGluLysValMetArgLeuAlaAsp---GlyValGluTyrGlnPheTrpThrPheGly 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGCAACCACATCCGCCTGGGGACAAGGCGCGGTGCGGAAGGCAACTGCGGCAGAAATA 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGGCAGGAGCCGCCCTGGCTGGG----
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GIYAYVNHNLIEAFELGAAAHFKYTGEWNDDLMTSVLAPSGT"
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03-3812-0544.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic
/strain="S-6"
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427.50
47.00%
33.68%
16.28%
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158
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ACCESSION AP005214.1 BA000035 VERSION AP005214.1 GI:23491835  KEYWORDS SOURCE Corynebacterium efficiens YS-314 Bacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaeae; Corynebacterium.  REFERENCE AUTHORS Ikeo,K., Suzuki,M., Mashima,J., Itoh,T., Yamagishi,A., Nishio,Y., Usuda,Y. and Sugimoto,S. TITLE JOURNAL Published Only in Database (2002) REFERENCE (bases 1 to 313200) Kawarabayasi,Y., Yamazaki,J., Hino,Y., Kikuchi,H. and Director-General of Biotechnology Center.	Oy 350 ValciuGlyGluGluAsnHisGluIleTyrSerHisLysGlnThrAspAlaValTyrLeu 369  1822 GTCACGGGTGAATGGAACGACGATCTGATGACGTCGGTTCTCGCA 1866  Oy 370 ProGluGly 372  Oy 370 ProGluGly 372  Ob 1867 CCATCTGGC 1875  RESULT 32 AP005214/c AP005214 DEFINITION Corynebacterium efficiens YS-314 DNA, complete genome, section 1/11	1582 292 • 1642 310 • 1702 330	207	Db 1174 TTGGGCGGCGGGCTGACCGAAATCAATCCGGAAAAAAAAA
· .				
CDS	CDS		FEATURES SOURCE CDS	JOURNAL COMMENT
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ddltgqdidyvaalsrlelpvlftrftndrdcptassealaeflhnadvrfedlpgel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVIAELRIFGPOAPSWRKGPLHVKGRGPRDTYG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mtededfiaqafervrreaqrrngrypdlnnrdafrrttprpig
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DAYQTIAPESRPAAVNYKTTIQGLAQFGEFDAGIIEATLLTELAAKRRREIERGMSL
VGPHRDDLELHLGGQPAKGFASHGETWSFALSMRIAEFNLLRSDGTDFILILDDVFSE
                                                                              TAAQTVNVTSQDAQGAADATSQEDVDQAQAEAE"
                                                                                                                                                                          GHNRWAREPVIVADRFVSFAGVLD"
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/db_xref="GI:23491842"
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/db_xref="GI:23491841"
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identity: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="CE0007"
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                                                                                                                                                                                                                                                                                                                           note="CE0008"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="CE0006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       071. .5652
note="CE0005,
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                   note="CE0009, similar to X65467-3|CAA46462.1| percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _table=11
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in 113 aa"
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n 685 aa"
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US-10-088-045-2 (1-502) x AP005214 (1-313200)
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                                                                                                                                                                                                                                                                                                                                                                                                     91 ValGluLysValMetArgLeuAlaAspGlyValGluTyrGlnPheTrpThrPheGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 AlaSerGlnGluHisGlnGlyGluLeuProValIleAspAlaIleValThrHisAlaPro 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 AlaGinProLysSerSerThrValAspAlaAlaAlaLysThrAlaAsnAlaAspAsnAla
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                                                                                                                                                                                                                                CAGGCGCCCGGACCCCTGCGCGCGACACCCTTCCGCATCACCCTG---
                                                                                                                                                                                                                                                                                   GlnValProGlyGlnMetIleArgValArgGluGlyAspThrIleGluValGlnPheSer 130
                                                                                                                                                                                                                                                                                                                                                  ACCGAGGAGGTCGCCAGGTCGCACCGGGTCATGAGCAGGTGGTCTTGGCTTTTCGACGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluValProProProValAspArgAspHisProAlaLysValValLysMetGluThr 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAITAATPEVPAAAEVTEVAGEGITGLVDGTRIAVGSPRWLAPGPLVGTVEDLEGKGM
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LAGSINISGVLEVBAFAAGTDNSLTTVVSLVEGAQAPERARIADRLARFLVPGVLI
LAGLIVAVIGSLIGDBDVMIERALVLVLVAASPCALAISVPUTVVSAIGAASRFGYVIK
GAAFERLGGIQHLALDKTGTLTRNQPTVADVVTTGATSRAEVLGMAAALEAHSTHPLA
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/product="hypothetical protein"
/protein_id="BAC16821.1"
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Srillslidapgypaolatelgltrtnvsnhlaclrdcgivvaepegrrtryeiadah
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/transl_table=
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/note="CE0010,
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AE005046.1 GI:10580716
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Ng, W.V., Kennedy, S.P., Mahairas, G.G., Berquist, B., Pan, M., Shukla, H.D., Lasky, S.R., Baliga, N., Thorsson, V., Sbrogna, J., Swartzell, S., Weir, D., Hall, J., Dahl, T.A., Welti, R., Goo, Y.A.,
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Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
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                                                                                                                   Proc. Natl. Acad. Sci.
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                                                                                                                   sequence of Halobacterium species NRC-1
Natl. Acad. Sci. U.S.A. 97 (22), 12176-1
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Leithauser, B., Keller, K., Cruz, R., Danson, M.J., Hough, D.W., Maddocks, D.G., Jablonski, P.E., Krebs, M.P., Angevine, C.M., Dale, H., Isenbarger, T.A., Peck, R.F., Pohlschrod, M., Spudich, J.L., Jung, K.-H., Alam, M., Freitas, T., Hou, S., Daniels, C.J., Dennis, P.P., Omer, A.D., Ebhardt, H., Lowe, T.M., Liang, P., Riley, M., Hood, L. and
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                                                                                                                                                                                                                                                                    /gene="pqqE"
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2187. .3257
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AVEHDAERQAAFAEHADTVSMNVFEEAAAELSVQWYELTPDSMSGRAGGHWTPPTTDD
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Best Local Similarity:
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                          spHisProAla----
   AC---ACGGACGGCAAGCGCCCACACACGCTGCATTTCCAC----
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US-10-088-045-2 (1-502) x AE005046 1.65e-07 258.00 40.24% 26.10% 9.82% (1-10159)Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 10159 107 58 151 94 20

3711 GCGTGCCCGGCCCCATCGTGCGCACCGAGGAAGGCCAGGACATCGAGGTGACGCTCGACA 3591 GCAACCAGGTGACGCTGAAAAGCGTGCCGGCGGTCCACGACGTCCACCCCTTGGATTCGA --ValProGlyGlnMetIleArgValArgGluGlyAspThrIleGluValGlnPheSerA TGGGCGGCCCGGTGAAGCTCCCCCGGGTGTGGGCGTTCGCCACCGAAGACGGCGACCCGA 3710 TCCCG-----ACCACGAGCCCGCCGGAGGTCGTCGACGCCACCGAGCAGG euProValIleAspAlaIleValThrHisAlaProGluValProProProValAspArgA CCGCTCCCGACGGTGGGGAGTCGGTGACGGACACGACCACTGCGGCCAAACAATCCGGAC erThrValAspAlaAlaAlaLysThrAlaAsnAlaAspAsnAlaAla-----GlyCysSer--------AsnGlnAlaAspLysAlaAlaGlnProLysSer-S TCCTTCCCAGACCGTAGGAACGATTCCCTGACCTGTGGAACCAGCGGGCTGCGATTAAGT euAlaAspGlyValGluTyr---GlnPheTrpThrPheGlyGlyGln-----CGCGGCGTGACTTCGTGGCGGCGACCGCTGGCGTCGGGACCGCTGCCATCGCCGGCTGCA GGCGGGCCATAGCACGGCGTGTATGACCGATCAGATCGGCGCTCCCGGCCTCGGCATCT SerLysProThrLeuIleLysThrThrLeuIleCysAlaLeuSerAlaLeuMetLeuSer LysValValLysMetGluThrValGluLysValMetArgL -----SerGlnGluHisGlnGlyGluL 3770 3650 3590 3425 131 97 79 3545 36 3365 111 59 3485 51 21

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AUTHORS
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                                                                                                                                           Ren,S.X., Fu,G., Jiang,X.G., Zeng,R., Miao,Y.G., Xu,H., Zhang,Y.X., Xiong,H., Lu,G., Lu,L.F., Jiang,H.Q., Jia,J., Tu,Y.F., Jiang,J.X., Gu,W.Y., Zhang,Y.Q., Cai,Z., Sheng,H.H., Yin,H.F., Zhang,Y.Q., Cai,Z., Sheng,H.L., Qian,Z., Wang,S.Y., Ma,W., Yao,Z.J., Zhu,G.F., Wan,M., Huang,H.L., Qian,Z., Wang,S.Y., Ma,W., Yao,Z.J., Shen,Y., Qiang,B.Q., Xia,Q.C., Guo,X.K., Danchin,A., Saint Girons, I., Somerville,R.L., Wen,Y.M., Shi,M.H., Chen,Z., Xu,J.G.
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Leptospira interrogans serovar lai str. 56601
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
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143 of 397 of the complete sequence
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                                                Unique physiological and pathogenic features of Leptospira interrogans revealed by whole-genome sequencing Nature 422 (6934), 888-893 (2003)
                                                                                                                           Girons, I., Sc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ren,S., Fu,G., Jiang,X., Zeng,R., Xiong,H., Lu,L., Lu,G., Jiang,H. Ding,Y., Jia,J., Tu,Y., Gu,W., Cai,Z., Sheng,H., Yin,H., Zhang,Y., Zhu,G., Wang,S., Shen,Y., Qiang,B., Chen,Z., Wen,Y., Xu,J. and
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VSFPKEGVFYYCSFHATEDGKNGMVGGIVCHVDPAKKSKSKWKNVSQFSGTTKK
VSFPKEGVFYYCSFHATEDGKNGMVGGIVCHVDPAKKSKSKWKNVSQFSGTTKK
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VSLIFILGCLLYTKIGLGGAGILWLFLVPVFCGIFLGRIITFWSYVITSLFVFSGIFF
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complement(6747. .70
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                                                                                                                                                                                       'locus_tag="LA1560"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'product="hypothetical protein"
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Query Match:
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214 ValMetGlnGly---AspPheTyrThrLysGlyLysTyrGlyGluGlnGlyLeuGlnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 MetArgLeuAlaAspGlyValGluTyrGlnPheTrpThrPheGlyGlyGlnValProGly 114
                                                                                                                                                                                     GlyLeuTyrValTyrHisCysAlaValAlaProValGlyMetHisIleAlaAsnGlyMet 193
                                                                 TACGGAGGTCTGATCGTGGATCCACCTGGAGGTCGTCCGCCTGCACATGAATTTATGCTG
                                                                                                     TyrGlyLeuIleLeuValGluProLysGluGlyLeuProLysValAspLysGluTyrTyr
                                                                                                                                               GGATTTCATCCGTATCATTGTCACGTTCCTCCATTGGCTAGTCATATGGCAAAAGGTCTT
                                                                                                                                                                                                                                                                 GluAlaSerPheThrAlaProGlyHisThrSerThrPheSerPheLysAlaLeuGlnPro 173
                                                                                                                                                                                                                                                                                                               SerlysMetProHisAsnValAspPheHisAlaAlaThrGlyProGly---GlyGlyAla 153
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SAVYKNGVLNLTLPKRKPLTKKIEVRSE"
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omplement(843.
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Nitrosomonas sp. TA-921i-NH4
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
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Submitted (22-JAN-
Hall, Princeton, N
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Casciotti, K.L. and Ward, B.B.
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Casciotti, K.L. and Ward, B.B.
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Princeton, NJ 08544, USA
Location/Qualifiers
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/strain="TA-921i-NH4"
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                                                                                                                                                                                                                                             Nostoc sp.
Kaneko,
Direct
                                                                                                                                          Kaneko,T., Nakamura,Y., Wolk,C.P., Kuritz,T., Sasamot
Watanabe,A., Iriguchi,M., Ishikawa,A., Kawashima,K.,
Kishida,Y., Kohara,M., Matsumoto,M., Matsuno,A., Mura
Nakazaki,N., Shimpo,S., Sugimoto,M., Takazawa,M., Yam
                                                                                                                                                                                                                                                                                               Nostoc sp. PCC 7120 DNA, complete genome, AP003594 BA000019 AP003594.1 GI:17132824
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                                                                  DNA Res. 8
21595285
                                                                           cyanobacterium Anabaena
DNA Res. 8 (5), 205-213
                                                                                               Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120
                                                                                                                                Yasuda,M. and Tabata,S.
                                                                                                                                                                                                                                 Bacteria;
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neko.T.
 Submission
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PCC 7120
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Muraki, A.,

Kimura, T.,

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Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
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GLLANPAAGAFLIIFRPFKVGDFITAAGITGTVSEIGLFTTDITTPDNVLTIVANKI
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TQLEHTLQHLQQTQLQLVQNEKMSALGNLVAGVAHEMNNPLGFIAVSLQHTQPTFADI
MEHLKLYQESLPHPGDKILHHAAQIDLDYILEDLPKLIEAMVMACDRLKNISTSLRTF
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GHLVGILYLENRLTRGVFTSGRLEVIR LLSAQAAVELEKARLY KQESQTKAQQLKQSLK
QQKILFNVVNQMRGSLDLAAI FCVYQNIR RILDVDRYG1 YQFHLDVDYFYGEFVABO
VSPAFPSALAVKVQDHCFGENYANLYKQGRI CAITDVQSSEILDCHRQILAQFHVRAS
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YHOQLLDFNLVTSANHCFVYMESALILLGKSADEISLRODAYAEKIVTEALASNDLWR
LFQFYLYRLVLUNFLLADPRAKODAEKAROYLTGCMGSVAEDIFYFYDSLTALASLDLWR
LFQFYLYRLVLUNFLLADPRAKODAEKAROYLTGCMGSVAEDIFYFYDSLTALASLHOS
PAGRDSOMORVRENOAILDKWADHAPMNYLHKWOLVAAETHRLLEOKTEAMEFYEMAI
KGAKENKYLRDEALAWELAAKY YLDWGKEKVYAAVYNGEAYYCYAFWEAKAKTNOLEKR
YFOLLOFILOEROFKENFOETIAVPGTSSTLSSTLGSTSISDTLDFASILKAAOVIS
TSLBLDELITNLTEIILENGGAKKSALLLPOEDIWOIKAMTLSNFOPNSSESTOTILE
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AKCPLDKYQVYQVKIQALTSRWELLBALAFGKSFLQELGVSLPDHFTPEDVQQAREEI
NRLIGDRLLGEFINLPKMTDBEKLAIMQISSSLIPACYMTGSLLYLLIVPLQVKLSLQ
FGNSLFSAHGYVSYAFHLSTTWQNMALAQQLGQIAYQLASEPEAKNIRAATFIVLGGY
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LQEGLIIPQSEVYKFFVGQEQEIDHAQTTEIVTYKFLHDRVQQAAYCLIPEAERAIAH
HHIGQLLLQKISPAAREEHIFEIVNQLNYGITLITQSERDELAQLNLNAAQKARAAT
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MNDTGYLLLIGAYRDNEVNPAHPLMLTVNEIGKNNGTIKKIDLAPLNQLKVNTLVAET
LKCSBETAQSLALLVFQKTQGNPFFTTQFLKALHQDNLIQFNYDLGCWQCDIAQVNHQ
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LRDYAQQQSLSLTEILTITIQLADILHHIYQQRIIHKDIKPANILINPETKQVKLIDF
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hypothetical protein"
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6804. .7658
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VFMNILANAIDALEDANNGLSYAEITANNNRIIIRTTQVNNHVRISITDNGIGMSEEL
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/gene="all3691"
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/gene="all3691"
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codon_start=1
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                                                                                                                                            note="ORF_ID:all3697"
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complement (12278. .13114)
                                                                      complement (
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unknown protein"
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KEYGGLYYFMDAAGHPPQQLEWDQKLWWVHLESLVALAMGYRLTGREVCWEWYQKMHD
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TYPGTRPMKALAVPNILANLTLEMEWLLPQETLENVLSATVQEVMSDFLDKERGLMYE
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GLLANFAAGAFLVIFRPFAVGDTIKAAGVTGKVEEIGLFTTTINTSDNVKTIIGNNKI
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               GlnProPheAspMetGluLysAlaIleArgGluAspAlaGluTyrValValPheAsnGly
                                                 ATAGTGCTGGTGATGGCTGGC---
                                                                                                                                            AsnGlyMetTyrGlyLeuIleLeuValGluProLysGluGlyLeuProLysValAspLys
                                                                                                                                                                                                   LeuGlnProGlyLeuTyrValTyrHisCysAlaValAlaProValGlyMetHisIleAla
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                                                                            GluTyrTyrValMetGlnGlyAspPheTyrThrLysGlyLysTyrGlyGluGlnGlyLeu
                                                                                                              AAAGGTTTATATGGAATGTTTATCATCGACCCACCGGCACCCCGTCCCCCAGCCGATGAG
                                                                                                                                                                                                                                            GAAATGGATGGTGCCGTCCTGTGAGTAATAATAGTGCCACCATCTACGAATTTGATGCT
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FLPDEQLPIAYQAANLTVMPSQSFEGFGLAITESLACGTPVLCTPIGGMPEILTPFSP
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FLAITIITADLTLSEVAENSDKKDLMGDIFADSQKSIQNYIEGIYVAPNGTVYTMSHE
DKAGAEASIXKDGNVIGULSDLDGWSBRRGGKAVTANSKYIYIAMSQGFWGKIDKDYP
EGTTWYCVRRYNLSGKPAPFANGRGWDKSMLIVNTKSEVTGLATKDKNLYVSDAANNK
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14028. .15197
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similar to glycosyltransferase"
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hepB_gene_product"
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347456 bp
Wallius Cereus ATCC 14579 section
AE017003 AE016877
AE017003.1 GI:2980F777
                                                                                                                                             Submitted (12-MAR-2003) INRA, Genetique Microbienne, Vilvert, Jouy en Josas 78352, France Location/Qualifiers join(1. 285893,347289. .347456) / Organism="Bacillus cereus ATCC 14579" / mol_type="genomic DNA" / strain="ATCC 14579" / strain="ATCC 14579"
                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 347456)
Ivanova, N., Sorokin, A., Anderson, I., Galleron, N., Candel, Ivanova, N., Bhattacharyya, A., Reznik, G., Mikhailova, N., Kapatral, V., Bhattacharyya, M., Goltsman, E., Larsen, N., D', Lapidus, A., Chu, L., Mazur, M., Goltsman, E., Larsen, N., D', Walunas, T., Grechkin, Y., Pusch, G., Haselkorn, R., Fonstein Ehrlich, D.S.D., Overbeek, R. and Kyrpides, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 347456)
Candelon, B., Gailloux, K., Ehrlich, D.S.
The number of ribosomal RNA operons in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus cereus ATCC 14579
Bacillus cereus ATCC 14579
Bacteria; Firmicutes; Baci
                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 423 (6935), 87-91 (2003)
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organism="Bacteriophage"
                                  285894.
                                                                                                                    db_xref="ATCC:14579"
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DGAYSAEELKQICKDGDEVIGVHIYRNDAPIPEGVMLVDTPGIDSTDDAHQLATESTII
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and Bacillus thuringiensis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mTGTLFGCAQDLPPKPNDNSCSDWDWDDELGVWQCDDSSSGYRG
HYPYGGRYYQNKSTFKNSSAFKSYQSSAEFKGGIGSGSKGGFGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mrleyrlndetkgypalwnyanisnseiiarmtceyfikeknty
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/db_xref="GI:29895272"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=
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LETEKGIEKLSYVFGSFLIAGKASSIGIRAGEKITGNESYYLPVGIKRRGKND"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative synthetase/amidase"
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7045. .7311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (6467.
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564. .8553.
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	erPheHisValIleGlyGlu 289	lyGlyProAsnLeuThrSerSerPheHisV	ValGlyAsnG	273	Ş
	CCATTAAAAGTGAATAAGGGAGATAACGTTCGTCTTAGA 268821	;	GGTGATTTAGTAGCG	268768	DЪ
	lyGluThrValArgLeuPhe 272	GlyAlaLeuThrGlyGluAsnAlaLeuLysAlaLysValGlyGluThrValArgLeuPhe		253	ફ
	   TCACAATCAATGGAAAAAGC 268767			268708	90
	heAsnGlySerVal 252	laGluTyrValVa		235	<b>.</b> 9
	AAGGAATGGACCATGGAAAT 268707	ATGAACATGGGCAGTGATAAAAAAGACTCTAGTAATATGGAAGGAA		268648	ß
	GlnGlyLeuGlnProPheAsp 234	G		228	Ş
	ACGGCATGGATCATTCTGAT 268647	tctaaaggtaatgaaaatggggaaaagaatgatgataagaacggcatggatcattctgat		268588	рb
	227			227	ş
	:::     AAGGGCAAATAGGTAATAAA 268587	GATAAAGAAGAAATGAATAAGCAGTTAAAAGAAATGACAAAAAGGGCAAATAGGTAATAAA		268528	Db
	TyrThrLysGlyLysTyrGlyGlu 227	TyrThrL		220	ફ
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	etGlnGlyAspPhe 219	svalaspiysGluTyrTyrValmetGlnGlyAspPhe	LysGluGlyLeuProLy	202	ई
	::::::       GAGCGCTCATTGTAGAAGAT 268473	CAATTAGATAGAGGTTTGTATGGAGCGCTCATTGTAGAAGAT		268417	ФФ
	TyrGlyLeuIleLeuValGluPro 201	leAlaAsnGlyMet		182	8
	CTCGCAT 2	AAAAGTTTCACTTACGAATTTGAAGCGAACGTACCAGGAACGTACTGGTATCACTCGCAT		U	망
	euTyrValTyrHisCysAla 181	HisThrSerThrPheSerPheLysAlaLeuGlnProGlyLeuTyrValTyrHi		162	Ś
	AAGATGCAGTTGAACCAGGA 268356	CTGTCCCAAATAACATGGATGGAATTCCAGGCGTGACACAAGATGCAGTTGAACCAGGA		268297	₽
	GlyAlaGluAlaSerPheThrAlaProGly 161		ThrGlyProGlyGly	147	Ś
	TGGATAT 26	GAATTATCTGCACCAGTAT		268243	B.
	snValAspPheHisAlaAla 146	ProAspSerLysMetProHisAsnValAspPheHi		127	Ś
	rgGiuGlyAspThrIleGlu 126 :::::   ::: ::::: AAAAAGGTGAAAAGGTGAAA 268242	Interestystychnyalfioglyginmetileargyalargginglyaspinrilegin 		268183	유 성
		Profile Clawar Tagaretta			?
	lyValGluTyrGlnPheTrp 106       GTGTTATTGTTCCAGTCTGG 268182	tGluThrValGluLy6ValMetArgLeuAlaAspClyValGluTyrGlnPheTr; 	LysMetGluThrVal	87 268135	음 성
	26	AC IGANACAGE IACAACACCA ITGAAAAGTTGAAAAAGGACCAGAAGTTACTTTAATAGCG		6/0897	5
	86	ThrHisAlaProGluValProProProValAspArgAspHisProAlaLysValValVal		9	\$ 8
		03 (1-347456)	-2 (1-502) x AE017003	0-088-045-	US-1
	347456 108 57 159 144 19	Length: Matches: Conservative: Mismatches: Indels: Gaps:	res: 6.81e-05 245.00 245.00 35.26% milarity: 23.08% 9.33%	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarit Query Match: DB:	Alignmen Pred. No Score: Percent Best Loc Query Ma DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356 HisGluIleTyrSerHisLysGlnThrAspAlaValTyrLeuProGluGlyAlaProGln
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                                                                                                                                                                                                                                                       Mesorhizobium sp. 4FB11
Mesorhizobium sp. 4FB11
Bacteria; Proteobacteria; Alphaproteobacteria;
Phyllobacteriaceae; Mesorhizobium.
1 (bases 1 to 537)
Song,B. and Ward,B.B.
Nitrite reductase genes in halobenzoate degradi
                                                                                                                                                                                                                                                                                                                                                                                                 537 bp DNA linear BCT 03-MAR-2002 Mesorhizobium sp. 4FB11 putative dissimilatory nitrite reductase (nirK) gene, partial cds.
AY078254
AY078254.1 GI:19072874
                                                                                                                    Submitted (08-FEB-2002) Geosciences,
Hall, Princeton, NJ 08544, USA
Location/Qualifiers
                                                                                                                                                                         Song, B. and Ward, B.B. Direct Submission
                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                         (bases 1 to 537)
                   /db_xref="taxon:126151"
<1. .>537
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/mol_type="genomic DNA"
/strain="4FB11"
/gene="nirK"
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Ensifer sp. 2FB8
Ensifer sp. 2FB8
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Ensifer.
1 (bases 1 to 537)
                                                                                                        AY078247
Ensifer sp. 2FB8 g
gene, partial cds.
                                                                                              AY078247
                                                                                  AY078247.1
                                                                                                                                                                                                                                                                                                                                                        GACAACGCGATGAAGTCCAAGGTCGGCGAGACGGTG---
                                                                                                                                                                                                                                                                                                                                                                      GluAsnAlaLeuLysAlaLysValGlyGluThrValArgLeuPheValGlyAsnGlyGly :::|||||||:::|| :::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACGGCAACTTCAAGAAGTTCGACTCCCTTGGCGAGAGCTACGAGGAGAGCGATGGAGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrGlyLeuIleLeuValGluProLysGluGlyLeuPro-----
                                                                                                                                                                                                                  GlyAlaAlaIleThrGluPheLysValAspValProGlyAspTyrValLeuValAspHis
                                                                                                                                                                                                                                               GAGGGCAAGTTCGCCAACCCGCCCGCCCAAGGATCTGGAGACCTGGTTCATCCGTGGCGGT
                                                                                                                                                                                                                                                                       GlyGlyLysGlyGluAsn------HisAsnIleGlnThrThrLeuIleProAlaGly
                                                                                                                                                                                                                                                                                                                           ProAsnLeuThrSerSerPheHisValIleGlyGluIlePheAspLysValHisPheGlu
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YTFLQPGVYAYVMHNLIEA"
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177 ValTyrHisCysAlaValAlaProValGlyMet-----HisIleAlaAsnGlyMet
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                                                                                                                                                                                                                                                                                                                                                                                                                         56 AACGGCGCCATCATGGTGCTGCCGCGCGACGGACTGAAGGACGAGAAGGGCCAGCCGCTG
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Song, B. and Ward, B.B.
Direct Submission
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GlyLysGlyGluAsnHis-----AsnIleGlnThrThrLeuIleProAlaGlyGly
                                                                                                                     CATGCTTTGACTGCGGCCGTGGGCGAG-----CGTGTGCTCGTCGTCCATTCGCAGGCC
                                                                                                                                                    AsnAlaLeuLysAlaLysValGlyGluThrValArgLeuPheValGlyAsnGlyGlyPro
                                                                                                                                                                                             CGCACGCTGACCCCGACCCACATCGTCTTCAACGGTGCGGTCGGCGCGCTGACCGGCGAC
                                                                                                                                                                                                                   ArgGlu----AspAlaGluTyrValValPheAsnGlySerValGlyAlaLeuThrGlyGlu
                                                                                                                                                                                                                                                                      GGGAACTACAAGAAGTACGAAACCCCCGGCGAAGCCTATGAAGATGCTGTCAAGGCGATG
                                                                                                                                                                                                                                                                                                                                                                        LysValAspLysGluTyrTyrValMetGlnGlyAspPheTyrThrLys--
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                                                                            AsnLeuThrSerSerPheHisValIleGlyGluIlePheAspLysValHisPheGluGly
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174 c 170 g
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                                                                                       207 LysValAspLysGluTyrTyrValMetGlnGlyAspPheTyrThrLys-----
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176 GGGAACTACAAGAAGTACGAAACCCCCCGGCGAAGCCTATGAAGATGCTGTCAAGGCGATG 235
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Ensifer sp. 4FB6
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Ensifer.
1 (bases 1 to 537)
Song,B. and Ward,B.B.
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Song, B. and Ward, B.B.
Direct Submission
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                            -----GlyLysTyrGlyGluGlnGlyLeuGlnProPheAspMetGluLysAlaile 239
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	His 334	334	8
520	GGAACCGCCGGCGCTGCCTTCTACACCTTCCGCCAGCCGGGTGTGTACGCCTACGTCAAC 520	461	망
ω ω	314 GlyGlyAlaAlaIleThrGluPheLysValAspValProGlyAspTyrValLeuValAsp 333	314	Ş
460	401 GCGACCGGCAAGTTCCGGCAACCCGGCGGATCTCGACCAGGAAACCTGGCTCATTCCGGGC 460	401	Вb
313	299 GlyLysGlyGluAsnHisAsn	. 299	Ş
400	AACCGCGATACGCGACCGCACCTGATCGGCGGGCATGGTGACTATGTCGGG 400	350	뫄
298	279 AsnLeuThrSerSerPheHisVallleGlyGluIlePheAspLysValHisPheGluGly 298	279	Ś
349	CATGCTTTGACTGCGGCGTGGGCGAGCGTGTGCTCGTCGTCGATTCGCAGGCC 349	296	В
278	AsnAlaLeuLysAlaLysValGlyGluThrValArgLeuPheValGlyAsnGlyGlyPro 278	259	Ş
295	236 CGCACGCTGACCCCGACCCACATCGTCTTCAACGGTGTGGTCGGCGGCGCTGACCGGCGAC 295	236	망
258	ArgGluAspAlaGluTyrValValPheAsnGlySerValGlyAlaLeuThrGlyGlu	240	Ş

Search completed: September 5, 2003, 12:57:48 Job time : 7408 secs

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## Run on: OM protein - protein search, using sw model August 27, 2003, 18:27:06 ; Search time 42 Seconds (without alignments) 1149.445 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-088-045-2 2626 1 MSKPTLIKTTLICALSALML.....NKGGQLSADDVAKAKKTKPN 502

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	28				24	23			20	19	18	17.	16	15	14	13	12	11	10	9	80	7	0	υ	4	ω	2	<b>-</b>	No.	Result	ļ
161	162	163	163	164.5	167	170	174.5	187	187	194	203.5	222	222	248.5	250.5	427.5	431	439.5	442	442	448	451	451	453	461.5	1386	1386	1388	Score		
6.1	•	•	6.2	•		6.5	6.6	7.1	7.1	7.4	7.7	8.5	8.5	9.5	9.5	16.3	16.4	16.7	16.8	16.8	17.1	17.2	17.2	17.3	17.6	52.8		52.9	Match I	Query	æ
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cytochrome c552 [v		L-ascorbate oxidas		copper resistance		. L-ascorbate oxidas	probable copper-co	multicopper oxidas			copper resistance	cytochrome c552 NM			membrane protein [	nitrite reductase	nitrite reductase	probable nitrite r	copper-containing	nitrite reductase,	rite reduct	7.	te	nitrite reductase	nitrite reductase	nitrite reductase	nitrite reductase	ctase	Description		

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	
142	143.5	144	144.5	145	145.5	146	149	150	150	151.5	153	153.5	154	158.5	159.5	
5.4	5.5	5. 5	5.5	5 5	ភ ភ	5.6	5.7	5.7	5.7	5.8	5.8	5.8	s.9	6.0	6.1	
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A36868	KFBO5	T05020	T44928	S23763	B49340	S14271	F83387	E83075	F83631	T04343	A83363	KSKVAO	T35030	F70813	C82845	
copA homolog - Xan	coagulation factor	L-ascorbate oxidas	L-ascorbate oxidas	pollen-specific pr	membrane-bound alc	membrane-bound alc	copper resistance	probable cytochrom	cytochrome c oxida	L-ascorbate oxidas	probable cytochrom	L-ascorbate oxidas	probable copper ox	hypothetical prote	copper resistance	

## ALIGNMENTS

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QPFDMEKAIREDAEYVVI      :  :          PFDMDKAVAEQPEYVVI	LQPGLYVYHCAVAPVGM                LQPGLYIYHCAVAPVGM	QVPGQMIRVREGDTIEV    :       bvpgrmirvregdtvevi	ASQEHQGELPVIDAVTI  ::        :   AAETPSGELPVIDAVTTI	Length 390; Indels 8; Gaps	eisseria meningi _change 19-Jan-2 , A.C.; Nelson, ischmann, R.D.; ischmann, R.D.; Masignani, V.; j Moxon, E.R.; dis serogroup B dis serogroup B
FN 249  -  - 	HI 189    HI 184	2F 129 :  EF 124	нд 69    Нд 64	ω 	tidis (strain M 1001 K.E.; Eisen, J. Dougherty, B.A. Pizza, M.; V strain MC58.

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RESULT 3
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A19208
nitrite reductase (EC 1.7.99.3) Panl [similarity] - intrite reductase (EC 1.7.99.3) Panl [similarity] - intrite reductase outer membrane protein Panl C;Species: Neisseria gonorrhoeae
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #C;Accession: A49208
C;Accession: A49208
R;Hoehn, G.T.; Clark, V.L.
Infect. Immun. 60, 4704-4708, 1992
A;Tille: The major anaerobically induced outer membr A;Reference number: A49208; MUID:93014188; PMID:1398
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A;Experimental source:
C;Genetics:
A;Gene: aniA; NMA1887
C;Keywords: oxidoreduct
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F;135,170/Binding site: cop
F;325/Binding site: cop
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Matches 263
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;Reywords: oxidoreductase
;130,171,179,184/Binding site: copper (His, Cys, His, Met) (type 1) #status predicted
;135,170/Binding site: copper (His) (type 2) (shared with trimeric partner 1) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkhill, J.; Achtman, M. James, Holroyd, S.; Jagels, K.; Leather, arure 404, 502-506, 2000
Title: Complete DNA sequence of a Reference number: A81775; MUID:20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession:
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MJID:20222556; PMID:10761919
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A;Accession: A49208
A;Status: preliminary; not c
A;Molecule type: DNA
A;Residues: 1-392 <HOE>
A;Note: sequence extracted f
C;Keywords: oxidoreductase
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 GSGAASA-PAASAPAASAPA
                         PEGAPQAIDTQEAPKTPAPA
                                                    IVPAGGSAIVEFKVDIPGSYTLVDHSIFRAFNKGALGQLKVEGAENPEIMTQKLSDTAYA
                                                                    LIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYL
                                                                                                         GHVGSIAGDNALKAKAGETVRMYVGNGGPNLVSSFHVIGEIFDKVYVEGGKLINENVQST
                                                                                                                           GSVGALTGENALKAKVGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTT
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No. 6.9e-87;
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RESULT 4 JC4648 nitrite reductase

nitrite reductase (EC 1.7.99.3) precursor - Achromobacter cycloclastes C;Species: Achromobacter cycloclastes C;Species: Achromobacter cycloclastes C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 08-Oct-1999 C;Accession: JC4648; A37260
R;Chen, J.Y.; Chang, W.C.; Chang, T.; Chang, W.C.; Liu, M.Y.; Payne, W.J.; LeGall, J. Biochem. Biophys. Res. Commun. 219, 423-428, 1996
A;Title: Cloning, characterization, and expression of the nitric oxide-generating nitri A;Reference number: JC4648; MUID:96193667; PMID:8605003
A;Accession: JC4648
A;Molecule type: DNA
A;Residues: 1-378 <CHE>
A;Residues: 1-378 <CHE>
A;Cross-references: EMBL:Z48635; NID:g1125638; PIDN:CAA88564.1; PID:e140933; PID:g11256

A;Experimental source: IAM1013
A;Note: The authors translated the codon GGT for residue 299 as His
R;Fenderson, F.F.; Kumar, S.; Adman, E.T.; Liu, M.Y.; Payne, W.J.; LeGall, J.
Biochemistry 30, 7180-7185, 1991
A;Title: Amino acid sequence of nitrite reductase: a copper protein from Achromobacter
A;Reference number: A37260; MUID:91308101; PMID:1830217
A;Accession: A37260

A;Status: preliminary
A;Molecule type: protein
A;Residues: 39-378 <FEN>
C;Comment: This enzyme is a copper-containing
it reduces nitrite ion to nitric oxide, and it

Comment: This enzyme is a copper-containing enzyme. It is involved in the alternative reduces nitrite ion to nitric oxide, and it receives electrons from the blue copper Genetics:

Gene: nir

C;Keywords: copper; electron transfer; oxidoreductase
F;1-38/Domain: signal sequence #status predicted <SIG>
F;39-378/Product: nitrite reductase #status predicted <MAT>

Query Match

17.6%; Score 461.5; DB 2; Length 378;

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RESULT 5
A48936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nitrite reductase (EC 1.7.99.3) - Pseudomonas (;Species: Pseudomonas sp. C;Date: 19-Dec-1993 #sequence_revision 18-Nov-C;Accession: A48936
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: isolate G-179
A;Note: sequence extracted from NCBI backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-379 <Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Ye, R.W.; Fries, M.R.; Bezborodnikov, S.G.; Averill, Appl. Environ. Microbiol. 59, 250-254, 1993
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reference number:
Accession: A48936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pl. Environ. Microbiol. 59, 250-254, 1993
Title: Characterization of the structural gene encoding a copper-containing nitrite
Reference number: A48936; MUID:93175864; PMID:8439151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: GB:M97294; NID:g151396; PIDN:AAC79132.1; PID:g151397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                      copper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-379 <YE1>
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                            TIEVQFSNHPDSKMPHNVDFHAATGPGGGAEASFTAPGHTSTFSFKALQPGLYVYHCAVA
                                                                            EQGLQPFDMEKAIRE-DAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNLTSSFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVHFEGGKGENH----NIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DMEKAIRE-DAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNLTSSFHVIGEIFD
               VIGEIFDKVHFEGGKGENH---NIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNK
                                                        SAGEAYPDVLEAMKTLTPTHVVFNGAVGALTGDNALQAKVGD--RVLILHSQANRDTRPH
                                                                                                                                                                    PVGM---HIANGMYGLILVEPKEGLPK-----VDKEYYVMQGDFYTK-----GKYG
                                                                                                                                                                                                                                                                                                                    VPPPVDRDH-----PAKVVVKMETVEKVMRLAD-GVEYQFWTFGGQVPGQMIRVREGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIANGMYGLILVEPKEGLP-----KVDKEYYVMQGDFYTK-----GKYGEQGLQPF
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                                                                                                                               PAGMVPWHVTSGMNGAIMVLPRDGLKDHKGHELVYDKVYYVGEQDFYVPKDENGKFKKYE
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                                                                                                                                                                                                                                                                                                                                                           Score 453; DB 2;
Pred. No. 2.2e-23;
5; Mismatches 119
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5; Mismatches
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             submitted to the EMBL Data L
A; Reference number: S32112
A; Accession: S32112
A; Status: preliminary
A; Molecule type: DNA
A; Cross-references: EMBL: Z21
C; Keywords: copper; oxidored
                                                                                                                                                        C;Species: Pseudomonas aureofaciens
C;Date: 20-Feb-1995 #sequence_revisi
C;Accession: S32112
R;Zumft, W.G.
                                                                                                                                                                                                                                          RESULT 7
$32112
(EC 1.7.2.1)
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A;Status: preliminary
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A;Title: Cloning, sequencing, and transcriptional
A;Reference number: JG0170; MUID:99160880; PMID:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nitrite reductase (EC 1.7.99.3) - Alcaligenes denitrificans subsp. C;Species: Alcaligenes denitrificans subsp. xylosoxydans C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11.
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A; Residues: 1-360 <SUZ>
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R; Suzuki, E.; Horikoshi, N.; Kohzuma,
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                 copper; oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALKAKVGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGEN---HNIQTTLIPAG--
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                                                                                                                                                                                                     #sequence_revision
                               EMBL: Z21945; *NID: g287906; PIDN: CAA79939.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.2%;
35.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 451; DB 2;
Pred. No. 2.8e-23;
5; Mismatches 135
                                                                                                                                                  March
                                                                                                                                                                                                         20-Feb-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ptional studies
PMID:10049725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135;
                                                                                                                                                                                                     #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #text_change 11-May-2000
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                                   PID:g287907
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nitrite reductase (EC 1.7.99.3) blue copper-containing - Achromobacter xylosoxid N,Alternate names: NiR
C;Species: Achromobacter xylosoxidans
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 07-May-1999
C;Accession: JE0215
R;Vandenberghe, I.H.M.; Meyer, T.E.; Cusanovich, M.A.; Van Beeumen, J.J.
Biochem. Biophys. Res. Commun. 247, 734-740, 1998
A;Title: The covalent structure of the blue copper-containing nitrite reductase A;Reference number: JE0215; MUID:98321197; PMID:9647763
A;Accession: JE0215
A;Molecule type: protein
A;Residues: 1-336 <VAN.
A;Residues: 1-336 <VAN.
A;Residues: 1-336 <VAN.
C;Keywoqds: oxidoreductase
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Matches 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIEVQFSNHPDSKMPHNVDFHAATGPGGGAEASFTAPGHTSTFSFKALQPGLYVYHCAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAPPLVHPHEQVVSGPPKVVQFRMSIEEKKMVIDDQGTTLQAMTFNGSMPGPTLVVHEGD
                                                                                                                                                                                                                                               LYVYHCAVAPVGM---HIANGMYGLILVEPKEGLP-----KVDKEYYVMOGDFY----
                                                                                                                                                                                                                                                                                   PTLVVHEGDTVQLTLVNPATNAMPHNVDFHGATGALGGAKLTNVNPGEQATLRFKADRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGALGILKVEGEENHEI 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVIGEIFDKVHFEGGKGEN---HNIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FDMEKAIRE-----DAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNLTSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POGMVPWHVVSGMNGALMVLPRDGLRDPQGKLLHYDRVYTIGESDLYIPKDKDGHYKDYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVGM---HIANGMYGLILVEPKEGL--PK-----VDKEYYVMQGDFY-TKGKYGEQGLQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPPPVDRDH-----PAKVV-VKMETVEKVMRLAD-GVEYQFWTFGGQVPGQMIRVREGD
                                                                                              GPNLTSSFHVIGEIFDKVHFEGGKGEN---HNIQTTLIPAG--GAAITEFKVDVPGDYVL 331
                                                                                                                                                                 TKGKYGEQGL---QPFDMEKAIRE-DAEYVVFNGSVGALTGENALKAKVGETVRLFVGNG 276
                                                                                                                                                                                                                TFVYHC--APEGMVPWHVVSGMSGTLMVLPRDGLKDPQGKPLHYDRAYTIGEFDLYIPKG
                                                                                                                                                                                                                                                                                                                QMIRVREGDTIEVQFSNHPDSKMPHNVDFHAATGPGGGAEASFTAPGHTSTFSFKALQPG
                                                                                                                                                                                                                                                                                                                                                   KLPHTKVTLVAPPQVHPHEQATKSGPKVTEFTMTIEEKKMVIDDKGTTLQAMTFNGSMPG
                                                                                                                                                                                                                                                                                                                                                                                     ELPVIDAIVTHAPEVPP---PVDRDHPAKVVVKMETVEKVMRLAD-GVEYQFWTFGGQVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLIGGHGDWV-WTTGKFANPPORNMETWFIPGGSAVAALYTFKOPGTYVYLSHNLIEAME
                                  VDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKTPAP
                                                                    QANRDTRPHLIGGHGDWV-WETGKFANPPQRDLETWFIRGGSAGAALYTFK--QFGVYAY 297
                                                                                                                                         PDGKYKDYATLAESYGDTVQVMRTLTPSHIVFNGKVGALTGANALTAKVGETVLLI--HS
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                                                                                                                                                                                                                                                                                                                                                                                                                                        17.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          blue copper-containing - Achromobacter xylosoxidans
                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 448; DB 2; 1; Pred. No. 4.1e-23; 44; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348
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Pred. No. 2.9e-23;
1; Mismatches 110
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     DLMKQIKAPAP
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nitrite reductase, copper-containing [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Oate: 11-Jan-2002 #text_change 18-Nov-2002 C;Accession: AB3095 C;Accession: AB3095 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, W.; Perry, M.; Grant, D.; Kutyavin, T.; Li, Karp, P.; Jung, M.; Krespan, M.; Krespan, M.; Krespan, M.; Krespan, M.; Krespan, M.; Krespan, M.; Krespan, M.; Krespan, M.; Krespan, M.; Krespan, M.; Krespan, M.; Krespan, M.; Krespan, M.; Krespan, M.; Krespan
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A;Accession: AB3095
A;Accession: Preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-411 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL45176.1; PID:g17742853; G:A;Experimental source: strain C58 (Dupont)
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A; Map position: linear chromosome
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                                                                                                                                                                                                      HFEGGKGENH----NIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTNELQHNIDFHSATGALGGGGLTIVNPGEKAILRFKATKAGVFVYHC--APPGMVPWHV
                                                                                                                                                                                                                                                                     LEVMRKLTPSHIVFNGAVGALTGEHALQAAVGE--KVLIVHSQANRDTRPHLIGGHGDYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANGMYGLILVEPKEGLPK-----VDKEYYVMQGDFYTK------GKYGEQGLQPFDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDSKMPHNVDFHAATGPGGGAEASFTAPGHTSTFSFKALQPGLYVYHCAVAPVGM---HI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGCSNQADKAAQPKSSTVDAAAKTANAD-----NAASQEHQGELPVIDAIVTHAPEVP
GEWNNTL 401
                                                                      GEENHEI
                                                                                                                                  -WATGKFRNPPDLDQETWFIPGGTAGAAFYTFEQPGIYAYVNHNLIEAFELGAAAHFKVT
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Pred. No. 1.4e-22;
""ematches 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56;
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McClell
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RESULT H98191

R;Goodner, B; Hinkle, G; Gattung, A; Liu, F; Wollam, C; Allinger, Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plan copper-containing nitrite reductase precursor C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-A; Accession: H98191 A; Status: preliminary A; Reference number: C; Accession: H98191 type: DNA uence of the Plant Pathogen and Biotechnology Agent Agrobacterium A97359; MUID:21608551; PMID:11743194 3 0 22-Oct-2001 Miller, N.; Blanchard, M.; Qurollo, Doughty, D.; Scott, C.; Lappas, C.; (cu-nir) [imported] - Agrobacterium #text_change 18-Nov-2002 B.; Goldman, Markelz, B.,

tumef.

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RESULT 11
A95347
                                                                                                                                                       A;Experimental source: strain 1021, megaplasmid pSymA

R;Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-376 <KUR>
A;Cross-references: GB:AEO06469; PIDN:AAK65339.1; PID:g14523797; GSPDB:GN00165
                                                                                                                                                                                                                                                                                                                                                                                       R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe, Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 983-988, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: A95347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 24-Au
C;Accession:
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C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 14-Sep-2001
C;Accession: A95347
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                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
 Best Local Sin
Matches 121;
                                                                         Keywords: oxidoreductase
                                                                                                                                            Contents: annotation
                                                                                       Genome: plasmid
                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANGMYGLILVEPKEGLPK-----VDKEYYVMQGDFYTK-----GKYGEQGLQPFDM
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   Conservative
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s: GB:AE007870; PIDN:AAK89058.1;
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                  16.7%;
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 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -EQXMILDDXGTEVHAMTFNGSVPGPLMVVHQDDYVELTLINP
                  Score 439.5;
Pred. No. 1.8
 Mismatches
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No. 1.6e-22;
                    1.8e-22;
                                  DB
 128;
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                                2;
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C;Accession: AC3633
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Iver, R; Mazur, M.; Goltsman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella me A;Reference number: AD3252; PMID:11756688
A;Accession: AC3633
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AC3633
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C; Keywords: oxi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-376 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nitrite reductase (EC 1.7.99.3) [imported] - Brucella melitensis (strain 16 C;Species: Brucella melitensis C;Species: Brucella melitensis (S;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002 C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keywords: oxidoreductase
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                                                                                                                                                                                                                                                              EYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPDSKMPHNVDFHAATGPGGGAEASFTAPG
KVGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNI--QTTLIPAGGAAITEF
                                                                                             YYVMQGDFYTK----
                                                                                                                                          EKTVLRFKATKPGVFVYHC--APPGMVPWHVVSGMNGAVMVLPREGLHDGKGNKLTYDKV
                                                                                                                                                                                      HTSTFSFKALQPGLYVYHCAVAPVGM---HIANGMYGLILVEPKEGLP-----KVDKE
                                                                                                                                                                                                                                     EVHAMTFNGTVPGPLMVVHQDDYLELTLINPETNTLLHNIDFHAATGALGGGGLTEINPG
                                                                                                                                                                                                                                                                                                                                 RKASAEEIAALPRO-KVELVDPPFVHA---HTQVAEGGPKVVQFTMVIEEKKIVIDDAGT
                                                                                                                                                                                                                                                                                                                                                                           KTANADNAASQEHQGELPVIDAIVTHAPEVPPPVDRDHPAKVVVKMETVEKVMRLAD-GV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAEASFTAPGHTSTFSFKALQPGLYVYHCAVAPVGM---HIANGMYGLILVEPKEGLP--
                                          YYVGEQDFYVPRDENGNYKTYEAPGDAYEDTVKVMRTLTPTHVVFNGAVGALTGDKALTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGALTGDSALKAAVGE--KVLIVHSQANRDTRPHLIGGHGDYV-WATGKFRNAPDVDQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGALTGENALKAKVGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENH---NIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----KVDKEYYVMQGDFY----TKGKY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGALTVVNPGDTTVLRFKASKAGVFVYHC--APPGMVPWHVTSGMNGAIMVLPREGLTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKIVIDEQGTELHAMTFNGSVPGPLMVVHQDDYVELTLINPDTNTLQHNIDFHSATGALG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - KVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPDSKMPHNVDFHAATGPGG
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                                                                                                                                                                                                                                                                                                                                                                                                                            16.4%;
llarity 34.8%;
Conservative 48
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                                                                                           --GKYGEQGLQPFDMEKAIRE-DAEYVVFNGSVGALTGENALKA
                                                                                                                                                                                                                                                                                                                                                                                                                            48;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 431; DB 2; 1
Pred. No. 6.9e-22;
8; Mismatches 147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 376;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Cloning and charcterization of nitrite reductase gene from Alcaligenes A;Reference number: I39582; MUID:93294530; PMID:8515232 A;Accession: I39582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Nishiyama, M.; Suzuki, J.; Kukimoto, M.; Ohnuki, T.; Horinouchi, J. Gen. Microbiol. 139, 725-733, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-376 < RES>
                                                                                                                                                    RESULT
E84274
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                                                                                                                                membrane protein [imported] - Halobacterium sp. NRC-1
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Best Local S
Matches 129
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Leithauser, B.; Keller, K.; Cruz, R.; Danson,
Jung, K.H.; Alam, M.; Freitas, T.
roc. Natl. Acad. Sci. U.S.A. 97, 12176-12181,
                                                                                       ;Species: Halobacterium sp. NRC-1;Date: 02-Feb-2001 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                          Accession:
                                     W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, thauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jab
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                                                                            E84274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVDVPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEG 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHVVSGMNGAIMVLPREGLHDGKGKALTYDKIYYVGEQDFYVPRDENGKYKKYEAPGDAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INPETNTLMHNIDFHAATGALGGGGLTEINPGEKTILRFKATKPGVFVYHC--APPGMVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNHPDSKMPHNVDFHAATGPGGGAEASFTAPGHTSTFSFKALQPGLYVYHCAVAPVGM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVPPPVDRDHPAKVVVKMETVEKVMRLAD-GVEYQFWTFGGQVPGQMIRVREGDTIEVQF
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                                                                                                                                                                                                                                                               VEGEENHEIYSHKQTDAVYLPEG 372
                                                                                                                                                                                                                                                                                                      DYVWATGKFNTPPDVDQETWF1PGGAAGAAFYTFQQPG1YAYVNHNL1EAFELGAAAHFK
                                                                                                                                                                                                                                                                                                                                                                                                      FDMEKAIRE-DAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNLTSSFHVIGEIF
                                                                                                                                                                                                                                                                                                                                         DKVHFEGGKGENHNI--QTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILK
                                                                                                                                                                                                                                                                                                                                                                              EDTVKVMRTLTPTHVVFNGAVGALTGDKAMTAAVGE--KVLIVHSQANRDTRPHLIGGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -HIANGMYGLILVEPKEGLP-----KVDKEYYVMQGDFYT----KGKYGE----QGLQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.3%; Score 427.5; DB 2
33.7%; Pred. No. 1.2e-21;
                                                                                                                                                                                                                              -SVLAPSG
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                                                                                             02-Feb-2001 #text_change
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                                                                                                 02-Feb-2001
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A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; A;Title: Genome sequence of Halobacterium species NRC-1. A;Reference number: A84160; MUID:20504483; PMID:11016950 A;Accession: E84274
                                                                                                                                                                                            A; Status Francis INA
A; Molecule type: DNA
A; Residues: 1-338 < KUR>
A; Cross-references: GB:BA000019; PIDN:BAB75641.1;
A; Cross-reference: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-379 <STO>
                                                                                                                                                                                                                                                                                                                      DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein all3942 [imported] - Nostoc sp. C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of C;Date: 14-Dec-2001 #sequence revision 14-Dec-2001 C;Accession: AG2298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                 R; Kaneko, T.; Nakamura,
                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                           A; Accession: AG2298
                                                                                                                                                                                                                                                                                                                                                                                         Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa,
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94;
                                    94 VMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPDSKMPHNVDFHAATGPGGGA
                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVMNGTFYPGGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLYHCHY-QTQRHIDMGMYGIFRIDPK-GYEPADKEYFMTVKDWDSRLNRSMAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDRDHPAKVV----VKMETVEKVMRLADGVEYQFWTFGGQ-----VPGQMIRVREGDTIEV
VIQLNSAVSYNIWDLNGRIPGPTLRAKQGDRIRVLF--HNQAGHSHSLHFHGV----HPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLHIHNHRFRMVEKDGGQIPAAAQHTMDITDMAPAERHTI-EFQADADPGIYLMHCHKVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----EDVDYSPRTRNPDVFTVNGKSAPRTLHPEDGSPIIVEQGDTVRLHLVNGG-YMNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKAIREDAEYV--VFNGSVGALTGENA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VHDVHPLDSMGGPVKLPRV-------WAFATEDGDPSVPGPIVRTEEGQDIEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Y.; Wolk, C.P.; Kuritz, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.5%; Score 250.5; DB 2
25.3%; Pred. No. 1.4e-09;
ative 52; Mismatches 133
                                                                                                   9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345
                                                                                Score 248.5; DB 2
Pred. No. 1.6e-09;
2; Mismatches 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ĠSQTAWEDDGVPTTTGIRVGPĞEKHTYTIPANVPĞT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp.
                                                                                                                                                                                                                               PID:g17133076;
                                                                                                                                                                                                                                                                                                                                                                                                M.; Yamada,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anabaena sp. #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TAPGHTSTFSFKALQPGL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LKAKVGETVRLFVGNGGPNLTS
                                                                                                                                                                                                                                                                                                                                                                                                                     Sasamoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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09-Dec-2002
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                                                                                  39;
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                                                                                                                                                                                                                                   GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                Watanabe, A.; ; Yasuda, M.;
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A; Lettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougl ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Dougl Science 287, 1809-1815, 2000
A; A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappu A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain A; Reference number: A81000; MUID:20175755; PMID:10710307
A; Molecule type: DNA A; Residues: 1-138 cTET>
A; Cross-references: GB:AE002426; GB:AE002098; NID:g7225939; PIDN:AAF41130.1; Pl A; Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0717
C;Keywords: Chromoprotein; electron transfer; heme; iron. monology
F;1-26/Domain: signal sequence #starron
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C;Species: Neisse
C;Date: 01-Sep-20
C;Accession: B811
R;Tettelin, H.;
                                                                                                                                                                cytochrome c552 NMA0925 precursor [similarity] - Neisseria meningitidis c;Speciles: Neisseria meningitidis c;Speciles: Neisseria meningitidis C;Date: 01-Sep-2000 #sequence_revision 01-Sep-2000 #text_change 02-Feb-2 C;Accession: F81938
C;Accession: F81938
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C;Accession
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F81938
  A; Molecule type:
A; Residues: 1-16:
A; Cross-reference
                                                                                    A; Title: Complete DNA sequer A; Reference number: A81775; A; Accession: F81938
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Best Local S
Matches 44
  Residues: 1-163 <PAR>
                                                                                                                                                                                                                                                        Date: 01-Sep-2000 #sequence_revision 01-Sep-2000 #text_change 02-Feb-2001 Accession: F81938
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114/Domain: cytochrome c6 homology <CY63
43,416/Binding site: heme (Cys) (covalent) #status predicted
43,7,97/Binding site: heme iron (His, Met) (axial ligands) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 GKATYDSNCAACHQPDGKGVPNAFPPLANSDYLNADHARAASIVANGLSGKITVNGNQYE
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Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFMPATAISDADIAAVATYIMNAFDNGGGSVTEKDVKQAKSKK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGDYVLVDHAIFRAFNKGALGILKV--EGEENH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYVLNIIEYDPAVT--FHLHANFFDVYRY--GMSMKASEKTDVITMGVAERHILEFAFRY 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFVGN---GGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGGAA--ITEFKVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVLVMAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQKVYESNCVACHGKKGEGRGTMFPPLYRSDF1MKKPQVLLHSMVKG1NGT1KVNGKTYN
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                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
GB:AL162754; GB:AL157959; NID:g7379424;
                                                                                                              sequence of a serogroup A strain of
B1775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.5%;
42.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 3.1e
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----YDVDDNSHND--FYAFNGLPHHYM-DNPIQIYQNQLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 222; DB 1;
Pred. No. 3.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                             S.D.; Churcher, C.; Klee, Mungall, K.; Quail, M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 138
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                                                                                                                                         Neisseria
  PIDN:CAB84197.1;
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; Dougherty, B.
; Pizza, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rappuoli, R.; strain MC58.
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  PID:g737963
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C;Genetics:
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A; Residues: 1-605 <BI
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  PEGAPQAIDTQEAPKTPAPANLQEQIKAGKATYD--
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RESULT 18
S52253
copper resistance protein pcoA precursor - Escherichia coli plasmid pRJ1004
N;Alternate names: copper-binding protein
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Oate: 07-May-1995 #sequence revision 21-Jul-1995 #text_change 11-Jun-1999
C;Accession: $70159; $52253
C;Accession: $70159; $52253
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C;Genetics:
A;Gene: NMA0919; NMA0925
C;Superfamily: T. aquaticus cytochrome c552; cytochrome c6 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metallopro
F;1-21/Domain: signal sequence #status predicted <MAT>
F;22-163/Product: cytochrome c552 #status predicted <MAT>
F;28-109/Domain: cytochrome c6 homology <CY6>
F;38,41/Binding site: heme (Cys) (covalent) #status predicted
F;38,41/Binding site: heme iron (His, Met) (axial ligands) #status [F;42,92/Binding site: heme]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Genome: plasmid pRU1004
C;Superfamily: laccase
C;Keywords: copper binding
E;1-32/Domain: signal sequence #status predicted
F;33-605/Product: copper resistance protein pcoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Molecular genetics and transport analysis of the copper-resistance A;Reference number: S70159; MUID:96130847; PMID:8594334 A;Accession: S70159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Brown, N.L.; Barrett, S.R.; Camakaris, Mol. Microbiol. 17, 1153-1166, 1995
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                                                        AAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYL-----
                                                                                                                                                                  KVGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPA-----GG
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                                                                                                                                                                                                                                                                                                                                           GVPGLSFMGIEPDDTYVYTFKVKQNGTYWYH---SHSGLQEQEGVYGAIIIDAREPEPFA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSERQAKTINGGLPGPVLRWKEGDTITLKVKNRLNEQTSIHWHGIILPANMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVEYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPDSK-----MPHNVDFHAATGPG
                                                                                                             TIAD--RKMWAEMKMNPTDLADVSG--YTYTYLMNGQAPLKNWTGLFRPGEKIRLRFING
                                                                                                                                                                                                                           YDREHVVMLSDWTDE------NPHSLLKKLKKQSDYYNFNKPTVGSFFRDVNTRGLSA
                                                                                                                                                                                                                                                                                                                                                                                                 GGAEASFTA--PGHTSTFSFKALQPGLYVYHCAVAPVGMHIANGMYGLILVEPKEGLP-K
SAMTYFDIRIPGLKMTVVAADGQYVNPVTVDEFRIAVAETYDVIVEPQGEAYTIFAQSMD 336
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Pred. No. 4e-06;
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Pred. No. 3.9e-08;
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SNC 406

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B83910
hypothetical protein BH2082 [imported] - Bacillus halodurans (strair C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-0
C;Accession: B83910
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacilla Complete genome sequence of the alkaliphilic bacterium Bacilla; Reseasion: B83910
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83910
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-500 < STO>
A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:B4
A;Experimental source: strain C-125
C;Genet: BH2082
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hypothetical protein AGR_L_1722 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-
                                                                                RESULT
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                                                                                                                                                                                                                             MLLGSDDGGDTFTINGKKFPNHEIYDVEEGDMVKFTIINDTDFDHPMHLHGDFFHVISKG
                                                                                                                                                                                                                                                                   SNCAACHQPD-----GKGVPN-----AFPPLANSDY-----LNADHARAASIV 441
                                                                                                                                                                                                                                                                                                                                                    ENHE-----IYSHKQTDAVYLPEGAPQAIDTQEAPKTPAPANLQEQIKAGKAT--YD 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACHQPDGKGVPN---AFPPLANSDYLNADHARAASI
                                                                                                                                                                                                                                                                                                              ENGERLOALIPLYYEEYEDEEL------OTVDSISSFFDLTTYGIPKELDIGDITKEYD
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#sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
                                                                                                                                                                                    KITVN---GNOYESVMPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----DDHSEMDHGNNQQDEQNEGTF---
                                                                                                                                                                                                                                                                                                                                                                                               -TAFRIAPAERYDLEIIMD----
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                                                                                                                                                                                       462
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                                                                                                                                                                                                                                                                                                                                                                                               -NPGAWGI-QVFAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134;
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                                            (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             halodurans
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                                          C58,
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                                            Cere
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002
C;Accession: AC3047
R;Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.;
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.;
Karp, P.; Romero, P.; Zhang, S.
science 294, 2317-2323, 2001

multicopper oxidase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

11-Jan-2002 #text_change 18-Nov-2002

D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, ID.; Kutyavin, T.; Levy, R.; Li, M.; McClell

ster, E.W. A;Title: The Genome of

of the Natural Genetic AB2577; MUID:21608550;

A; Authors: Yoo, H.;

Tao,

Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm

Engineer Agrobacterium PMID:11743193

tumefaciens

A;Reference number: A A;Accession: AC3047 A;Status: preliminary

A;Cross-references: GB:AE008689; PIDN:AAL44793.1; PID:g17742433; GSPDB:GN00187 A;Experimental source: strain C58 (Dupont) C;Genetics:

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C;Accession: A98239
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurc A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, Science 294, 233-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent A;Reference number: A97359; MUID:21608551; PMID:11743194
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A; Residues: 1-449 < KUR >
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene: AGR_L_1722
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372
                                 384 KTPAP----
                                                                                                                                                                          286 VI---GEIFDKVHFEGG--KGENHNIQTTL-IPAGGAAITEFKVDVPGDYVLVDHAIFRA
                                                                                                                                                                                                               210
                                                                                                                                                                                                                                                 226 GEQGLOPFDMEKAIREDAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNLTSSFH
                                                                                                                                                                                                                                                                                     157 EFDLVKSGTFMYH-PHSDEMVQMAMGMMGFFVIHPKDPAFMPVDRDFVFLLNAF-----
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                                                                                                                                                                                                                                                                                                                                                                                             114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
                                                                                                                                                                                                                                                                                                                                                                                                                             43 VKPTTGPDYNPVVTINGWTLPFRMNNGVKEFHLVAEPVEREM--AEGMTARLWGYNGOSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 ICALSALMLSGCSNQADKAAQPKSSTVDAAAKTANADNAASQEHQGELPVIDAIVTHAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97;
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                                                                                                                                                                                                                                                                                                                                                                                          GOMIRVREGDTIEVOFSNHPDSKMPHN--VDFHAATGPG-----GGAEASFTAPGHTSTF
                                                                                                                                                                                                                                                                                                                                                          GPTIEAVEGDRVRIFVTN----KLPEHTTIHWHGMILPSGMDGVGGLSQPHIPVGKTFVY
ENTVPMMTGWGPHGPIEMGGMFSVVKVREGISAGDYT
                                                                       MN--AMG-
                                                                                                      FNKGALGILKVEGEENHEIYSHKQTDAV----
                                                                                                                                        PIHMHGYDFEVTCTDGGWVRPEARWPEVSIDIPVGAMRAYEFDAKYVGDWAIHCHKSHHT
                                                                                                                                                                                                               ---DINPGASVPKIMTMTDFNLWAWNSRVFPGIDPLVVSKNDRVRVRVG----NLTMTNH
                                                                                                                                                                                                                                                                                                                      SFKALQPGLYVYHCAVAPVGMHIANGMYGLILVEPKE-GLPKVDKEYYVMQGDFYTKGKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPPPVDRDHPAKVVVK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLGVSAAMVSSA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.1%;
                                                                       -HDVPTFIGVDKKTVTEKIRKIRPDYMPMGTAGMADMGAMEMEIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 187; DB
Pred. No. 3.6e-
63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:AAK89435.1; PID:g15159296; GSPDB:GN00170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.; Miller, N.; Blanchard, M.; Qurollo, M.; Doughty, D.; Scott, C.; Lappas, C.;
                                   -ANLQEQIKAGKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187; DB 2; I
No. 3.6e-05;
smatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --AWAKTSNSS------LPEAALMETAATQAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----METVEKVMRLADGVEYQFWTFGGQVP
                                                                                                      -----YLPEGAPQAID----TQEAP
 408
                                   401
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Markelz, B.,
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L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium mellioti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE006469; PIDN:AAK65221.1; PID:g14523669; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barl
pela, D.; Chain, F.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable copper-containing oxidase [imported] - Sinorhizobium meliloti (strain C;Species: Sinorhizobium meliloti C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                A;Gene: SMa1038
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432 A;Accession: C95332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
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A; Map position: linear chromosome
                                                                                                                                                 A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-449 < KUR>
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  Query Match
Best Local S
Matches 92
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Best Local S
Matches 97
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                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---DINPGASVPKIMTMTDFNLWAWNSRVFPGIDPLVVSKNDRVRVRVG----NLTMTNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEQGLQPFDMEKAIREDAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNLTSSFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPTIEAVEGDRVRIFVTN----KLPEHTTIHWHGMILPSGMDGVGGLSQPHIPVGKTFVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQMIRVREGDTIEVQFSNHPDSKMPHN--VDFHAATGPG-----GGAEASFTAPGHTSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKPTTGPDYNPVVTINGWTLPFRMNNGVKEFHLVAEPVEREM--AEGMTARLWGYNGQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLGVSAAMVSSA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MN--AMG-----HDVPTFIGVDKKTVTEKIRKIRPDYMPMGTAGMADMGAMEMEIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIHMHGYDFEVTCTDGGWVRPEARWPEVSIDIPVGAMRAYEFDAKYVGDWAIHCHKSHHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENTVPMMTGWGPHGPIEMGGMFSVVKVREGISAGDYT
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    Conservative
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                     6.6%;
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55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
                   Score 174.5; DB 2; Pred. No. 0.00025;
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - ANLOEQI KAGKAT
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  63;
Gaps
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                                                                                                                                                                                                                                                                                            F.; Barloy-Hubler,
N.A.; Fisher, R.F.
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                   J. Mol. Biol. 206,
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A;Title: Refined crystal structure of ascorbate oxidase at 1.9 A;Reference number: A58657; MUID:92194315; PMID:1548698 A;Contents: annotation; X-ray crystallography, 1.9 angstroms A;Note: the sequence reported in A51027 is attributed to R. Pet R;Messerschmidt, A.; Luecke, H.; Huber, R. submitted to the Brookhaven Protein Data Bank, November 1992 authorized to the Brookhaven Protein Data Bank, November 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Messerschmidt, A.; Ladenstein, R.; Huber, submitted to the Brookhaven Protein Data BaA;Reference number: A51027; PDB:1AOZ
    A;Contents: annotation; X-ray crystallography, R;Messerschmidt, A.; Rossi, A.; Ladenstein, R.;
                                                A; Reference number: A51621; PDB: 1ASQ
                                                                        R;Messerschmidt, A.; Luecke, H.; Huber, R
submitted to the Brookhaven Protein Data
                                                                                                                A;Reference number: A51620; PDB:1ASP
A;Contents: annotation; X-ray crystallography,
                                                                                                                                                                                    A;Reference number: A51619; PDB:1ASO
A;Contents: annotation; X-ray crystallography,
R;Messerschmidt, A.; Luecke, H.; Huber, R.
                                                                                                                                                                                                                                                                                                                                                                                                R;Messerschmidt, A.; Ladenstein, R.; Huber, R.; Bolognesi, M.; Avigliano, J. Mol. Biol. 224, 179-205, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 52-67;100-108, 'H'; 445-454; 498-517 < ROS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A30066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Contents: sequence; X-ray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A30066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Rossi, A. unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not A;Molecule type: mRNA; protein
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A;Accession: A51027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Cucurbita pepo var. melopepo (zucchini)
C;Date: 08-Nov-1989 #sequence_revision 14-Nov-1997
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                                                                                                                                                                submitted to the Brookhaven Protein Data Bank,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.; Petruzelli, R.
hed results, cited by Messerschmidt,
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2.32 angstroms,
; Huber, R.; Bol
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  oms, azide form,
Bolognesi, M.;
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    residues :
Gatti, G.;
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A.; Rossi, A.; 6, 513-529, 1989 structure

of the blue

oxidase ascorbate oxidase from zucchini. An

Gatti,

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A;Reference number: A30633; MUID:89236417; PMID:2716059
A;Contents: annotation; X-ray crystallography, 2.5 angstroms
C;Complex: homotetramer
C;Function:
A;Description: catalyzes the oxidation of L-ascorbate to dehydroascorl
C;Superfamily: laccase
C;Superfamily: laccase
C;Keywords: copper; glycoprotein; homotetramer; metalloprotein; oxido:
C;Keywords: copper; glycoprotein; beta-barrel #status experimental <BB1>
F;1-133/Domain: amino-terminal beta-barrel #status experimental <BB1>
                                                                                                                                                                                    A;Cross-
C;Geneti
A;Gene:
                                                                                                                                                                                                                                                                                                                                        cytochrome c family protein [imported] - Caulobacter crescentus

(;Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C;Accession: F87384

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kol

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.

proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: F87384
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F;345-538/Domain: carboxyl-terminal beta-barrel #status experimental <BB3>
F;19-201,811-538,180-193/Disulfide bonds: #status experimental <BB3>
F;60,448/Binding site: copper (His) (type 2) #status experimental 
F;62,104,106,450,506,508/Binding site: 2Cu-O cluster (His) (copper type 3) #status 
F;62,104,106,450,506,508/Binding site: 2Cu-O cluster (His) (copper type 3) #status 
F;92/Binding site: carbohydrate (Asn) (covalent) #status experimental 
F;163,362,443,512/Binding site: substrate (Trp, Trp, Glu, His) #status predicted 
F;325,440/Binding site: carbohydrate (Asn) (covalent) #status predicted 
F;445,507,512,517/Binding site: copper (His, Cys, His, Met) (type 1) #status experi
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F87384
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A; Residues: 1-130
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Best Local S
Matches 81
                                                                               Query Match
Best Local S
Matches 37
                                                                                                                                                                                                                                                                                                                  Status: preliminary
                                                                                                                                                                                                                                     Cross-references: GB:AE005673; NID:g13422394; PIDN:AAK23074.1;
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                                                                               Similarity
37; Conserv
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GKATYDSNCAACHOPDGKGVPNAFPPLANSDYLNADHARAASIVANGLSGKITVNGNQYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSIAAKYDSNLEPCKLKGSESCAPYIFHVSPKKTYRIRI------AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGTPWADGTASISQCAINPGETFFYNFTVDNPGTFFYH---GHLGMQRSAGLYGSLIVDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEYMFWAPNCNENIVMGINGQFPGPTIRANAGDSVVVELTNKLHTEGVVIH----WHGILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTRARHPNTPPGLTLLNYLPNSVSK-LPTSPPPQTPA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTALAALNFAIGNHOLLVVEADGNYVOPFYTSDIDIYSGESYSVLITTDONPSENYWVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTLIPAGGAAITEFK---VDVPGDYV----LVDHAIFRAFNKGALGILKVEGEENHEI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SVGALTGEN--ALKAKVGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQ
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                                                                                  15;
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                                                                               Score 167; DB 2; 1 Pred. No. 0.00016; 5; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 170; DB 2; Length 552; Pred. No. 0.00067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 129;
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                                                                                                                             Length
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A;Gene: copA
C;Superfamily: laccase
C;Superfamily: laccase
C;Keywords: copper; tandem repeat
F;1-32/Domain: signal sequence #Scatus predicted <SIG>
F;33-609/Product: copper resistance protein A #status
F;367-434/Region: 8-residue repeats (D-H-x-X-M-X-G-M)
F;542,591,596,601/Binding site: copper (His, Cys, His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Mellano, M.A.; Cooksey, D.A.
J. Bacteriol. 170, 2879-2883, 1988
A;Title: Nucleotide sequence and organization of copper A;Reference number: A32018; MUID:88227880; PMID:3372485
A;Accession: A32018
A;Molecule type: DNA
A;Residues: 1-609 <MEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     copper resistance protein precursor A - Pseudomonas syringae C;Species: Pseudomonas syringae pv. tomato C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_chan C;Accession: A32018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110
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                                                                                                                                                                                                                                                        AAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEGAPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVMPAIA--LSDQQIANVITYTLNSFGNKGGQLSADDVAKAK 497
                                                                                                                                                SMDRTGYARGTLAVREGLVAQVPPLDPRPLVTMDDMGMGGMDHGSMDGMSGMDSGADDGM
                                                                                                                                                                                  AID---
                                                                                                                                                                                                                      SAMTYFDIRIPGLKMTVVASDGQFVNPVEVDELRIAVAETFDVIVEPTAEAYTV---FAQ
                                                                                                                                                                                                                                                                                            AATVADRKMWAEMKMNPTDLADVSGATY--TYLLNGQAPNMNWTGLFRPGEKLRLRFING
                                                                                                                                                                                                                                                                                                                                  P----
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AMSPTAKLNDPGLGLRNNGRKVLTY
                                  SVMPAIALSDOQIA----NVITY
                                                                        QTMSSMGGDSMP-AMDHSKMSTMQGMDHGAMSGMDHGAMGGMVMQSHPASENDNPLVDMQ
                                                                                                          AACHOPDGKGVPNAFPPLANSDYLNADHARAASIVANGLSGKI-----
                                                                                                                                                                                                                                                                                                                                                                    DWTDE------DPVSLMRTLKKQSDYYNFH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -PGHTSTFSFKALQPGLYVYHCAVAPVGMHIANGMYGLILVEPKEGLP-KVDKEYYVMQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKSLYMDNCSACHQATGKGVKGAFPALAGTPLVQGPPKVLITTVLNGRAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.3%;
                                                                                                                                                                                                                                                                                                                              ---NLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPA---
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                                                                                                                                                                                  --TOEAPKTPAPANLQEQIKAGKATY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 164.5;
Pred. No. 0.0
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   477
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--hes 179;
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copper-binding protein [imported] - C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revisiC;Accession: H87368

#sequence_revision

20-Apr-2001

#text_change

20-Apr-2001

Caulobacter crescentus

H87368

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                                                                                                                                                                                                F;375-568/Domain: carboxyl-terminal beta-barrel #status predicted F;49-231/Disulfide bonds: #status predicted F;90,478/Binding site: copper (His) (type 2) #status predicted F;92,134,136,480,536,538/Binding site: 2Cu-o cluster (His) (copper F;111-568/Disulfide bonds: #status predicted F;193,392,473,542/Binding site: substrate (Trp, Trp, Glu, His) #st
                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
'A;Residues: 31-48 <ESA>
C;Superfamily: laccase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Molecular cloning and nucleotide sequence of full-length A;Reference number: S11027; MUID:90361033; PMID:2143984 A;Accession: S11027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L-ascorbate oxidase (EC 1.10.3.3) precursor - Cucurbita cv. Ebis C;Species: Cucurbita cv. Ebisu Nankin C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change C;Date: 21-Nov-1993 #sequence_Craccession: S11027; S36936 R;Esaka, M.; Hattori, T.; Pujisawa, K.; Sakajo, S.; Asahi, T. Eur. J. Biochem. 191, 537-541, 1990
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A;Molecule type: DNA
A;Residues: 1-570 <STO>
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87368
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S36936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-579 < EUR>
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                                                                                                                                                                                 210-223/Disulfide bonds: #status predicted
                                                                                            Matches
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                          101 VEYQFWT------FGGQVPGQMIRVREGDTIEVQFSN--HPDSKMPHNVDFHAATG
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                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIANGMYGLILVEPK-EGLPKVDKEYYVMQGDFYTKGKYGEQGLQPFDMEKAIREDAEYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDEDT--SIHWHGLLVPFQMDGVPGVSFPGIKPGETFTYEFPIRQSGTYWWH---SHSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDSKMPHNVDFHAATGP---GGGAEASFTA--PGHTSTFSFKALQPGLYVYHCAVAPVGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPALSGEE----IKL-TVGHTMAKIDGKAGHAVTVNGAIPGPLIRLKEGQNVRLSVTNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPPVDRDHPAKVVVKMETVEKVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSNH
VEYMFWAPDCNENIVMGINGQFPGPTIRANAGDTVVVELINKLHTEGVVIH----WHGILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNWTGLFAPGERVRLRFINAG--AMTIENVRIPG 289
                                                                                            Conservative
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                                                                                       6.2%; Score 163; DB 2; I
24.6%; Pred. No. 0.0021;
htive 44; Mismatches 130;
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Pred. No. 0.0021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN:CAA39300.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327
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                                                                                                                                Length 579;
                                                                                                                                                                                                                                               (His) (copper type 3) #status
                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PID:g18252
                                                                                                                                                                                                       #status
                                                                                                                                                                                                                                                                                                                      <BB3>
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                                                                                       Gaps
  96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;373-565/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>
F;87,475/Binding site: copper (His) (type 2) #status predicted
F;89,131,133,477,533,535/Binding site: 2Cu-O cluster (His) (copper type 3) #status predicted
F;108-565/Disulfide bonds: #status predicted
F;108-565/Disulfide bonds: #status predicted
F;109,390,470,539/Binding site: substrate (Trp, Trp, Glu, His) #status predicted
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A; Residues: 1-578 < KAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: cDNA cloning and gene expression of ascorbate oxidase A;Reference number: S66353; MUID:96194464; PMID:8624413 A;Accession: S66353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kato,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: S66353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L-ascorbate oxidase (EC 1.10.3.3) precursor - commo C;Species: Nicotiana tabacum (common tobacco) C;Date: 28-Oct_1996 #sequence_revision 13-Mar-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;207-221/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:D43624; NID:g599593; PIDN:BAA07734.1; PID:g599594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: laccase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 GTRGRHPNTPPGLTLLNYLPNSVSK-LPTSPPPETPA 346
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Similarity 22.9%;
                                                                                                                                                                                                                                                                                                                                                                   IGTPWADGTAAISQCAINPGETFLYRFKVDKAGTYFYH---GHYGMQRSAGLYGSLIVEV
GESYSVLFKTDQDPTKNYWISINVRGREPKTPQGLTL-----LNYLPNSAS-----
                                          HKQTDAVYLPEGAPQ-----AIDTQ-EAPKTPAPANLQEQIKAGKATYDSNCAACHQPDG
                                                                                          RVASTTALGSLSLAIGGHKMVVVEADGNYV--
                                                                                                                                                                                                                                                                                                                    KEGLPK---VDKEYYVMQGDFYTKGKYGEQGLQPFDMEKAIREDAEYVVFNGSVGALTGE 258
                                                                                                                                                                                                                                                                                                                                                                                                            PG-----GGAEASFTA--PGHTSTFSFKALQPGLYVYHCAVAPVGMHIANGMYGLILVEP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEKVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSN--HPDSKMPHNVDFHAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSIAAKYDSNLEPCKLKGSEPCAPYI-
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                                                                                                                                  ---QTTLIPAGGAAITEFK---VDVPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYS
                                                                                                                                                                               NPLR-WIGEPQTLLLNGRGQYNCSLAARFSKPPLPQCKLRGGEQYAPQILRVRPNKIYRL
                                                                                                                                                                                                                          NALKAKVGETVRLFV-GNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEYIHWSPDGEESVVMGINGQFPGPTIRAKAGDTVAVHLTNKLHTEGVVIH----WHGIRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SHKQTD-----AVYLPEGAPQAIDTQEAPKTPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTLIPAGGAAITE---FKVDVPGDYV----LVDHAIFRAFNKGALGILKVEGEENHEIY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQGKKEPFHYDGEINLLLSDWCHQSIHKQEVGLS----SKPIRWIGEPQTILLNGRGQFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEGLPK---VDKEYYVMQGDFYTKGKYGEQ-GLQPFDMEKAIR--EDAEYVVFNG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SVGALTGEN--ALKAKVGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30, 833-837, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 162; DB 2; Pred. No. 0.0025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                          ----QPFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162;
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cytochrome c552 |
C;Species: Thermu
C;Date: 04-Dec-19
C;Accession: A001
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A;Contents: annotation; X-ray crystallography, 1.28 angstroms
C;Comment: This cytochrome appears to function as an electron donor to cytochrome oxid C;Superfamily: T. aquaticus cytochrome c552; cytochrome c6 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; pyroglutamic C;Ceywords: chromoprotein; electron transfer; heme; iron; metalloprotein; pyroglutamic P;2-87/Domain: cytochrome c6 homology cCT69
F;11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11,14/Binding site: heme (Cys) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-131 <TIT>
A;Note: the source was designated as Thermus thermophilus
A;Note: the source was designated as Thermus thermophilus
R;Than, M.E.; Hof, P.; Huber, R.; Bourenkov, G.P.; Bartunik, H.D.; Buse,
submitted to the Protein Data Bank, June 1997
A;Reference number: A77356; PDB:1C52
A;Reference number: A77356; PDB:1C52
A;Contends: annotation; X-ray crystallography, 1.28 angstroms, residues
A;Contends: annotation; X-ray crystallography, 1.28 angstroms, residues
A;Contends: annotation; X-ray crystallography, G.P.; Bartunik, H.D.; Buse,
J. Mol. Biol. 271, 629-644, 1997
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A;Molecule type: DNA
A;Residues: 1-611 <SIM>
A;Residues: 1-611 <SIM>
A;Cross-references: GB:AE003866; GB:AE003849; NID:g9104906; PIDN:AAF82945.1; GSPDB:GN00i
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, I
                                                                                                                                                                                          A; Note: for a complete list A; Accession: C82845
                                                                                                                                                                                                                  A,Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 be
                                                                                                                                                                                                                                                                                           C;Accession: C82845
R;anonymous, The Xylella fastidiosa
Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                  copper resistance protein A precursor XF0132 [imported] - Xylella fastidiosa
C;Species: Xylella fastidiosa
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Best Local (
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                                                                                                                                                                  Status: preliminary
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Pred. No. 0.00042;
3; Mismatches 39;
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A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.D.; Junqueira, M.L.; Kemner, E.L., vi--i--
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C; Superfamily:
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                                                                            APANLQEQIKAGKATYDSNCAACHQPDGKGVPNAFPPLANSDYLNADHARAAS
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RPRLTMQDMGHGMAHGQHGSRASEMAD --
                                                                                                                                                        HPVTVDBLRIALAETYDVLIQPHGQDAFAIFAQDMGRTGYACGTLAVRPGLHAPLPALDP
                                                                                                                                                                                                                                                                                                                 LFRPGEKVLLRLINGSAMTYFDVRIPG---
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                                                                                                                                                                                                                                ---DAVYLPEGAPQ-AIDTQEAPKT--
                                                                                                                                                                                                                                                                                                                                                                                     GAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYS
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Pred. No. 0.0
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        ---MPGMTHPGRL-GDHASHAS
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, I.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, Nature 393, 537-544, 193.

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Nature hypothetical protein Rv0846c - Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis A;Cross-references: GB:AL022004; GB:AL123456; NID:g3261550; PIDN:CAA17652.1; PID:g291690 A; Residues: 1-504 < COL> A; Molecule type: DNA A; Accession: F70813 A; Status: preliminary; Accession: F70813 Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 nucleic acid sequence pMID:9634230 not shown; translation (strain H37RV) C.; Harris, D not complete B.G D.; တ Holroyd, Gordon, genome

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strain

H37Rv

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probable copper oxidase - Streptomyces coelicolor C.Species: Streptomyces coelicolor C.Date: 05-Nov-1999 #sequence_revision of No. C.Accession: T15020
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C;Geneti
A;Gene:
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                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-343 <SEE>
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C;Superfamily: laccase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 104
                                                                                                                                                 Query Match
Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                               ;Cross-references: EMBL:AL079355; PIDN:CAB45586.1;
;Experimental source: strain A3(2)
;Genetics:
                                                                                                                                                                                                                           SCOEDB:SC4C6.22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 NGMYGLILVEPKEGLPKVDKEYYVMQGDFYTKG-----KYGEQGLQPFDMEKAIREDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 D--PTSVHWHGIALRNDMDGTEPATANIGPGGDFTYRFSVPDPGTYWAHPHVGLQGDH--
116: AMNKSDVEPGGTRTYTWRTHKPGRRDDGTWRPGSAGYWHYHDHV--VGTEHGTGGIRNGL
                               152 GAEASFTAPGHTSTFSFKALQP------GLYVYHCAVAPVGMH-----IANGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 TGMPEGEGVDSNLLGGDGGDIAYPYYLINGRIP--VAATSFKAKPGQRIRIRIINSAADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 SKMPHNVDFH--AATGPGGGAEASFT--APGHTSTFSFKALQPGLYVYHCAVAPVGMHIA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 6.0%; al Similarity 20.8%; 104; Conservative 5
                                                                    57 KLADGOMGYGFEKGKASVPGPLIEVNEGDTLHIEFTNTMDVRASLHVHGLDYEISS-DGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
                                                                                                         96 RLADG-VEYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPD---SKMPHNVDFHAATGPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLSGKI - - TVNGNOYESVMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQEAP 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTMAKYDWTINGEPYSTTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SPPDPQFRPDELNWRVGTVEMF 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFRIALAGHSMTVTHTDGYPVIPTEVDALLIGMAERYDVMVT--AAGGVFPLVALAEGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARIDLGGPIVSTL------TYGNTIPGPLIRATVGDEIVVSVTNRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----EYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGFALAAC----ASKPTAS--GAAGMTAAIDAAEAARPHSGR--TVTATLT-----PQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GLYLPVVVDDPTEPGHYDAEWIIILDD-WTDGIGKSPQQLYGEL----TDPNKPTMQNT
                                                                                                                                                 Conservative
                                                                                                                                           5.9%; Score 154; DB 2; Length 343;
22.0%; Pred. No. 0.0044;
vative 48; Mismatches 114; Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 158.5; DB 2; ; Pred. No. 0.0036; 51; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              461
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                                                                                                                                                                                                                                                                                  GSPDB:GN00070;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----VTLG 396
                                                                                                                                                                                                                                                                                  SCOEDB: SC4C6
                                                                                                                                               Gaps
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 173
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Db	γ	Db Qy	Db Q	Query M Best Lo Matches	C;KeYwc F;1-34-58 F;38-16 F;38-17 F;54-23 F;54-23 F;97,13 F;97,13 F;4-23	A; Molecule A; Residues: A; Cross-ref. C; Comment: C; Superfami	R;Ohkaw Proc. N A;Title A;Refer	RESULT 33 KSKVAO L-ascorbate N;Alternate C;Species: 0 C;Date: 30-0 C:Accession	Ф	Q	Ф	γQ	Дb	Qy	Дb	Ογ
:  :  ::  :: ::      :  :: ::    159	202 KEGLPKVDKEYYVMQGDFYTKGKYGEQ-GLQPFDMEKAIREDAEYVVFNG 250	149 PGGGAEASFTAPGHTSTFSFKALQPGLYVYHCAVAPVGMHIANGMYGLILVEP 201 	101 VEYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPDSKMPHNVDFHAATG 148	Query Match 5.8%; Score 153.5; DB 1; Length 587; Best Local Similarity 28.0%; Pred. No. 0.0097; Matches 49; Conservative \$1; Mismatches 60; Indels 35; Gaps 10;	C;Reywords: copper; glycoprotein; oxidoreductase f;1-35/Domain: signal sequence #status predicted <sig> F;1-37/Domain: signal sequence #status predicted <amt> F;34-58//Product: L-ascorbate oxidase #status predicted <bb1> F;36-346/Domain: middle beta-barrel #status predicted <bb2> F;16-346/Domain: carboxyl-terminal beta-barrel #status predicted <bb2> F;379-574/Domain: carboxyl-terminal beta-barrel #status predicted <bb3> F;379-574/Domain: carboxyl-terminal beta-barrel #status predicted F;36,483/Binding site: Copper (His) (type 2) #status predicted F;95,483/Binding site: Copper (His) (type 2) #status predicted F;95,483/Binding site: carbohydrate (Asn) (covalent) #status predicted F;360,401,475/Binding site: carbohydrate (Asn) (covalent) #status predicted predicted F;360,401,475/Binding site: carbohydrate (Asn) (covalent) #status predicted predicted F;360,401,475/Binding site: carbohydrate (Asn) (covalent) #status predicted predicted F;360,401,475/Binding site: carbohydrate (Asn) (covalent) #status predicted F;360,401,475/Binding site: carbohydrate (Asn) (covalent) #status predicted predicted F;360,401,475/Binding site: carbohydrate (Asn) (covalent) #status predicted F;360,401,475/Binding site: carbohydrate (Asn) (covalent) #status predicted F;360,401,475/Binding site: carbohydrate (Asn) (covalent) #status predicted F;360,401,475/Binding site: carbohydrate (Asn) (covalent) #status predicted F;360,401,475/Binding site: carbohydrate (Asn) (covalent) #status predicted F;360,401,475/Binding site: carbohydrate (Asn) (covalent) #status predicted F;360,401,475/Binding site: carbohydrate (Asn) (covalent) #status predicted F;360,401,475/Binding site: carbohydrate (Asn) (covalent) #status predicted F;360,401,475/Binding site: carbohydrate (Asn) (covalent) #status predicted F;360,401,475/Binding site: carbohydrate (Asn) (covalent) #status predicted F;360,401,401,405/Binding site: carbohydrate (Asn) (covalent) #status predicted F;360,401,401,405/Binding site: carbohydrate (Asn) (covalent) #status predicted F;360,401,401,405/B</bb3></bb2></bb2></bb1></amt></sig>	A;Molecule type: mRNA A;Residues: 1-587 <ohk> A;Residues: 1-587 <ohk> A;Cross-references: GB:U04494; NID:g167512; PIDN:AAA33119.1; PID:g167513 C;Comment: This enzyme, which catalyzes the oxidation of L-ascorbate to dehydroascorbate C;Comment: This enzyme, which catalyzes the oxidation of L-ascorbate to dehydroascorbate</ohk></ohk>	R;Obkawa, J; Okada, N.; Shinmyo, A.; Takano, M. R;Ohkawa, J; Okada, N.; Shinmyo, A.; Takano, M. Proc. Natl. Acad. Sci. U.S.A. 86, 1239-1243, 1989 A;Title: Primary structure of cucumber (Cucumis sativus) ascorbate oxidase deduced from A;Reference number: A30094; MUID:89145218; PMID:2919172	33  rbate oxidase (EC 1.10.3.3) precursor - cucumber  rnate names: ascorbase  les: Cucumis sativus (cucumber) : 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999  ssion- A3004	GTIPGYEPHEHGGATAKSC	358 IYSHKQTDAVYLPEGAPQAIDTQEAPKTPAPANLQEQIKAGKATYDSNCAACHQ 411	245 TGILTGPDDPSRVIDNKIYGPADSFGFQIIAGEGVGAGAWMYHCH 289	306 IQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVEGEENHE 357	198MTINNRKPHTGEDFEATVGDRVEIVMITHGEYYHTFHMHGHRWADNR 244	253 GALTGENALKAKVGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHN 305	::	,   VEPKEGLPKVDKEYYVMQGPFYTKGKYGEQGLQPFDMEKAIREDAEY

probable cytochrome c precursor PA2266 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: A83363 X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; .; Lory, S.; Olson, M.V.

M.J.; Br K.; Lim,

PAO1)

RESULT 34 A83363

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L-ascorbate of C;Species: O: C;Date: 23-A; C;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportun A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportun A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: A83363

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-439 <STO>

A;Cross-references: GB:AE004652; GB:AE004091; NID:g9948287; PIDN:AAG05654.1;
A;Cross-references: GB:AE004652; GB:AE004091; NID:g9948287; PIDN:AAG05654.1;
A;Experimental source: strain PA01
C;Genetics:
C;Genetics:
A;Gene: PA2266
C;Superfamily: membrane-bound alcohol dehydrogenase cytochrome c; cytochrome C;Keywords: Chromoprotein; heme; iron; metalloprotein
F;40,43/Binding site: heme (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Tabata, K.; Hirose, A.; Esaka, M. submitted to the EMBL Data Library, June 19: A; Description: Gene expression and function A; Reference number: Z15298
A; Accession: T04343
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A;Cross-references: EMBL:AB004799; PIDN:BAA20520.1
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밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -ascorbate oxidase (EC 1.10.3.3) - rice
;Species: Oryza sativa (rice)
;Date: 23-Apr-1999 #sequence_revision 23-
;Accession: T04343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: membrane-bound alcohol dehydrogenase cytochrome c; cyt; Superfamily: membrane-bound alcohol dehydrogenase cytochrome c; cyt; Keywords: chromoprotein; heme; iron; metalloprotein; Ad, 43/Binding site: heme (Cys) (covalent) #status predicted; 44/Binding site: heme iron (His) (axial ligand) #status predicted; 188,191/Binding site: heme (Cys) (covalent) #status predicted; 192/Binding site: heme iron (His) (axial ligand) #status predicted; 324,327/Binding site: heme (Cys) (covalent) #status predicted; 328/Binding site: heme iron (His) (axial ligand) #status predicted
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-237/Disulfide bonds:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: laccase
Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: translated from
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Local Similarity 35.5%;
tee 38; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                        VEYQFWT-----FGGQVPGQMIRVREGDTIEVQFSN--HPDSKMPHNVDFHAATG
                                                                                                                                 LPKVDKEYY------VMQGDFYTKGKYGE-QGLQPFDMEKAIREDAEYVVFNG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYES-VMPAIA--LSDQQIANVITYTLNSFGNKGGQLSADDVAKAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTGAALYVDNCGACHRTDGKGYARVFPALAGNPVVTGSDPTSLVHIVLKG--GTLPATHQ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAGKATYDSNCAACHOPDGKGVPNAFPPLA-NSDYLNADHARAASIVANGLSGKITVNGN
CTLGPARKSFEKLLNQERGDPASTIRRCAATRRSAEEERVGPYCPRSQCAPVVFNVEQGK
                                           -SVG--
                                                                                                                                                                                                                                                                   VEYVLWAPDCQQRVMIGINGRFPGPNITARAGDVISVTMNNKMHTEGVVIHWHGIRQFGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APSSFTMPPFGWRMNDQEIADVVNFIRTSWGNQAPSVSVDEVRRLRK 418
                                                                                                                                                                             PWADGTASISQCAVNPGETFVYKFVADKPGTYFYH---GHFGMQRAAGLYGSLIVLDSPE
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                           5.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            #status predicted
                                                                                                                                                                                                                       PGHTSTFSFKALQPGLYVYHCAVAPVGMHIANGMYGLILVEPKEG
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                                                                                                                                                                                                                                                                                                                                                           47;
                                                                                                                                                                                                                                                                                                                                                                           Score 151.5; DB Pred. No. 0.0075
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Pred. No. 0.0071;
5; Mismatches 48
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                                           ALTGENALKAKV---
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                                                                                                                                                                                                                                                                                                                                                           138;
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.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01,
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Restidues: 1-374 <STDA
A;Cross-references: GB:AE004449; GB:AE004091; NID:g9945928; PIDN:AAG03495.1; GSPDB:GN001
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytochrome c oxidase, subunit II cyspecies: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revC;Accession: F83631
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                     coxB;
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                                                                                                                                             241
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                                 456
                                                                                        396 KAGKATYDSNCAACHOPDGKGVPNAFPPLANSDYLNADHARAASIVANGLSGKITVNGNO
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                                                                                                                                                                                                                                                                                                                              VGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQT----TLIPAGGA-----
                              YESVMPAIA--LSDQQIANVITYTLNSFGNKGGQLSADDVAKAKKTK 500
                                                                                                                                                                                                                  TSSDVIHSWWVPAFAVKRDAIPGFVNEAWTKVDEPGIYRGQCAELCGKDHGFMPIVVD--
                                                                                                                                                                                                                                                                                                                                                                                                                                     PA0105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDVPG
--TAMAAFGKQLNEVDLAAVITYERNAWGNDDGDMVTPKDVVAYKQK
                                                                     ARGDKVYHTI CAACHQAEGQGMPPMFPALKGSKI VTGPKEHHLEVVFNGVPG
                                                                                                                                                                               IFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKTPAPANLQEQI
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                                                                                                                                                                                                                                                                                                                                                                                5.7%;
22.0%;
                                                                                                                                             - VKPKAEFDQWLAKRKE-EAAKVKE-----LTSKEWTK-----EELV
                                                                                                                                                                                                                                                        ---AITEF-----KVDVPGDY------VLVDHA
                                                                                                                                                                                                                                                                                          ------DQIHNRQAKDEHYLLEVDEPLVLPVGTKVRFLI
                                                                                                                                                                                                                                                                                                                                                                 38;
                                                                                                                                                                                                                                                                                                                                                                               Score 150; DB 2;
Pred. No. 0.0093;
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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A.; Larbig,
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K.; Lim,
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Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
Nature 406, 959-964, 2000
A,Title: Complete genome sequence of Pseudomonas aeruginosa PAO1,
A,Title: Complete genome sequence of Pseudomonas aeruginosa PAO1,

R;Stover, C.K.; Pham, X.Q.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.; Lory, S.; Olson, M.V.

Coulter,

A.L.; Mizoguchi, S.D.; Coulter, S.N.; Folger, I

Kas,

; Hickey, ; Larbig,

M.J.; Br K.; Lim,

an

opportunistic

patho

C; Accession: C;Date: 15-Sep-2000 C;Accession: E83075

probable cytochrome c PA4571 [imported]
C:Species: Pseudomonas aeruginosa

#sequence_revision

15-Sep-2000

#text_change

31-Dec-2000

Pseudomonas aeruginosa (strain

PAO1

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A;Experimental source: strain PAO1
C;Genetics:
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A; Reference number: A82950;
A; Accession: F83387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody, .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        copper resistance protein A precursor PA2065 [imported] - Pseudomonas aeruginosa C_\ell; Species: Pseudomonas aeruginosa
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A; Residues: 1-675 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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 325
                              353
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                                                                                                                         WAEMKMSPTDLADVSGYTYTYLLNGQPPDGNWTGLFR---
                                                                                                                                                                                      LLSDWSDE
                                                                                                                                                                                                                  MOGDFYTKGKYGEQGLQPFDMEKAIREDAEYVVF----
                                                                                                                                                                                                                                                                            --TAPGHTSTFSFKALQPGLYVYHCAVAPVGMHIANGMYGLILVEPKEGLP-KVDKEYYV
                                                                                                                                                                                                                                                                                                             TINGSLPGPTLRWREGDNVTLRVRNRLAEDTSIHWHGIILPANMD------GVPGLSF
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ERAYTLFAQSMDRSGY-ARGTLALAEGLSAPVPTPDPRPLIGMDDMGMGGMDHGAMGHGA
                             EENHEIYSHKQTDAVYLPEGAPQAIDTQEAP-KTPAPANLQEQIKAGKATYDSNC---AA
                                                          ----VNASAMSYFDVRIPGLKMTVVAADGQHVEPVSVDELRIAVAETYDV----IVEPGG
                                                                                            TLIPAGGAAITEFKVDVPG-----
                                                                                                                                                    --ALK----AKVGETVRLFVGNGGP---NLTSSFHVIGEIFDKVHFEGGKGENHNIQT
                                                                                                                                                                                                                                                 EGIAPGGLYEYRFKVRQNGTYWYH---SHSGLQEQAGVYGALVIDAREPEPFSYDRDYVV
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                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       5.7%; Score 149; DB 2
21.3%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence of Pseudomonas aeruginosa PA01,
50; MUID:20437337; PMID:10984043
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                                                                                                                                                                                   - KPORILAKLKKOSDYYNFHKRTVGDFIDDVSANGWAATLADRKM
                                                                                                                                                                                                                                                                                                                                                                          59;
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Pred.
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Coulter, S.N.; Folger, 1
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                         -DYVLVDH---AIFRAFNKGALGILKVEG
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Larbig,
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383
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K.; Lim,
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F:24-468/Product: membrane-bound alcohol dehydrogenase cytochrome c (F:320-403/Domain: cytochrome c6 homology <CY6-
F:320-403/Domain: cytochrome c6 homology <CY6-
F:45-48/Binding site: heme (Cy8) (covalent) #status predicted
F:49/Binding site: heme iron (His) (axial ligand) #status predicted
F:193,196/Binding site: heme (Cy8) (covalent) #status predicted
F:197/Binding site: heme (Cy8) (covalent) #status predicted
F:330,333/Binding site: heme (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: membrane-bound alcohol dehydrogenase cytochrome c;
C;Keywords: alcohol metabolism; blocked amino end; chromoprotein;
F;1-23/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-468 < TAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Tamaki, T.; Fukaya, M.; Takemura, H.; Tayama, K.; Okumura, Biochim. Biophys. Acta 1088, 292-300, 1991
A;Title: Cloning and sequencing of the gene cluster encoding A;Reference number: S14270; MUID:91159482; PMID:2001402
A;Accession: S14271
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                                             468
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394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        names: membrane-bound
                                           QQIANVITYTLNSFGNKG~GQLSADDVAKAKKT
                                                                                           NDGGGVARMFPPLAGNPVVVTENPTSLVNVIAHG--GVLPPSNWAPSAVAMPGYSKSLSA
                                                                                                                                                                                    GN----YTYDPSTANMLASG----NTASVP--
                                                                                                                                                                                                                                                                                AVF-GGMGD--
                                                                                                                                                                                                                                                                                                                         VHFEGGKGENHNIQTTLIPAGGAAITEFKVDVPGDYVLVD--HAIFRAFNKGALGILKVE
                                                                                                                                                                                                                                                                                                                                                                                                                    AIREDAEYVVFNGSVGALTGENALKAKVGETVR----LFVGNGGPNLTSSFHVIGEIFDK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLSMRWPLGIWRMMFSPSPKDFTPAPGTDPEIARGDYLVTGP-GHCGACHTPRGFAMQEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVGMHIANGMYGLIL-VEPKEGLPKVDKEYYVMQGDFYTKGKYGEQGL----QPFDM-EK 237
QQIADVVNFIRTSWGNKAPGTVTAADVTKLRDT
                                                                                                                                  PDGKGVPNAFPPLANSDYLNADHARA-ASIVANGLSGKITVNGNOYESV-MPAI--ALSD
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brane-bound alcohol dehydrogenase
                                                                                                                                                                                                                                                                           -----VVAWSTQYFTDDDLHAIAK-YLKSLPPVPPSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.6%; Score 146; DB 1; Length 468, 25.2%; Pred. No. 0.023; tive 50; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                      -GGPDFLSGGAPIDNWVAPSLRNDPVVGLGRWSEDDIYTFLKSGRIDHS
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l dehydrogenase 44K (
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membrane-bound alcohol dehydrogenase (EC 1.1.-.-) cytochrome c precursor N;Alternate names: membrane-bound alcohol dehydrogenase 44K chain C;Species: Acetobacter pasteurianus C;Date: 07-Apr-1994 #sequence_revision 09-Aug-1996 #text_change 17-Nov-20 C;Accession: B49340 R;Takemura, H.; Kondo, K.; Horinouchi, S.; Beppu, T.

09-Aug-1996 #text_change 17-Nov-2000

Acetobacter

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A;Cross-references GB::13893; NID:g517067; PIDN:BAA02993.1; PID:g452587
A;Experimental source: strain NCI1380
C;Complex: heterodimer of 72K and 44K (cytochrome c) chains
C;Superimental; membrane-bound alcohol dehydrogenase cytochrome c; cytochrome c6 homology
C;Keywords: alcohol metabolism; blocked amino end; chromoprotein; electron transfer; hen
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-472/Product: membrane-bound alcohol dehydrogenase cytochrome c chain #status predicted
F:321-404/Domain: cytochrome c6 homology <CYC>
F:46,49/Binding site: heme (Cys) (covalent) #status predicted
F:198/Binding site: heme (Cys) (covalent) #status predicted
F:198/Binding site: heme (Cys) (covalent) #status predicted
F:331,334/Binding site: heme (Cys) (covalent) #status predicted
F:331,334/Binding site: heme (Cys) (covalent) #status predicted
F:331,334/Binding site: heme iron (His) (axial ligand) #status predicted
F:331,334/Binding site: heme iron (His) (axial ligand) #status predicted
F:331,334/Binding site: heme iron (His) (axial ligand) #status predicted
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A; Title: Induction by ethanol of alcohol dehydrogenase activity in Acetobacter pasteuria
A; Reference number: A49340; MUID:94042848; PMID:8226628
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Search completed: August 27, 2003, 18:32:44
Job time : 46 secs
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A;Residues: 1-472 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.5%;
Best Local Similarity 33.3%;
Matches 39; Conservative 1
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                                                                                                                                                        371
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                                                                                                                                                                                                                           456 YESVMP-----AIA-----LSDQQIANVITYTLNSFGNKG-GQLSADDVAKAK 497
                                                                                                                                                                                                                                                                                                      322 AGAKTYVEQCAICHRNDGGGVARMFPPLAGNPVVVSDNPTSVAHIVVDG------ 370
                                                                                                                                                 --GVLPPTNWAPSAVAMPDYKNILSDQQIADVVNFIRSAWGNRAPANTTAADIQKLR 425
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%; Pred. No. 0.025;
18; Mismatches 31;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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2452.304 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07
2: /cgn2_6/ptodata/2/pubpaa/PCT 1
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                      /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09_RUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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	104	104	104	104	104	104	104	104	104	104	104	104	104.5	105	105	106.5	107.5	107.5	108	108	108.5	108.5	109	109	110.5	113	•	113.5	114.5	٠
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	12	12	12	12	12	12							15						12	9	11	9	9	9.	16	14	10	10	14	14
ALIGNMENTS	US-10-141-704-234	US-10-141-702-234	-10-141-698	US-10-140-926-234	-10-140-924		US-10-140-807-234	US-10-140-471-234	US-10-140-274-234	US-10-140-021-234	US-10-140-018-234	US-10-137-870-234	US-10-156-761-14797	US-10-193-764-55	US-10-193-764-57	US-10-156-761-10292	US-10-043-487-383	US-09-738-363-6	US-10-238-075-877	US-09-765-272-84	US-09-769-787-2	US-09-874-069-4	-SD	US-09-118	US-10-174-693-290	US-10-095-	US-0	•	-10-080-233-	US-10-080-210-2
		234,	Sequence 234, App	234,		234,	234,	Sequence 234, App	234,	234,	234,	234,	1479	Sequence 55, Appl		Sequence 10292, A	e Se		e B	٠.	Sequence 2, Appli	4	Н	N			2	13,	'n	Sequence 2, Appli

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317 183	265 VGETVRLFVGNGGPNLTSSFHVIGEI   :     135 LGQDVEYFSNLATPQ	Query Match 5.7%; Score 150; DB 15; Best Local Similarity 22.0%; Pred. No. 2.2e-05; Matches 63; Conservative 38; Mismatches 86	; ORGANISM: Pseudomonas aeruginosa US-10-127-032-116	; SEQ ID NO 116 ; LENGTH: 374 . TYPE: DPT	; NUMBER OF SEQ ID NOS: 170 ; SOFTWARE: FastSEQ for Windows Version 4.0	; PRIOR FILING DATE: 2001-10-24	PRIOR FILING DATE: 2001-04-20	; CURRENT FILING DATE: 2002-04-19 ; PRIOR APPLICATION NUMBER: US 60/285,190	CURRENT APPLICATION NUMBER: US/10/127,032	; TITLE OF INVENTION: BIOFILM FORMATION	INVENTION: M			; APPLICANT: Whiteley, Marvin	; GENERAL INFORMATION:	; Sequence 116, Application US/10127032 ; Publication No. US20030113742A1	RESULT 1 US-10-127-032-116
	11	B 15; Length 374; e-05; 86; Indels 100; Gaps									ONS FOR THE MODULATION OF						
40	316 182	11;															

Result No.

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Query Match Length DB

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Description

SUMMARIES

141 140.5 136.5 135.5 135.5 128.5 128.5 128.5 124.1 124.5

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574 529 529 575 575 575 5724 539 539

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US-09-738-626-6780
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US-09-869-877-8
US-09-732-350-8
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US-10-115-563-14
US-09-732-350-7
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Best Local Similarity
Matches 103; Conserv
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Patent No. US20010031490A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: ROZEK, CATOl
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 521
TELECOMMUNICATION INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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CITY: New York
TMATE: NY
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ADDRESSEE: No. US20010031490A10 No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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   115
                                 165 TFSFKALOPGLYVYHCAVAPVGMHIANGMYG-LILVEP----KEGLPKVDKEYYVMQGDF
                                                                                                           117 IRVREGDTIEVQFSNH----PDSKMPHNVDFH-----AATGPGGGAEASFTAP-----GHTS 164
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   EIPLRG-QTGTMWYH---AHLASQYVDGLRGPLVIYDPNDPHKSRYDVDDASTVVMLEDW
                                                                        ITANKGDTLRINVTNQLTDPSMRRATTIHWHGLFQATTADEDGPAFVTQCPIAQNLSYTY
                                                                                                                                                   LPLLAAVST------PAFAAVRNYKFDIKNVNVAPDGFQRSIVSVNGLVPGTL
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llarity 20.4%; Pred. No. 0.00026;
Conservative 60; Mismatches 216;
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US-09-869-877-5
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US-09-869-877-5
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LENGTH: 529
TYPE: PRT
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APPLICANT: Danielsen, Steffen
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Laccase Mutants
FILE REFERENCE: 10179.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/O:
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
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 269
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                                 325 VPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQE---
                                                                                                         270 RLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGG-----AAITEFKVD
                                                                                                                                                                                      220 Y-----TKGKYGEQG---LQPFDMEKAIREDAEYVVFNGSVGALTGENALKAKVGETV
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                                                                                                                                                 YHTPAPVLEKOMFSTNNTALLSPVPDSGLINGKGRYV-----GGPAVPRSVINVKRGKRY 225
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Pred. No. 0.00026;
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RESULT 4
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US-09-738-626-6780
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NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6780
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Best Local (
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
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TYPE: PRT
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                              GNGGPNLTSSFHVI--GEIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDVP---GD
                                                                      HNGRMGMGGHGQMMHGTPDRVLGGDVGDVMYPHYLINGRIPRAHRTFEARPGDKARLRFI
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
                                                                                                                                          GLQLDRGLHAPLIIRDPQDAEDQDVEWTIVLDDWVD----GIQGTPDDELDKLTGMGSGD
                                                                                                                                                                                                                   ITNELPESTSIHWHGIALHNAADGVPGMTQDPIEPGESFSYVFEVPHGGTYFYH---SHT
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OZAKI, AKIO
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19.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 140.5; DB 1
Pred. No. 0.00026;
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                                                                                                        -TGENALKAKVGETVRL-FV
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-RVDVEVILGD
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RESULT 6
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US-10-174-693-291
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CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: US 09/615,192
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 291, Application US/1017, publication No. US20030131373A1 GENERAL INFORMATION: APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 291
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Materials and Methods for TITLE OF INVENTION: Modification of Plant Lig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                     113 LWLRATLHGAIVILPKRGVPYPFPKPHKEVVVVLGEWWKSDTEGVISQAIKSGLAP----
                                                                                                                                                                                                                                                                                                                      237 KAIREDAEYVVFNGSVGALT-----GENALKAKVGETVRLFVGNGGPNLTSSFHVIGEIF 291
                                                                                                                                                                                                                                                                                                                                                                                                                187 MHIANGMYGLILVEPKEGL----PKVDKEYYVMQGDFYTKGKYG-----EQGLQPFDME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 PHNVDFH------AATGPGGGAEASFTAPGHTSTFSFKAL-QPGLYVYHCAVAPVG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323 GIFPLTALAVGKDDRAFAVIRTAGGQAPRPDVDFPELSSTGLLLSSLKPADRALLPEGTP
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                                                                                                                                    GEENHEIYSHKQTDAVYLPEG----APQAIDTQEAPKT
                                                                                                                                                                                                                              DKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVE
                                                                                                                                                                                                                                                                           ---NVSDAHTINGHPGPSSNCPSQGGFTLPVESGKKYMLRIINAALNEELFFKIAGH--
                                                                                       GOTTNALISTDOSSGKYMVAASPFMDSPIAVDNMTATAT
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o. US20030131373A1
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Sequence 8, Application US/09732350
Patent No. US2001031490A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Xu, Feng
TITLE OF INVENTION: LACCASE MUTAN
UMBER OF SEQUENCES: 10

Xu, Feng NVENTION: LACCASE MUTANTS

CORRESPONDENCE ADDRESS

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US-09-732-350-8
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Best Local (
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TOPOLOGY: lin
MOLECULE TYPE:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 212-867-014
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
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Similarity 20.0%;
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                                                                                                                               EQIKAGKATYDSNCAACHQPDGKGVPNAFPPL-----
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                                                                                                                                                                                                                                                               EPDTYWINAPLTNVPNKTAQALLVYEEDRRPYHPPKGPYRKWSVSEAIIKYWNHKHKHGR 337
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                                                                                         LDL----TFGLNFATGHWMI-NGIPYESPKIPTLLKILTDEDGVTESDFTKEEH---TV 448
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    ILPKNKCIEFNIKGNSGIPITHPVHLHGH----TWDVVQFGN
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                                                                                                                             US-09-738-626-4553; Sequence 4553; Application US/09738626; Publication No. US20020197605A1
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GENERAL INFORMATION:
APPLICANT: NAKAGAMA, (APPLICANT: NIZOGUCH, (APPLICANT: ANDO, SEI)
APPLICANT: HAYASHI, (APPLICANT: OCHIAI, K)
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US-09-869-877-8
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Publication No. US20020192792A1
GENERAL INFORMATION:
APPLICANT: Schneider, Palle
APPLICANT: Danielsen, Steffen
APPLICANT: Svendsen, Allan
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Best Local Similarity
Matches 105; Conserv
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Laccase Mutants FILE REFERENCE: 10179.204-US
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                      338 GLISGHGGLKARMIEGSHHLHSRSVVKRONETTTVVMDESKLVPLEYPGAACGSKPADLV 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 GILKVEG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 EPDTYWINAPLTNVPNKTAQALLVYEEDRRPYHPPKGPYRKWSVSEAIIKYWNHKHKHGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 -PGDYVL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 RFSV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 SFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDV-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 SHLSSQYVDGLRGPLVIYPKDPHRRLYDVDDEKTVLIIGDWY-------HESSKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 APVGMHIANGMYGLILVEPKE---GLPKVDKEYYVM-QGDFYTKGKYGEQGLQPFDMEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 RTTSIHWHGLLQHRNADDDGP-----SFVTQCPIVPRESYTYTIPLDDQTGTYWYH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 VLARTVEYGLKISDGEIAPDGVKRNATLVNGGYPGPLIFANKGDTLKVKVQNKLTNPEMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 VKMETVEKVMRLA-----DGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSN----HPDSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPHNVDFHAA-----TGPGGGAEASFT----APGHTSTFSFKA-LQPGLYVYHCAV
                                                                                                                                                                                                                                                                                                                                                                                            EQIKAGKATYDSNCAACHOPDGKGVPNAFPPL-----ANSDYLNADHARAAS
  ANDO, SEIKO
HAYASHI, MIKIF
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                 ILPKNKCIEFNIKGNSGIPITHPVHLHGH----
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                                          MIZOGUCHI, H
ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.1%; Score 135; DB 10; ilarity 20.0%; Pred. No. 0.0011; Conservative 63; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                    -TFGLNFATGHWMI-NGIPYESPKIPTLLKILTDEDGVTESDFTKEEH---TV
                                                                                       SATOSHI
                          MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EENHEIYS-----HKQTDAVYLPEGAPQAIDTQEAPKTPAPANLQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----EGHKV--TVIAADGVSTKPYQVDAFDILAGQRIDCVVEANQ
                                                                                                                                                                                                                                                                 -TWDVVQFGN
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US-10-115-563-14
; Sequence 14, Application US/10115563
; Publication No. US20030008307A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VEY: 3.0
SEQ ID NO 4553
LENGTH: 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 00/159162 PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Corynebacterium
                                              APPLICANT: Griffin, John H
Greengard, Judith S
TITLE OF INVENTION: METHODS FOR DIAGNOSING ACTIVATED PROTEIN
C RESISTANCE ASSOCIATED WITH A FACTOR V GENETIC MUTATION
AND COMPOSITIONS THEREOF
                   NUMBER OF SEQUENCES: 28 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          385
                                                                                                                                                                                                                                                                                                                                           396 KAGKATYDSNCAACHQPDGKGVPNAFPPLANSDYLNADHARAA 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119
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                                                                                                                                                                                                                                                                                                       QRVDVVIDHD-----QPEVWIVIN-----DNSDWPHNFHVHDA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANGITNAHFDATTRRVRFRVLNGSNMRFY-----NLAFSDTRTFQVIASDSGLLDEPQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNL----TSSFHVIG-----EIFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKLPAIADGGPHSPIGPGQTWSPTWTVANDAATLWYHPHTHGL-----TGLHAYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - KMPHNVDF - - HAATGPGGGAEASFTAPGHTSTFSFKALQPGLYVYHCAVAPVGMHIANG
                                                                                                                                                                                                                                                                                                                                                                                                                              ILKVEGEENHEIYSHKQTDAVYLP-----EGAPQAIDTQEAP---KTPAPANLQEQI 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVVKMETVEKVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPDS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTTLAIGPGERWEIVVELEP--GEDVTLESVGFEDNYGVPDDEFVPDFGMSDSFQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVHFEGGKGENHNIQTTLIPAGGAAIT-----EFKVDVPGDYVLVDHAIFRAFNKGALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAGMIIVE-DEATDKLDLPREYGVDDIPLVIMDHRFLEDGSLDEEDLP--DLGLLGDTPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGAGVLAATVVGAQVLVACSSDDVRGYGGEPRTLPI-----PPADLGTREGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKEDA, MASATO
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The
                                      AND: 28
Scripps Research Institute,
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                                                                                                                                                                                                                                                                                                                                                                                      DAAQAPALPGVLVKSTEPDVIDATERTFIMNTFSINDLQMDM
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Office of
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RESULT 10
US-10-172-712-31
; Sequence 31, Application US/10172712
; Publication No. US20030125232A1
; GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2224 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid .
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: 441
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/410,488 FILING DATE: 24-MAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 92037
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     581
                                                                                                                                                                                                                                                              297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 KEDGILGPIIRAQVRDTLKIVFKNMASRPYSIYPHGVTFSPYEDE----VNSSFTS-GRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 ----VPGQMIRVREGDTIEVQFSN---HPDSKMPHNVDFHAATGPGGGAEASFTAPGHTS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 EVIWDYAPVIPANMDKKYRSQHLDNFSNQIGKHYKKVMY----TQYEDESFTKHTVNPNM
                                                                                                                                           670 PRSKKLRLKFRDVKCIPDDDEDSYEIFEPPESTVMATRKMHDRLEPEDEESDADYD
                                                                                                                                                                                354 ENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKTPAPA-----NLQEQIKAGKATYD 403
                                                                                                                                                                                                                                                                                                                                            254 ALTGENALKAKVGETVRLFVGNGGPNLTSSFHVIGEIFD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 DAIVTHAPEVPPPVDRDHPAKVVVKMET-----VEKVMRLADGVEYQFWTFGGQ-----
                                                                                                                                                                                                                                                                                                                                                                                 RSLDRRGIQRAADIEQQAVFAVFDENKSWYLEDNINKFCENPDEVKRDDPKF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/115,563
FILING DATE: 02-Apr-2002
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                       TGHSFIYGKRHEDTLTLFPMRGESVT
                                                                                                                                                                                                                                                            EGGK----GENHNIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVEGE
                                                                                                                                                                                                                                                                                                     ----YESNIMSTINGYV-----PESITTLGFCFDDTVQWHFCSVGTQNEILTIHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent Counsel
STREET: 10666 No. US20030008307Alth Torrey Pines Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 619-554-6312
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19.7%; Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449.0
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APPLICANT: GRIFFIN,

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RESULT 11
US-09-732-350-7
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US-10-172-712-31
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PRIOR FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 31
LENGTH: 2224
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09732350 Patent No. US20010031490A1
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Best Local Similarity
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Su, Feng
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US20010031490Alo No. US20010031490Aldisk of No. US20010031490Alth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 4198-4001US1
CURRENT APPLICATION NUMBER: US/10/172,712
CURRENT FILING DATE: 2002-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GETZOFF, ELIZABETH D.
APPLICANT: PELLEQUER, JEAN-LUC
TITLE OF INVENTION: STABILIZED PROTEINS WITH ENGINEERED DISULFIDE BONDS
                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 EVIWDYÄPVIPANMÖKKYRSQHLDNFSNQIGKHYKKVMY----TQYEDESFTKHTVNPNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 DAIVTHAPEVPPPVDRDHPAKVVVKMET----VEKVMRLADGVEYQFWTFGGQ-----
                                                                                                                                                            10174
                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRSKKLRLKFRDVKCIPDDDEDSYEIFEPPESTVMATRKMHDRLEPEDEESDADYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKTPAPA-----NLQEQIKAGKATYD 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTGENALKAKVGETVRLFVGNGGPNLTSSFHVIGEIFD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSLDRRGIQRAADIEQQAVFAVFDENKSWYLEDNINKFCENPDEVKRDDPKF------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEDGILGPIIRAQVRDTLKIVFKNMASRPYSIYPHGVTFSPYEDE---VNSSFTS-GRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGGK---GENHNIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVEGE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----YESNIMSTINGYV-----PESITTLGFCFDDTVQWHFCSVGTQNEILTIHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGLPK-----VDKEYYVMQGDF-YTKGKYGEQGLQPF--DMEKAIREDAEYVVFNGSVG
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                                                                                                                                                                                                                                          405 Lexington Avenue
                                                                                                                                                                                USA
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      NUMBER:
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    US/09/732,350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 128.5; DB Pred. No. 0.036;
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                                                 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KVHF 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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; LENGTH: 572
; TYPE: PRT
; ORGANISM: Rhizoctonia solani
US-09-869-877-7
                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-869-877-7
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                                                                                                                               APPLICANT: Schneider, Palle
APPLICANT: Schneider, Steffen
APPLICANT: Danielsen, Steffen
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Laccase Mutants
FILE REFERENCE: 10179.204-US
CURRENT APPLICATION NUMBER: U$/09/869,877
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09869877 Publication No. US20020192792A1 GENERAL INFORMATION:
                                                                                       SOFTWARE: PatentIn
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: ROZEK, CALUL
NAME: ROZEK, CALUL
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5200
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 212.867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Rozek, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 EIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGIL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 QYVDGLRGPLVIYDPKDPHRRLYDIDDEKTVLIIGDWYHTSSKAILATGNITLQQPDS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 MPHNVDFHAA-----TGPGGGAEASFTAPGHTSTFSFK-ALQPGLYVYHCAVAPVGM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 HIANGMYG-LILVEPKEGLPKV----DKEYYVMQGDFY-TKGK----YGEQGLQPFDMEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 RTTSIHWHGLLQHRNADDDGPAFVTQCPI-VPQASYTYTMPLGDQTGTYWYH---SHLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 VLARTVEYNLKISNGKIAPDGVERDATLVNGGYPGPLIFANKGDTLKVKVQNKLTNPDMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 VKMETVEKVMRLA-----DGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSN---HPDSK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRRPYHPPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----RMSIQGHK-----MTVIAADGVSTKPYQVD-
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21.4%; Pred. No. 0
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Gaps

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RESULT 13
US-09-732-350-1
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Best Local
                                                                                     ATTORNEY/AGENT INFORMATION:

NAME: ROZEK, CATOl

REGISTRATION UNMBER: 36,993

REFERENCE/DOCKET NUMBER: 5200

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123
                                 TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARPLICANT: Svendsen APPLICANT: Xu, Feng TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                     SOFTWAKE: .....CATA:
CURRENT APPLICATION DATA:
US/09/732,350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US20010031490Alo No.
STREET: 405 Lexington Avenue
                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
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                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity
79; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKT---PAP-ANLQEQIKAGKATYDS 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGIL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ATINGK-GRFDPDNTPANPNTLYTLKVKRGKRYRLRVINS--SAIASF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIREDAEYVVFNGSVGALTGEN------ALKAKVGETVRLFVGNGGPNLTSSFHVIG 288
 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTTSIHWHGLLQHRNADDDGPAFVTQCPI-VPQASYTYTMPLGDQTGTYWYH---SHLSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLARTVEYNLKISNGKIAPDGVERDATLVNGGYPGPLIFANKGDTLKVKVQNKLTNPDMY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SFDILAGQRIDAV-----VEANQEPDTYWINAPLTNVANKTAQALLIYED
                   539 amino acids
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SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 539
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Matches
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APPLICANT: Danielsen, Steffen
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Laccase Mutants
FILE REFERENCE: 10179.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/869, CURRENT FILING DATE: 2001-07-06
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TOPOLOGY: lir
MOLECULE TYPE:
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165 TLADWYHIPAPSIQG-----AAQPDA--TLINGKGRYVGGPAAELSIVNVEQGKKYR
                                  216 Q-GDFYTKGKYGEQGLQPFDMEKAIREDAEYVVFNGS---VGALTGE-NALKAKVGE--T 268
                                                                     108 GHAFLYKFTPAGHAGTFWYH---SHFGTQYCDGLRGPMVIYDDNDPHAALYDEDDENTII 164
                                                                                                                                                                                112 VPGQMIRVREGDTIEVQFSN---HPDSKMPHNVDFHA-----ATGPGGGAEASFTAP
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                                                                                                                                               49 VHGPLIRGGKNDNFELNVVNDLDNPTMLRPTSIHWHGLFQRGTNWADGADGVNQCPI-SP
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US-09-338-723A-2
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PATENT NO. US20020019038A1
GENERAL INFORMATION:
APPLICANT: Huaming, Wang
TITLE OF INVENTION: Phenol Oxidizing Enzymes
FILE REFERENCE: GC561-2
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Best Local (
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LENGTH: 594
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                                                                                                                                                                                                                                                              TKGKYGEQGLQPFDMEKAIREDAEYVVFNGSVGALTGENA-----
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PFPPHKEGPADKHFKFERSNGHYLINDVGFADVNERVLAKPELGTVEVWELENSSGGWSH
                                 -----GAAITEFKVDVPGDYVLVDHAIF-----RAFNKGALGILKVEGEEN-----H
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; TYPE: PRT
; ORGANISM: Stachybotrys
US-10-080-210-2
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US-10-080-210-2
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PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 09/338,723
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 2
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Best Local Similarity
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APPLICANT: Bodie, Elizabeth A.
TITLE OF INVENTION: Phenol Oxidizing Enzymes
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CURRENT FILING DATE: 2002-02-19
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                   PFPPHKEGPADKHFKFERSNGHYLINDVGFADVNERVLAKPELGTVEVWELENSSGGWSH
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19.0%; Pred. No. 0.092;
ative 72; Mismatches 2
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; TYPE: PRT
; ORGANISM: Stachybotrys
US-10-080-233-2
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US-10-080-233-2
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Matches 123
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Publication No. US20020151450A1
GENERAL INFORMATION:
APPLICANT: Wang, Huaming
TITLE OF INVENTION: No. US200201514
FILE REFERENCE: GC567
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CURRENT FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 5
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19.0%; Pred. No. 0.092;
ative 72; Mismatches 226;
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US-09-995-749A-2
; Sequence 2, Application US/09995749A
; Patent No. US20020155568A1
; GENERAL INFORMATION:
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APPLICANT: VAN GEBL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
FILLE REFERENCE: BO43388-CIP
CURRENT APPLICATION NUMBER: US/09/995,749A
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APPLICANT: LEER, RÖBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
FILE REFERENCE: BO43388-CIP
CURRENT APPLICATION NUMBER: US/09/995,749A
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR APPLICATION NUMBER: 09/604,957
PRIOR APPLICATION NUMBER: EPO 00201871.1
PRIOR APPLICATION NUMBER: EPO 00201871.1
PRIOR FILING DATE: 2000-05-25
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; LENGTH: 535
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/09995749A Patent No. US20020155568A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VAN GEEL-SCHUTTEN, G
APPLICANT: DIJKHUIZEN, LUBBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Lactobacillus reuteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 TFSFKALQPGLYVY----HCAVAPVGMHIANGMYGLILVEPKEGLPKVDKEYYVMQGDFY 220
                                                                                             ANPDVSGYL---AVWVPVGASDNQDARTAPST----EKNSGNSAYRTNAAF----D 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFTFEDEQKGIDAYIQDQNSTVKKYNLYNIPASYAILLTN-KDTIPRV---YY---GDLY
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SNVIFEAFSNFVYTPTKESERANVRIAQNADFFAS
                                            GKGVPNAF----PPLANSDYLNADHARAASIVAN 443
                                                                                                                                       ENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKTPAPANLQEQIKAGKATYDSNCAACHQPD
                                                                                                                                                                                      -----GAPVA--MTDENGDLYLSSHNL--VVNGKEEADTAVQGY 382
                                                                                                                                                                                                                                VHFEGGKGENHNIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVEGE
                                                                                                                                                                                                                                                                                    TGTDETRTQGIGVVVSNTPNLKLGVNDKVVLHMGAAHKNQQYRAAVLTTTDGVINYTSDQ
                                                                                                                                                                                                                                                                                                                                                                                 TDGGQYMEHQTRYYDTLTNLLKSRVKYVAGGQSMQTMSVGGNNNILTSVRYGKGAMTATD
                                                                                                                                                                                                                                                                                                                                                                                                                              TK-GKYGEQGLQPFD-MEKAIREDAEYVVFNGSV------GALTGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 113.5; DI
Pred. No. 0.097,
3; Mismatches 1
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462
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APPLICANT: Stepan, Tony
APPLICANT: Munson, Keith
TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Fac
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 35052/204375
CURRENT APPLICATION NUMBER: US/10/095,718
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/689,430
PRIOR APPLICATION NUMBER: 09/689,430
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LERCTH: 1411
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PRIOR APPLICATION NUMBER: 09/604,957
PRIOR FILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PACENTIN VET. 2.1
SEQ ID NO 2
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                                                                                                      US-10-095-718-4
Query Match
Best Local Similarity
Matches 82; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10095718 Publication No. US20020131956A1
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Best Local Similarity
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APPLICANT: Chao, Hengjun
APPLICANT: Burstein, Haim
APPLICANT: Lynch, Carmel
                                                                                                                                                   LENGTH: 1431
TYPE: PRT
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TYPE: PRT
                                                                                                                        ORGANISM: canine
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     Conservative
                                                                                                                          B-domain deleted factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Christopher
                         20.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------GAPVA--MTDENGDLYLSSHNL--VVNGKEEADTAVQGY 1361
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     66;
  Score 113; DB 14;
Pred. No. 0.5;
6; Mismatches 154;
                                               Length 1431;
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  Indels 102;
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  Gaps
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CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR APPLICATION NUMBER: US 09/615,192
PRIOR APPLICATION NUMBER: US 09/615,192
                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 86; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 290
LENGTH: 440
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                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin FILE REFERENCE: 11000.1003c5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 407
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-07-12:
                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Eucalyptus
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                  217
                                                                                               131 OSYTYNFTLTGORGTLLWHAHVS----WLRSSIHGPIIILPKRNESYPFEKPSKEVPIIF 186
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  187
                                                                                                                                              165 ---TFSFKAL-QPGLYVYHCAVAPVGMHIANGMYGLILVEPK--EGLP--KVDKEYYVMQ
                                                                                                                                                                                                                               111 QVPGQMIRVREGDTIEVQFSNHPDSKMPHNVDFH-----AATGPGGGAEASFTAPGHTS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 734 DTYEDIPTPLLNENNVIKPRSFSQNSRHPSTKEKQLKMKREDFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 TEFKVDVPGDYVLVDH-AIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEGAPQAI 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          641 SVCLHEVAYWYILSVGAQTD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       581 SDKRNVILFSVFDENRSWYLTENMQRFLPNADVVQPHDPEFQLSNIMHSINGYVFDNLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 VDKEYYVMQGDF-YTKGKYGEQGLQPF--DMEKAIREDAEYVVFN--GSVGALTGEN-AL
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                                                                                                                                                                                           QYPGPPLVAREGONILVKVVNH----VAANVTIHWHGVRQLRTGWADGPAYVTQCPIQTN 130
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                                               GDFYTKGKYGEQGLQPFDMEKAIRED-----AEYVVFNGSVGALTGENA-----LK
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                                                                                                                                                                                                                                                                                        4.2%; Score 110.5; D
19.7%; Pred. No. 0.14;
tive 51; Mismatches
  -VDPEAVIAQALQSGGGPNVSDAYTINGLPGPLYNCSSKDTFKLK 235
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                                                                                                                                                                                                                                                                                             136;
                                                                                                                                                                                                                                                                                             Indels
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QY 24 SNQADKAAQPKSSTVDA-AAKTANADNAASQEHQGELPVIDAIVTHAPEVPPPVDRD 79	Query Match 4.2%; Score 109; DB 9; Length 969; Best Local Similarity 18.8%; Pred. No. 0.64; Matches 119; Conservative 72; Mismatches 188; Indels 254; Gaps 25;	; TYPE: AMINO ACID ; STRANDEDNESS: SINGLE ; TOPOLOGY: LINEAR US-09-118-276-2	(703) 8 R SEQ II RACTERII	196; 43,07 6201-0003 DN:	INONE TION:	; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/09/118,276	25998	ა ஜ "	7 D	R R R D O M	; TITLE OF INVENTION: METHODS AND MEANS TO MODULATE PROGRAMMED ; TITLE OF INVENTION: CELL DEATH IN EUKARYOTIC CELLS	KUSHNIR, DE BLOCK	; Patent No. US20010011381A1 ; GENERAL INFORMATION: ; APPLICANT, BARTYCHTE FIRMA:	276-		Qy 450 TVNGNQYESVMPAIAL 465	Db 401 NKF 412	Qy 390 NLQEQIKAGKATYDSNCAACHQPDGKGVPNAFPPLANSDYLNADHARAASIVANGLSGKI 449	QY 356 -HEIYSHKQT	296 TKTDFPNSTFLMAAWPYFTGMGTFDNSTVAGILEYEHPKSSNYPP	QY 308 TTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVEGEEN 355	236 VKPGKTYLLRLINAALNDELFFSIANHAVTVVEVDAVYTKPFSAGCLHLTPGQTMVVLLK	Qy 263 AKVGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQ 307
; PRIOR AFFLICATION DATA: NONE ; ATTORNEY/AGENT INFORMATION: ; NAME: SCHULMAN, ROBERT M.; SALEN, KENNETH H. ; REGISTRATION NUMBER: 31,196; 43,077 ; REFERENCE/DOCKET NUMBER: 6201-0003	IWARE: ASCII NT APPLICATION DATA LICATION NUMBER: U LICATION 17-JUL-1	7 9 A	WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN, WCLEAN	NUMBER OF INVENTION: CELL DEATH IN BOWNSTOIL CELLS  NUMBER OF SEQUENCES: 21  CORRESPONDENCE ADDRESS:  ADDRESSEE: SIXBEY, FEREDWAN, LEEDOM, & FERGUSON  CORREST: 8186 (SPECISONS DELVE SULTE 800	NI: DE BLOCK, MARC; NI: INZE, DIRK F INVENTION: METHODS AND MEANS TO MODU		RESULT: 23 US-09-118-276-11 ; Sequence 11, Application U\$/09118276 ; Fatent No. U\$20010011381A1 ; GENERAL INFORMATION:	Db 703 PSIHPHIIRDEDDLMIKAKMLEALQDIEIASKI 735	Qy 461 PAIALSDQQIANVI 474	648	405 NCAACHQPDGKGVPNAFPPLANSDYLNADHARAASIVANGLSGKITVNGNQYESVM	Qy 368YLPEGAPQAIDTQEAPKTPAPANLQEQIKAGKATYDS 404	Db 531 QDDGSECYVFRKWGRVGSEKIGGQKLEEMSKTEAIKEFKRLFLEKTGNSWEAWECKT 587	484RSAVHESSGLQDTAHILEDGKSIYNATLNMSDLALGVNSYYVLQIIE	Qy 277 GPNLTSSFHVIGEIFDKVH-FEGGKGENHNIQTTLIPAGGAAITEFKVDVPGDYVLV 332	425 LDNENAEVRKARRLKIPIVREGYIGECVKKNKMLPFDLYKLENALESSKGSTVTVKVKG-	Db 365 SKATQRTSLLSSKGLDKLRFSVVGQSKEAANEWIEKLKLAGANFYARVVKDIDCLIACGE 424 Ov 239 -IREDAEYVVENGSVGALTGRNALKAKVGETVELFVGNG 276	Oy 239 238	305 SGNVSEWSKCTYSATEP	197ILVEPKEGLPKVDKEYYVMQGDFYTKGKYGEQGLQPFDMEKA-	Db 269 ERHLID-RCADGMIGGALGPCPVCANGMYYYYGOYOC 304	223	Oy 80 HPAKVVVKM-ETVEKVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPDSKMP 138

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Sequence 4, Application US/09874069
PATENT NO. US/20020064826A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Cytokine Receptor-like Po
FILE REFERENCE: PT021P1
CURRENT APPLICATION NUMBER: US/09/874,069
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: PCT/US00/32525
PRIOR APPLICATION NUMBER: 60/168,621
                                                                                                                                                                                                     RESULT 24
US-09-874-069-4
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TELEPHONE: (703) 790-9110
TELEPAX: (703) 883-0370
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: LINEAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 4.2%; Score 109; DB 9; Length 980; Similarity 18.8%; Pred. No. 0.65;
                                                                                                                                                                                                                                                                                                                                                                                                                            NFRKQPGRFYPLDVDYGVKKAPKRKDISEMKSSLAPQLLELMKMLFNVETYRAAMMEFEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIEQNKGSKRKKSENDIDSYKSARLDESTSEGTVRNKGQL------VDPRGSNT
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                                                                                                                                                                                                                                                                                 PSIHPHIRDEDDLMIKAKMLEALQDIEIASKI 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----YLPEGAPQAIDTQEAPKTPAPANLQ-----
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                                                                                                            Polynucleotides, Polypeptides, and Antibod
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Sequence 2, Application US/09769787
Publication No. US20030091577A1
GENERAL INFORMATION:
                                                 APPLICANT: Microbial Technics.Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PMC/P21129W
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
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   SEQ ID NO 2
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Best Local :
                  NUMBER OF SEQ ID NOS: 388 SOFTWARE: PatentIn Ver. 2
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PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 988
TYPE: PRT
930 TVTNSTSTQQGSLFRPKASRTPTPQN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 ASFTAPGHTS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 ---WTFGGQV-----PGQMIRVREGDTIEVQFSNHPDSKMPHNVDFHAATG-PGGGAE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   559 SWEAPQFPNGILEGYRLVYEPCSPVDGVSKIVTVDVKGNSPLWLKVKDLAEGVTYRFRIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 VKLKNLTGYTAYMVSVAAFNA-AGDGPRSTPTQGQTQQA-APSASSSVKFSELTTTSVNV
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                                                                                                                                                                               PSPGSLHYSDEDVTKYN--
                                       ---QAIDTQE-----APKTPAPANLQEQIKAGKATYDSNCAACHQPDGKGVPNAFPPL
                                                                                      SNHQKAHSFVNHYISDPTYYNSWRRQQKGISRAQA-----YSYTESDS-----GEPDHT
                                                                                                                              VPG-----DYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEGAP---
                                                                                                                                                                                                                         NLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGGAAIT-----EFKVD.324
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Pred. No. 0.74;
5; Mismatches
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--PPNPPSQQSTLYRPPSSLAPGSRAPI
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US-09-765-272-84
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                                                                                                                                                                                                                                                                                                          Sequence 84, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
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                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genom
STREET: 9410 Key West
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                                 SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
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                                                                                                                                                     CITY: Rockville
STATE: Maryland
COUNTRY: USA
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 APPLICATION NUMBER: US/09/765,272 FILING DATE: 22-Jan-2001
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                                                                                                                                         20850
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                                                                                                                                                                                                                         Genome Sciences,
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Pred. No. 2.0
                                                                                                                                                                                                         Avenue
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                                                                                                       storage
                                                                                                                                                                                                                                                                          Antigens and Vaccines
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                                                                            RESULT 27
US-10-238-075-877
; Sequence 877, Application US/10238075
; Publication No. US20030148324A1
; GENERAL INFORMATION:
; APPLICANT: I.N.S.E.R.M.
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FILE REFERENCE: BLANDINE
CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
                                                TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (301) 30 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID
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APPLICATION NUMBER: 08/961,
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                         GIVSVEEVSVTTPIAEAPQLPESVRTYDSN-----
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                                                                                                                                                                                                                                                                                            --YDKGFPKTHKVTWQAIPKEKLDSYQTFEVLGKVEGIDLE-ARA-
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                                                                                                                                                                                                                                                                                                                            ATYDSNCAACHQPDGKGVP-----NAFPPLANSDYLNADHARAASIVANGLSGKITVN 452
                                                                                                                                                                                                                                                                                                                                                              AVTLNAEYEGAKDQVELTIQANTEKKIAQSIRPVNVVTDLHQEPSLPATVTVE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LQTYAIQ--FLEEAPKIAHL----SLQVEKADSLKEDQTVKLSV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  ----RAHYQDG-----TQAVLPADKVT---FSTSGEGE-VAIRKGMLELHKPG
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19.8%;
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Pred. No. 0.
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RESULT 28
US-09-738-363-6
; Sequence 6, Application US/09738363
; Patent No. US20010010932A1
; GENERAL INFORMATION:
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US-10-238-075-877
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Best Local Simi
Matches 127;
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PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
SOPTWARE: PatentIn version 3.1
SEQ ID NO 877
LENGTH: 1684
              TITLE OF INVENTION: Nematicidal NUMBER OF SEQUENCES: 40 CORRESPONDENCE ADDRESS:
                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 DAAAKTA---NADNAASQEHQGELPVIDAIVTHAPEVPPPVDRDHPAKVVVKMETVEKVM
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ADDRESSEE:
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                                                                    Schwab, George E. Schwab, George E. Payne, Jewel M. Narva, Kenneth E. Foncerrada, Luis
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Jay M. Sanders
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Pred. No. 1.9;
                                                      Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/076,137
FILING DATE: 12-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: YES ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-20CCCD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
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VRLFVGNGGPNLTSSFHVI ----
                                  NOOTLIFEFHASKTAOYTIRIRYASTOGTKGYFRLDNOELOTLNIPTSHNGYVTGNIGEN
                                                                                                                 LRDFINVYTLISTPTINELSTEKIKGFP-AEKGYIKNQGIMKYYGKPEY-INGAQPVNLE
                                                                                                                                                                                          YKAIAGSSVLVNFK---DGTQGYAFAQAPTGGAWDHSFIESDGAPEGHKLNYIYTSPGDT
                                                                                                                                                                                                                                                                       AKIFTGIRNTFYKSPNTHETYHVDFSYNTQSSGNISRGSSNPIPIDLNNPIISTCIRNSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NGLDKF---KSLDVNSYNKKANYIKGMTE-----MVLDLVA-----LWPTFDPDHYQKE 290
                                                                                                                                                                                                                                 ----GHTSTFSFKALQPGLYVYHCAVAPVG-----
                                                                                                                                                                                                                                                                                                              -----KMP-----HNVDFHAATGPGGGAEASFTAP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Bacillus thuringiensis INDIVIDUAL ISOLATE: PS33F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/738,363 FILING DATE: 15-Dec-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1.3;
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-GEIFDKVHFEGGKGENHNIQTTLIPAGGAAITE
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APPLICANT: Pierre, LEGRAIN

TITLE OF INVENTION: Protein-protein interactions bet

TITLE OF INVENTION: mammalian polypeptides

FILE REFERENCE: B4778A

CURRENT APPLICATION NUMBER: US/10/043,487

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/261,130

PRIOR FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 561

SOFTWARE: Patentin version 3.1

SEQ ID NO 383

LENGTH: 2609

TYPE: PAT

ORGANISM: Shigella Flexneri

US-10-043-487-383
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US-10-043-487-383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                             -----GHGGDPGLVSAY-----GAGLEGGVTGNPAEFVVNTSNAGAGALSVTIDGPS
                                                                                                                                                         CYVTEID---QDKYAVRFIP-----RENGVYLIDVKFNGT--HIPG-SPFKIRVGEP
                                                                                                                                                                                             YYVMQGDFYTKGKYGEQGLQPFDMEKAIREDAEYVV---FNGSVGALTGENALKAKVGET 268
                                                                                                                                                                                                                                                                         TAP-----GHTSTFSFKALQ-PGLYVYHCAVAPVGMHIANGMYGLILVEPKEGLPKVDKE 211
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                                                                                                                                                                                                                                                                                                                                                                                           AEMGTHTVSVKYKGQHVPGSPFQFTVGPLGEGGAHKVRAGGPGLE---RAEAGVPAEFSI 2223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSVANVGSHCDLS-LKIPEISIQ-DMTAQVTS----PSGKTHEAEIVEGENHTYCIRFVP 2166
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                                                                                                                VRLFVGNGG-PNLTSSFHVIGEIFDKVHFEGGKGEN---HNIQTTLIPAGGAAIT----
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20.8%; Pred
71;
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Pred. No. 4.1;
71; Mismatches 217;
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10292
LENGTH: 482
TYPE: PRT
ORGANISM: Streptomyces avermitilis
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APPLICANT: SAKAKI, YASHIYUKI
APPLICANT: HATTORI, MASHIRRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JU
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                                                     VNGNOYESVMPAIAL 465
                                                                                                                                    QIKAGKATYDSNCAACHQPDGKGVPNAFPPLAN--SDYLNADHARAASIVANGLSG-KIT 450
                                                                                                                                                                                                              HAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKTPAPANLQE 393
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                    INGSA-GTTMAAMAM 384
                                                                                               WVRGGSGTYDFLTVT---PDASDTPDALPSSLNTITRYDTTDF--AARTITLGQSGASML 370
                                                                                                                                                                                                                                                                                                                                                                       --GDF-YTKGKYGEQGLQPFDMEKAIREDAEYVVFNGSVGALTGENALKAKVGETVRLFV 273
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HORIKAWA, HIROSHI
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                                                                                                                                                                         -SDAVTL----QAVVT-----
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RESULT 32
US-10-193-764-55
; Sequence 55, Application US/10193764
; Publication No. US20030133943A1
; GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver.
SEQ ID NO 57
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APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS
FILE REFERENCE: 1038-1239MIS
CURRENT APPLICATION UMMBER: 105/10/193,764
CURRENT FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: 09/167,568
PRIOR FILING DATE: 1998-10-07
                      APPLICANT: LOOSMORE, Sheena M.
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS
FILE REFERENCE: 1038-1239MIS
CURRENT APPLICATION NUMBER: US/10/193,764
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                                                                                                                                                                                                                                                                                                                                                                                       452 NGN------QYESVMPAIALSDQQIANVITYTLNSFGNKGGQLSADDVAKAK 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    550 NISQKEGNLTISSDKINITNQITIKAGVDGENSDSDATNN---ANLTIKTKELKLTQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 -YSHKQ------TDAVYLPEGAPQAIDTQEAPKTPAPANLQEQIKAGKATYDSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 ----QGLQPFDMEKAIREDAEYVVFNGSV-----GALTGENALKAKVGETVRLFVGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 VKQGSVANFSFKAKNDTNHA-NQLP--IQFNSNISVDGGGKVLFCI---TSNYSGRSV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 VREGDTIEVQF-----SNHPDSKMPHNVDFHAATGPGGGAEASFTAPGHTSTFSFKALQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GIGMSSINVSDGSNLTFNSSIRGQEAF-NISKDLTINATGSFFELGQYSD
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; Pred. No. 1.6;
71; Mismatches 182;
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RESULT 33 US-10-156-761-14797

Sequence 14797, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:

SATOSHI , HARUO

APPLICANT: OMURA, APPLICANT: ISHIK APPLICANT: ISHIK APPLICANT: HORIK APPLICANT: SHIBA

APPLICANT: SHIBA, TÄDAYOSHI APPLICANT: SATAKI, YOSHIYUKI APPLICANT: HATTORI, MASAHIRA TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

ISHIKAWA, JUN HORIKAWA, HIROSHI

NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14797
LENGTH: 625
TYPE: PRT

ORGANISM: Streptomyces avermitilis

CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02

FILE REFERENCE: 249-262

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SEQ ID NO 55
LENGTH: 998
TYPE: PRT
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PRIOR APPLICATION NUMBER: 09/167,568
PRIOR FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Haemophilus influenzae
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  671
                                                                                                                                                                                                                                                                                                                                  438
                                    452 NGN------QYESVMPAĮALSDQQIANVITYTLNSFGNKGGQLSADDVAKAK 497
                                                                               613 ISGFNKAEITAKDGSDLTIGNTN--SADSTNAKKVTFNQVKDSKISAGDHNVTLNSKVET
                                                                                                                                                                                                                                                498 NISQGVVKLGNVTNDGDLNITTHAKHNQRSIIGGDIINKKGSLNI--TDSNKNAEIQIGG
                                                                                                                                                                                                                                                                                                                                                                                                                 382 TFNGNGFN----HDAIKSTHNISILGGNVTLGGQDSSSTITGNINISQAANVTLRAYNGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 VREGDTIEVQF-----SNHPDSKMPHNVDFHAATGPGGGAEASFTAPGHTSTFSFKALQP 173
                                                                                                                      406 CAACHQPDGKGVPNAFPPLANSDYLNADHARAASIVAN------GLSGKITV 451
                                                                                                                                                               556 NISOKEGNLTISSUKINITNOITIKAGVDGENSDSDATNN---ANLTIKTKELKLTODLN
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SGNTDNTGDGSGNNAGLTIAAKNVEVKNNIT-----SNKTVNITASEKLTTK 717
                                                                                                                                                                                                                                                                                       TEFK-----VDVPGDYVLVDHAIFRAFN-----KGALGILKVEGEENHEI----
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19.0%; Pred. No. 1.
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RESULT 34
US-10-137-870-234
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                                                                                                                                                                                                                                                                                                                                                   Sequence 234, Application US/10137870 Publication No. US20030138883A1
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT:
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CURRENT
             TITLE OF INVENTION: SECRETED AND TRANSMEMERANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C155
                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 HPDSKMPHNV-DFHAATGPGGGAE-----ASFTAPGHT-STFSFKALQPGLYVYH 179
APPLICATION NUMBER: US/10/137,870
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                                                                                                                                                                                                                                                                                                                        Baker, Kevin P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIWESKNVTMRSMNAYYLQSFGVVGQFSENISIDKVNFAPD------PRSGRST 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----PNLT-----SSFHVIGEI-----FDKVHFEGGKGENHNIQTTLIPAGGAAI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HDPEAQRTWRGDNPLFN-DVAAVTDLGGRRIRIDYTTAARPADAGLVYQMRLIERTEPGA
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                                                                                                                                                                                                                      Gao, Wei-Qiang
Gerritsen, Mary E.
                                                                                                            Stewart, Timothy A. Tumas, Daniel
                                                                                                                                                                                                                                                       Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                        Beresini, Maureen
                                                                          Watanabe, Colin K
Wood, William
                                                                                                                                                         Sherwood, Steven
                                                                                                                                                                           Gurney, Austin L.
                                                                                                                                                                                          Godowski, Paul J.
                                                                                                                                                                                                       Goddard, Audrey
                                                                                                                                                                                                                                                                                       DeForge,Laura
                                                               Zhang, Zemin
                                                                                                                                           Smith, Victoria
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Pred. No. 0.85;
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RESULT 35
US-10-140-018-234
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Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550 SEQ ID NO 234 LENGTH: 1160 TYPE: PRT
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Prior Application removed - See |
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 234
LENGTH: 1160
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Best Local Similarity
                                                                                                                             APPLICANT: Tumas Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C158
                                                                                           CURRENT APPLICATION NUMBER: US/10/140,018
CURRENT FILING DATE: 2002-05-06
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                                                                                                                                                                                                                                                                                 Smith, Victoria
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Godowski, Paul J.
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o. US20030138885A1
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Pred. No. 2
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; ORGANISM: Homo Sapien US-10-140-018-234

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US-10-140-021-234
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                                                                                                                                                                                            Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 234
LENGTH: 1160
TYPE: PRT
                                                                                              Query Match
Best Local Similarity
Matches 69; Conserv
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Best Local S
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CURRENT FILING DATE: 2002-05-06
                                                                                                                                                                                                                                                                                                           APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SCRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C167
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                              791 EYTDGTF--RIPRPRTGPEEHLGILGPLIKGEVGDILTVVFKN--NASRPYSVHAH----
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Similarity 19.7%; Pred. No. 2.
PGGGAEASFTA-----PGHTSTFSFKALQ---PG-----LYVYHCAVAPVGMHIANG
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Wood, William
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Smith, Victoria
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Godowski, Paul J.
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19.7%; Pred. No. 2.5;
vative 58; Mismatches 116;
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                                                            GOMIRVREGDTIEVOFSNHPDSKMPHNVDFHAATG 148
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; ORGANISM: Homo US-10-140-274-234
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US-10-140-274-234
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                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/140,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                        193 MYGLI-----LVEPKEGLPKVDKEYYVM-----QGDFYTKGKYGEQGLQPFDMEKAIR 240
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                                                                                   ---GVLESTTVWPLAAEPGEVVTYQWNIPERSGPGPNDSACVSWIYYSAVDPI-KDMYSG
                                                                                                                                PGGGAEASFTA-----PGHTSTFSFKALQ---PG-----LYVYHCAVAPVGMHIANG 192
                                                                                                                                                                           EYTDGTF -- RIPRPRTGPEEHLGILGPLIKGEVGDILTVVFKN -- NASRPYSVHAH -- --
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Godowski, Paul J.
Gurney, Austin L.
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b. US20030143674A1
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19.7%; Pred. No. 2.5;
vative 58; Mismatches 116; Indels 108;
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US-10-140-471-234
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LENGTH: 1160
TYPE: PRT
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-10-140-471-234
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CURRENT APPLICATION NUMBER: US/10/140,471

CURRENT FILING DATE: 2002-05-06

Prior Application removed - See File Wraj

NUMBER OF SEQ ID NOS: 550
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APPLICANT:
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Similarity 19.7%;
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                              GALGILKVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKTPAPANLQE
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                                                                                                                                 QDETFLESN-KMHAINGKLYANLRGLTMYQGERVAWYMLAMGQDVDLHTIHFHAESFLY-
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Gurney, Austin L.
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removed - See File Wrapper or
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Pred. No. 2.5;
TEHL----SPLTVITKETEKVP-PRDIEE 1092
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 234
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CURRENT APPLICATION NUMBER: US/10/140,807

CURRENT FILING DATE: 2002-05-07
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Godowski, Paul J.
Gurney, Austin L.
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                            GOMIRVREGDTIEVQFSNHPDSKMPHNVDFHAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1160;
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RESULT 40 US-10-140-922-234

Sequence 234, Application US/10140922
Publication No. US20030138889A1
GENERAL INFORMATION:
APPLICANT: Baker, Keyin P.

APPLICANT:

Beresini, Maureen

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Search completed: August 27, 2003, 18:34:16 Job time : 33 secs
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US-10-140-922-234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C179
CURRENT APPLICATION NUMBER: US/10/140,922
CURRENT FILING DATE: 2002-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                         1069 ----
                                                                                                                                                                             1015 -----RNGENYRADVVDLFPGTFEVVEMVASNPGTWLMHCHVTDHVHAGMETLFTVFSR 1068
                                                                                                                              343 GALGILKVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKTPAPANLQE 393
                                                                                                                                                                                                                                                                                                                                                             899 LVGPLAICQKGILEPHGGRSDMDREFALLFLIFDENKSWYLEENVATHGSQ--DPGSINL 956
                                                                                                                                                                                                                            293
                                                                                                                                                                                                                                                                    957 QDETFLESN-KMHAINGKLYANLRGLTMYQGERVAWYMLAMGQDVDLHTIHFHAESFLY- 1014
                                                                                                                                                                                                                                                                                                              241 EDAEYVVFNGSVGALTGE----NALKAKVGETVRLFVGNGGPNL---TSSFHVIGEIFD 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                       843 --- GVLESTTVWPLAAEPGEVVTYQWNIPERSGPGPNDSACVSWIYYSAVDPI-KDMYSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 EYQFWTFGGQVP------GQMIRVREGDTIEVQFSNHPDSKMPHNVDFHAATG 148
                                                                                                                                                                                                                                                                                                                                                                                                        193 MYGLI-----LVEPKEGLPKVDKEYYVM-----QGDFYTKGKYGEQGLQPFDMEKAIR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 PGGGAEASFTA-----PGHTSTFSFKALQ---PG-----LYVYHCAVAPVGMHIANG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           791 EYTDGTF--RIPRPRTGPEEHLGILGPLIKGEVGDILTVVFKN--NASRPYSVHAH----
                                                                                                                                                                                                                     KVHFEGGKGENHNIQTTLIPAGGAAITEFKVDVPGDYVL----VDH-----AIFRAFNK 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J. Gurney, Austin L. Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumas, Daniel
Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith, Victoria
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.0%; Score 104; DB 12; Length 1160; .
19.7%; Pred. No. 2.5; ative 58; Mismatches 116; Indels 108;
                                                                                         -TEHL----SPLTVITKETEKVP-PRDIEE 1092
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OM protein - protein search, using sw model
                                                                                         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Title: Perfect score: US-10-088-045-2 2626 August 27, 2003, 18:28:17; Search time 29 Seconds (without alignments) 732.416 Million cell updates/sec

Run on:

Sequence: 1 MSKPTLIKTTLICALSALML.....NKGGQLSADDVAKAKKTKPN 502

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

328717

328717 seqs, 42310858 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	% Query Match Length	DB	ID	Description
- :	163.5	6.2	645	4	US-09-252-991A-25253	Sequence 25253,
2	163	6.2	442	ω	-09-296-	26
w	163	•	478	w	-09-296	equence
4	153	5.8	751	4.	-09-252	e 25
₅	ū	5.7	444	4	-09-252-991A-1733	e 1733
6	150	5.7	712	4	-09-252-991A-2148	
7	147.5	5.6	658	4.	-09-252-991A-	መ
œ	146	5.6	468	μ	-07-985-458-4	4, Ap
9	146		593	4.	-09-252	306
10	145	٠	559	Н	US-08-030-096-6	
11	141	5.4	529	ш	US-08-172-331B-14	14
12	141	5.4	529	μ.	-037-2	25,
. 13	141	5.4	529	N	US-09-005-397-25	е 2
14	141	5.4	529	2		5, ,
15	141	5.4	529	N	-08-993-318A	ۍ '
16	141	•	529	w	•	Sequence 5, Appl:
17	141	5.4	529	w		e v
18	141	•	529	w	-09-576-281-	ю 5
19	136.5		326	4		e 29
20	136		320	4	US-09-252-991A-23061	e 23
21	135	5.1	575	N	-09-032-	e 8,
22	135		575	N	-993-	e 8,
23	135	5.1	575	ω	US-09-399-886-8	е В,
24	135	5.1	575	w	US-09-396-260-8	е 8,
25	135	5.1	575	ω	-09-576-281-	e 8
26	133.5	5.1	576	H	US-08-172-331B-2	Ø
27	132	'n	117		110 00 000 000	2

Sequence 2, Ap	3 US-09-324-867-2	w	2343	4.6	120.5	45
Sequence 1, App	3 US-09-576-281-1	w	539	4.6	121.5	44
Sequence 27, App	3 US-09-181-827A-27	w	539	4.6	121.5	43
Sequence 27, App	3 US-09-389-528-27	w	539	4.6	121.5	42
Sequence 1, Appl	3 US-09-396-260-1	w	539	4.6	121.5	41
Sequence 1, Ap	3 US-09-399-886-1	w	539	4.6	121.5	40
Sequence 27, A	3 US-08-689-421-27	ω	539	4.6	121.5	39
Sequence 1, Appl:	2 US-08-993-318A-1	2	539	4.6	121.5	38
Sequence 1, Ap	0S-09-032-315-1	2	539	4.6	121.5	37
Sequence 7, Ap	3 US-09-576-281-7	ω ω	572	4.7	124	36
Sequence 7, Ap	3 US-09-396-260-7	ω ω	572	4.7	124	5
Sequence 7, Ap	3 US-09-399-886-7	ω ω	572	4.7	124	4
Sequence 7, Appl.	2 US-08-993-318A-7	2	572	4.7	124	33
Sequence 7, Ap	2 US-09-032-315-7	2	572	4.7	124	32
Sequence 23088, A	1 US-09-252-991A-23088	4.	310	4.8	125.5	31
Sequence 7, Ap	3 US-08-687-580B-7	u	540	4.9	. 129	30
Sequence 5, Ap	3 US-08-746-111-5	w	2183	5.0	130	29
Sequence 8029,	1 US-09-328-352-8029	4	97.0		131.3	2

## ALIGNMENTS

Qy 264 KVGET :    Db 289 RPGER	Oy 222 Db 232 FDFFR	Qy 188 HIANG       Db 173 QELTG	Qy 133 PDSKM : : : Db 117 -KLRE	Qy 73 PPPVD Db 82	Qy 19 MLSGC : :  Db 41 VLAGL	Query Match Best Local Similarity Matches 93; Conser	RESULT 1 US-09-252-991A-2523 / Sequence 2523, Applicatio / Patent No. 6551795 / GENERAL INFORMATION: / APPLICANT: MARC J. Ruben TITLE OF INVENTION: AUCL / TITLE OF INVENTION: AUCL / TITLE OF INVENTION: AUCL / TITLE OF INTENTION: NUMBE / CURRENT FILING DATE: 1996 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING DATE: 1998 / PRIOR FILING
KVGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKV 323 	KGKYGEQGLQPFDMEKAIREDAEYVVFNGSVGALTGENALKA 263	HIANGMYGLILVBPKEGLPKVDKEYYVM	PDSKMPHNVDFHAATGPGGGAEASFTAPGHTSTFSFKALQPGLYVYHCAVAPVGM 187 	PPPVDRDHPAKVVVKMETVEKVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSNH 132  NFTGKPGVATTINGSLPAPTLRWREGDTVTIRVTN- 116	MLSGCSNQADKA-AQPKSSTVDAAAKTANADNAASQEHQGELDVIDAIVTHAPEV 72 : :	6.2%; Score 163.5; DB 4; Length 645; larity 21.8%; Pred. No. 2.1e-06; Conservative 52; Mismatches 141; Indels 141; Gaps 21;	91A-25253 2525, Application US/09252991A 25253, Application US/09252991A 25253, Application US/09252991A 25253, Application US/09252991A T: MARC J: Rubenfield et al. T: MARC J: Rubenfield et al. T: INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS ENERGIE: 107196.136 APPLICATION NUMBER: US/09/252,991A FILING DATE: 1999-02-18 PLICATION NUMBER: US 60/074,788 LING DATE: 1998-02-18 PLICATION NUMBER: US 60/094,190 LING DATE: 1998-07-27 PF SEQ ID NOS: 33142 645 RT M: Pseudomonas aeruginosa

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TYPE: PRT
; ORGANISM: Gluconobacter suboxydans
US-09-296-284-26
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                                                                                                                                                                                                SOFTWARE: Pa
SEQ ID NO 5
LENGTH: 478
                                                                Query Match
Best Local Similarity
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SOFTWARE: PatentIn Ve
SEQ ID NO 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Applic Patent No. 6204040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Choi, Eui-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Gluconobacter S
TITLE OF INVENTION: and Methods of
FILE REFERENCE: 1533.087000
                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes TITLE OF INVENTION: and Methods of Use Thereof FILE REFERENCE: 1533.0870000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/296,284A CURRENT FILING DATE: 1999-04-22
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APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
                                                                                                                                                      ORGANISM: Gluconobacter suboxydans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.2%; Score 163; DB 3; Length 442;
Local Similarity 37.3%; Pred. No. 1.2e-06;
hes 50; Conservative 17; Mismatches 57; Indels
369 LPEGAPQAIDTQEAPKTPAPANLQEQIKAGKATYDSNCAACHQPDGKGVPNAFPPLANSD 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       429 YLNADHARA-ASIVANGLSGKITVNGNQYESV-MPAIA--LSDQQIANVITYTLNSFGNK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 VPEGKNLG---QDDGKATALLEAGGKGDAGAEVYLHNCAICHMNDGTGVNRMFPPLAGNP 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 LPEGAPOAIDTQEAPKTPAPANLQEQIKAGKATYDSNCAACHQPDGKGVPNAFPPLANSD 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 PKTPAPA 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APGTLSASDIRKLR 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09296284A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes
                                      6.2%; Score 163; DB 3; 1
37.3%; Pred. No. 1.4e-06;
17. Mismatches 57;
                                                                                  Length 478;
                                           Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                         Gaps
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/0
PRIOR APPLICATION NUMBER: US 60/0
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25481
LENGTH: 751
TYPE: PRI
ORGANISM: Pseudomonas aeruginosa
FEATURE:
NAME VEEV
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; LOCATION: (339)
; OTHER INFORMATION:
US-09-252-991A-25481
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                                                                              PRIOR FILING DATE: 1:
NUMBER OF SEQ ID NOS:
SEQ ID NO 17336
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APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                              Sequence 17336, Appatent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25481,
Patent No. 65517
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Best Local Similarity
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                                                                                                                          CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
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TITLE OF INVENTION:
FILE REFERENCE: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
ORGANISM: Pseudomonas aeruginosa
)9-252-991A-17336
                                          TYPE: PRT
                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 KAGKATYDSNCAACHQPDGKGVPNAFPPLA-NSDYLNADHARAASIVANGLSGKITVNGN 454
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VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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1998-02-18
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Pred. No. 2.5e-05;
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RESULT 6
US-09-252-991A-21481
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US-09-252-991A-24910
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US-09-252-991A-21481
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Best Local S
Matches 46
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Best Local S
Matches 63
                       GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 21481
LENGTH: 712
                                                                                      Sequence 24910, Application US/09252991A
Patent No. 6551795
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PRIOR APPLICATION NUMBER: US 6
PRIOR TITING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 199-02-18
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
       REFERENCE:
                                                                                                                                                                                                                                    447
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                                                                                                                                                                                                 396 GWKTAETATHSRVYTMPGFAQLEDREIAEILSFVRSSWGNQGSSIDAGQVKKLRQ 450
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                                                                                                                                                                                                                                                                                                      APANIQEQIKAGKATYDSNCAACHQPPGKGYPNAFPPLANSDYLNADHARAASIVANGLS 446
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ilarity 26.3%;
Conservative 2
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         107196.136
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BER: US 60/074,788
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Pred. No. 4.4e-05;
wismatches 73;
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US-07-985-458-4
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SEQ ID NO 24910
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APPLICANT: Tamaki
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
ZIP: 10010-2007
COMPUTER REALABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.72 mb
COMPUTER: IBM PC compatible (NI
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                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Frishauf, Holtz,
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                                                                         COUNTRY:
ZIP: 100
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                                                                                                                                                                                                                                                                                      Kawamura,
                                                                                                                                                                                                                                                                                                      Okumura, Hajime and
                                                                                                                                                                                                                                                                                                                            Fukaya, Masahiro;
                                                                                                                                                                                                                                                                                                                                                             Takemura, Hiroshi;
                                                                                                                                                                                                                                                                                                                                                                            Tamaki, Toshimi;
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412 PDGKGVPNA-----FPPLANSDYLNADHARAASIVANGL 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 LLSDWSDE------KPQRILAKLKKQSDYYNFHKRTVGDFIDDVSANGWAATLADRKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 MQGDFYTKGKYGEQGLQPFDMEKAIREDAEYVVF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 EGIAPGGLYEYRFKVRONGTYWYH---SHSGLQEQAGVYGALVIDAREPEPFSYDRDYVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 -- TAPGHTSTFSFKALQPGLYVYHCAVAPVGMHIANGMYGLILVEPKEGLP-KVDKEYYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 TINGSLPGPTLRWREGDNVTLRVRNRLAEDTSIHWHGIILPANMD-------GVPGLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 TFGGQVPGQMIRVREGDTIEVQFSNH--PDSK-----MPHNVDFHAATGPGGGAEASF 157
                                                                                                                                                                                                                                                                                                                                                            INVENTION: Structural Gene of Membrane-Bound
INVENTION: Alcohol Dehydrogenase Complex, Plasmid
INVENTION: Containing The Same And Transformed Act
INVENTION: Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMGHGAATRPASEMDHSKMSGMDMKGMDHSKMAGMDMNGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERAYTLFAQSMDRSGY-ARGTLALAEGLSAPVPTPDPRPLIGMDDMGMGGMD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EENHEIYSHKQTDAVYLPEGAPQAIDTQEAP-KTPAPANLQEQIKAGKATYDSNCAACHQ 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VNASAMSYFDVRIPGLKMTVVAADGQHVEPVSVDELRIAVAETYDV----IVEPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLIPAGGAAITEFKVDVPG-------DYVLVDH---AIFRAFNKGALGILKVEG
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(NEC PC-9801 ES)
                                                                                                                                                                                                                                                                    Goodman & Woodward,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461
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                                                                                                                                                                                                                                                                                                                                                                                                      Acetic Acid
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368 352 270

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CURRENT APPLICATION DATA:

APPLICATION NUMBER: U

US/07/985,458

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Best Local Similarity
Watches 84; Conservi
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LENGTH: 468 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 972-1400
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/658,221
FILING DATE: 20-FEB-1991
APPLICATION NUMBER: 73440/1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                              PAGES: 292
DATE: 1991
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                                                                                                                                                                                                                                                                                                                                                                                                              VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MATURE PEPTIDE LOCATION: 24 to 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS:
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   412
                                 300
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                                                                                                                              294 VHFEGGKGENHNIQTTLIPAGGAAITEFKVDVPGDYVLVD--HAIFRAFNKGALGILKVE 351
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                                                                                                                                                                                                                              149
                                                                                                                                                                                                                                                             184 PVGMHIANGMYGLIL-VEPKEGLPKVDKEYYVMQGDFYTKGKYGEQGL----QPFDM-EK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodman, Herbert
                                                              GEENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKTPAPANLQEQIKAGKATYDSNCAACHQ 411
                                                                                                                                                                                              AIREDAEYVVFNGSVGALTGENALKAKVGETVR----LFVGNGGPNLTSSFHVIGEIFDK 293
PDGKGVPNAFPPLANSDYLNADHARA-ASIVANGLSGKITVNGNQYESV-MPAI--ALSD 467
                                GN----YTYDPSTANMLASG----NTASVP---
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                                                                                                                                                                AL--DAA-----GGPDFLSGGAPIDNWVAPSLRNDPVVGLGRWSEDDIYTFLKSGRIDHS 260
                                                                                                                                                                                                                              PLSMRWPLGIWRMMFSPSPKDFTPAPGTDPEIARGDYLVTGP-GHCGACHTPRGFAMQEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Beppu, Teruhiko
Cloning and Sequencing of the Gene Cluster
Encoding Two Subunite of Membrane-Bound
Alcohol Dehydrogenase from Acetobacter
                                                                                                                                                                                                                                                                                                                                                                                             292-300
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Fukaya, Masahiro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okumura, Hajime;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tayama, Kenji;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (212)370-1622
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Horinouchi, Sueharu and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takemura, Hiroshi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawamura, Yoshiya;
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                                                                                                                                                                                                                                                                                                          Score 146; DB 1; Length 468; Pred. No. 5.2e-05;
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                                                                                                                                                                                                                                                                                             Mismatches 127;
                                                                                              ---VVAWSTQYFTDDDLHAIAK-YLKSLPPVPPSQ 299
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                                ----GADTYVKECAICHR 335
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US-09-252-991A-30673
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US-09-252-991A-30673
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30673
LENGTH: 593
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Patent No. 6551795
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                              367
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538 RMOPMPGFAGKLDDEQLTDLLNYLRQTWGGLPGDLGPQQVAQLK 581
                                                                                479
                                                                                                                   397 AGKATYDSNÇAACHQPDGKGVPN-AFPPLANSDYLNADHARAASIVANGLSGKITVNGNQ
                                                                                                                                                              423
                                                                                                                                                                                                  344 ALGIL-----KVEGEENHEIYSHKQTDAVY-LPEGAPQAIDTQEAPKTPAPANLQEQIK 396
                                                                                                                                                                                                                                                                                    301 GENHNIQTTLIPAGGAAITEFKVD---
                                                                                                                                                                                                                                                                                                                                                                                                            262 SADEFFAAL----TEGKRKDGAYLYPAMPYTSYHLIEREDADAIYAYLMAQEPIARPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 KVDKEYYVMQGDFYTKGKYGEQG----LQPFDMEKAI-REDAEYVV---------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 HPRAEPDPAEVRRPVRLPVQL------LRAGLRQRRHRAGGKSPAPADQAQRAGAGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 HAPEVPPPVDRDHPAKVVVKMETVEKVMRLADGVEYQFWTFGGQVPG----QMIRVREGDT
                                     YESVMPAIA--LSDQQIANVITYTLNSFGNKGGQLSADDVAKAK 497
                                                                              RGRQQYLNVCAGCHGGEGEGKPHIAVAMNGNTTLRLQDPRNLLRVIEDGIVEQ-QFTGFE
                                                                                                                                                              AQGSMFNEMFPVVHHSTQHLDDSDLAAMATYLLGDQPPPAKVVQALPE--
                                                                                                                                                                                                                                            GECHTPRN----LAGALEQDKRLSGGLLNGYLAPSLLPGDLAARGWTQPDLASFLKHGMS
                                                                                                                                                                                                                                                                                                                          QTSLSFPFNVRMG-LAGWNLL---YGKSVRLQPEEGRSEAWKRGQYMVEVL-----GHC
                                                                                                                                                                                                                                                                                                                                                                  ----FNGSVGALTGENALKAKVGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGK 300
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22.1%; Pred. No. 7.7e-05;
tive 61; Mismatches 219
                                                                                                                                                                                                                                                                                  ---VPGD----YVLVDHAIFRAFNKG
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RESULT 10 US-08-030-096-6

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RESULT 11
US-08-172-331B-14
; Sequence 14, Application US/08172331B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION DATA:
PRIOR APPLICATION UNMBER: US 07/556,917
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
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APPLICATION NUMBER:
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REGISTRATION NUMBER: ?
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F: 3000 K Street, N.W., Suite 500
Washington, D.C.
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APPLICANT: Wahleit
APPLICANT: Christe
APPLICANT: Schneid
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Best Local Similarity
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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VPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQE---
                                                                                                                      RLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGG-----AAITEFKVD 324
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Pred. No. 0.00019;
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US-08-706-037-25
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                                                                                                                                                                   Query Match 5.4%;
Best Local Similarity 20.4%;
Matches 103; Conservative 6
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APPLICANT: Xu, Feng
APPLICANT: Berka, Randy M.

APPLICANT: Wahleithner, Jill A.

TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTS WITH

TITLE OF INVENTION: ENHANCED ACTIVITY
                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
FILING DATE: 1-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ADDRESSEE: No. 57704190 No.
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                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET_NUMBER: 4526.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/706,037 FILING DATE: 30-AUG-1996 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Harrington, James J
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                                                     IRVREGDTIEVQFSNH----PDSKMPHNVDFH----AATGPGGGAEASFTAP-----GHTS 164
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                     ITANKGDTLRINVTNQLTDPSMRRATTIHWHGLFQATTADEDGPAFVTQCPIAQNLSYTY 114
                                                                                              LPLLAAVST-
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                                                                                                                                                                                                                                                                                                                   529 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           us 60/002,800
                                                                                                                                                                     60;
                                                                                                                                                                 Score 141; DB 1; 1
Pred. No. 0.00019;
0; Mismatches 216;
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                                                                                                                                                                   Indels 126;
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US-09-005-397-25
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                                                                        TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                     CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US OF
PRICE DATE: 30-AUG-1996
                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Harrington James
                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                     SEQUENCE CHARACTERISTICS
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TYPE: am:
TOPOLOGY:
                                                                                                                                                NAME: Harrington, James J. REGISTRATION NUMBER: 38,711 REFERENCE/DOCKET NUMBER: 45
                                                                                                                                                                                                                         FILING DATE: 30-AUG
APPLICATION NUMBER:
FILING DATE: 1-SEP
                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP:
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                     : 529 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
7: United States
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RESULT 14
US-09-032-315-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59858180 No. 5985818disk of No. 5985818th America,
    ATTORNEY/AGENT INFORMATION:
NAME: ROZEK, CATO1
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 52/
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Svendsen, Allan APPLICANT: Xu, Feng TITLE OF INVENTION: LACCAS
                                                                                                                                                                                                                                                                                                    STREET: ***
CTTY: New York
                                                                                   FILING DATE: 2 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                     UMBER: US/09/032,315
27-FEB-1998
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        5200.200-US
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Pred. No. 0.00019;
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                                                                                                                                                                                                                                                                             Sequence 5, Application US/08993318A
Patent No. 5998353
GENERAL INFORMATION:
APPLICANT: Pedersen, Anders
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
ZIP: 10174
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                            APPLICANT: Cherry, Joel TITLE OF INVENTION: LAC
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MOLECULE TYPE:
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                                                                                                                                         CORRESPONDENCE ADDRESS
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TYPE: amino ac
STRANDEDNESS:
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                                                              COUNTRY: USA
                                                                                     CITY:
                                                                                                     STREET:
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                                                                                                   405 Lexington
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                                                                                                                                                                                                                     Svendsen, Allan
Schneider, Palle
Rasmussen, Grethe
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                                                                                                                       No. 59983530 No.
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Pred. No. 0.00019;
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                                                                                                                       5998353disk of No.
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US-09-399-886-5
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                                     Sequence 5, Application US/09399886
Patent No. 6140092
GENERAL INFORMATION:
APPLICANT: Pedersen, Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 103;
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REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
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LENGTH: 529 amino acids
   APPLICANT:
                     APPLICANT:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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TOPOLOGY: li
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                                                                                                                                                                                            IHLHGH-----VFDIVKSLGGTPN
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ilarity 20.4%;
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.00019;
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Best Local :
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APPLICATION NUMBER:
FILING DATE: Decembe
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Re-lease #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TITLE OF INVENTION: LAC
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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 329 AIGTALVEENLHALINPGÄPGGSAPADVSLNLAIGRSTVDGILRFTFNNIKYEAP----
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Sequence 5, Applicati Patent No. 6184015 GENERAL INFORMATION:

APPLICANT: Svendsen APPLICANT: Xu, Feng TITLE OF INVENTION:

CITY: New York STATE: NY STREET:

10174

USA

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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: ROZEK, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/032,315
FILING DATE: 27-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for CURRENT APPLICATION DATA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61840150 No. 6184015disk of No. 6184015th America,
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                                                                                                                                      115 EIPLRG-QTGTMWYH---AHLASQYVDGLRGPLVIYDPNDPHKSRYDVDDASTVVMLEDW
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RLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGG-----AAITEFKVD 324
                                                                                                                                                                                                                                                       IRVREGDTIEVQFSNH----PDSKMPHNVDFH----AATGPGGGAEASFTAP-----GHTS 164
                                                                                                                                                                                                                                                                                              LPLLAAVST-----PAFAAVRNYKFDIKNVNVAPDGFQRSIVSVNGLVPGTL
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                                                                                                Y-----TKGKYGEQG---LQPFDMEKAIREDAEYVVFNGSVGALTGENALKAKVGETV 269
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US-09-576-281-5
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                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAMME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 503:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                      TYPE:
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                                                                             103;
                                    59 LPVIDAIVTHAPEVPPPVDRDHPAKVVVK--METVEKVMRLADGVEYQFWTFGGQVPGQM 116
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ilarity 20.4%;
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Schneider, Palle
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                                                                         Score 141; DB 3; 1
Pred. No. 0.00019;
0; Mismatches 216;
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                                                                                                                Length 529;
                                                                             Indels 126;
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Matches Query Match

103;

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Local

Similarity

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LENGTH:

TELEPHONE:

CLASSIFICATION: FILING DATE: OPERATING SYSTEM:

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US-09-615-192A-291
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                                                                                                                                                                                                       Query Match
Best Local
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GENERAL INFORMATION:
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                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                             LENGTH: 326
TYPE: PRT
ORGANISM: Eucalyptus
-09-615-192A-291
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CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Materials and Methods TITLE OF INVENTION: Modification of Plant
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APPLICANT: Havukkala,
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                                    KYNVTIHWHGIRQLRTGWADGPAYITQCPI-QPGQSYVYNFTITGQRGTLLWHAHI----
                                                                       PHNVDFH-----AATGPGGGAEASFTAPGHTSTFSFKAL-QPGLYVYHCAVAPVG 186
                                                                                                                                               RDHPAKVVVKMETVEKVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPDSKM 137
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MHIANGMYGLILVEPKEGL----PKVDKEYYVMQGDFYTKGKYG-----EQGLQPFDME 236
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                                                                                                            RNYTFNVVMKNTT-----RLCS--SKPIVTVNGMFPGPTLYAREDDTVLVRVSN----RV
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                                                                                                                                                                                    Score 136.5; DB 4;
Pred. No. 0.00022;
6; Mismatches 129;
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; Sequence 8, Application US/09032315
; Patent No. 5985818
; GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Xu, Feng
TITLE OF INVENTION: LACCASE MUTAN'; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
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US-09-032-315-8
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US-09-252-991A-23061
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23061
LENGTH: 320
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GENERAL INFORMATION:
GENERAL INFORMATION: Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MARC J. RUBENFIELD ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: """""TINDEA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                  ---GEPETIKTTIM-AG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYLALYPGLGTWKGLMPGYQSADEFADKEK-GWTGVHQWEKEMA-KADEKYGPIFAKFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GQTTNALISTDQSSGKYMVAASPFMDSPIAVDNMTATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEENHEIYSHKQTDAVYLPEG----APQAIDTQEAPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---NVSDAHTINGHPGPSSNCPSQGGFTLPVESGKKYMLRIINAALNEELFFKIAGH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAIREDAEYVVFNGSVGALT-----GENALKAKVGETVRLFVGNGGPNLTSSFHVIGEIF
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25.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 136; DB 4;
Pred. No. 0.00024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                -RHAAMPAWGE----VIGEEGVKNVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80;
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LACCASE MUTANTS

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 27-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
   22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
CITY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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                                                         449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 MPHNVDFHAA-----TGPGGGAEASFT----APGHTSTFSFKA-LQPGLYVYHCAV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 VKMETVEKVMRLA-----DGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSN---HPDSK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APVGMHIANGMYGLILVEPKE----GLPKVDKEYYVM-QGDFYTKGKYGEQGLQPFDMEKA
                                                                                       IVANGLSGKITVNGNQYESVMPAIALSDQQIANVITYTLNSFGN
                                                                                                                                                              EQIKAGKATYDSNCAACHQPDGKGVPNAFPPL------ANSDYLNADHARAAS
                                                                                                                                                                                                GLLSGHGGLKARMIEGSHHLHSRSVVKRQNETTTVVMDESKLVPLEYPGAACGSKPADLV 397
                                                                                                                                                                                                                                 GILKVEG-----EENHEIYS-----HKQTDAVYLPEGAPQAIDTQEAPKTPAPANLQ 392
                                                                                                                                                                                                                                                                                                                                                                             SFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHLSSQYVDGLRGPLVIYPKDPHRRLYDVDDEKTVLIIGDWY-----HESSKA
                                                                                                                             LDL----TFGLNFATGHWMI-NGIPYESPKIPTLLKILTDEDGVTESDFTKEEH---TV
                                                                                                                                                                                                                                                                                                                                                                                                                   ILASGNITRORPVSATINGK-GREDPDNTPANPDTLYTLKVKRGKRYRLRVINSSEIASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    I-----REDAEYVVFNGSVGALTGEN-----ALKAKVGETVRLFVGNGGPNLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTTSIHWHGLLQHRNADDDGP----SFVTQCPIVPRESYTYTIPLDDQTGTYWYH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLARTVEYGLKISDGEIAPDGVKRNATLVNGGYPGPLIFANKGDTLKVKVQNKLTNPEMY
                                                      ILPKNKCIEFNIKGNSGIPITHPVHLHGH-----
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20.0%;
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; Pred. No. 0.00077;
63; Mismatches 176;
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                                                        -TWDVVQFGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gregg, Valeta A.
REGISTATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 50.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08 FILING DATE: December 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 575 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: No. 59983530 No.
                  346
                                                                                       326
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                                                      278 EPDTYWINAPLTNVPNKTAQALLVYEEDRRPYHPPKGPYRKWSVSEAIIKYWNHKHKHGR 337
                                                                                                                                                                                                                                                                                                        183 APVGMHIANGMYGLILVEPKE---GLPKVDKEYYVM-QGDFYTKGKYGEQGLQPFDMEKA 238
                                                                                                                                                                                                                                                                                                                                              77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 VKMETVEKVMRLA-----DGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSN---HPDSK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New
GILKVEG------EENHEIYS------HKQTDAVYLPEGAPQAIDTQEAPKTPAPANLQ 392
                                                                                                                                                                                                                                                                       SHLSSQYVDGLRGPLVIYPKDPHRRLYDVDDEKTVLIIGDWY------HESSKA 175
                                                                                                                                                                                                                                                                                                                                                                             MPHNVDFHAA-----TGPGGGAEASFT----APGHTSTFSFKA-LQPGLYVYHCAV 182
                                                                                         -PGDYVL--
                                                                                                                       RFSV-----EGHKV--TVIAADGVSTKPYQVDAFDILAGQRIDCVVEANQ 277
                                                                                                                                                          SFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDV-------
                                                                                                                                                                                                                                                                                                                                            RTTSIHWHGLLQHRNADDDGP-----SFVTQCPIVPRESYTYTIPLDDQTGTYWYH---
                                                                                                                                                                                                                                                                                                                                                                                                                 VLARTVEYGLKISDGEIAPDGVKRNATLVNGGYPGPLIFANKGDTLKVKVQNKLTNPEMY
                                                                                                                                                                                              ILASGNITRORPVSATINGK-GRFDPDNTPANPDTLYTLKVKRGKRYRLRVINSSEIASF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212-878-9655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pedersen, Anders
Svendsen, Allan
Schneider, Palle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rasmussen, Grethe
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linear
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20.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/993,318A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 135; DB 2; ]; Pred. No. 0.00077; 63; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5032.200-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 180;
                                                                                       VDHAIFRAFN---KGAL 345
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US-09-399-886-8
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/993,31
FILING DATE: December 18, 199
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CÜRRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: N
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                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
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CITY: New York
                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                 APVGMHIANGMYGLILVEPKE---GLPKVDKEYYVM-QGDFYTKGKYGEQGLQPFDMEKA 238
                                                                                                       MPHNVDFHAA-----TGPGGGAEASFT----APGHTSTFSFKA-LQPGLYVYHCAV 182
                                                                                                                                          VLARTVEYGLKISDGEIAPDGVKRNATLVNGGYPGPLIFANKGDTLKVKVQNKLTNPEMY 76
                                                                                                                                                                                                                                                                                                      TYPE: protein
 SHLSSQYVDGLRGPLVIYPKDPHRRLYDVDDEKTVLIIGDWY---
                                                                        RTTSIHWHGLLQHRNADDDGP-
                                                                                                                                                                              VKMETVEKVMRLA-----DGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSN---HPDSK 136
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                                                                                                                                                                                                                                                                                                                                                                           575 amino acids
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E: No. 61400920 No. 6140092disk of No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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Rasmussen, Grethe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Svendsen,
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                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                             Score 135; DB 3; Length 575;
Pred. No. 0.00077;
63; Mismatches 176; Indels 1
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                                                                      ----SFVTQCPIVPRESYTYTIPLDDQTGTYWYH--- 127
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                                                                                                                                                                                                                 Indels 180;
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   --HESSKA 175
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US-09-396-260-8
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                                                                        US-09-396-260-8
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Query Match
Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Svendsen APPLICANT: Xu, Feng TITLE OF INVENTION:
                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                       TOPOLOGY: 1: MOLECULE TYPE:
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CTTY: New York
                                                                                                                                                                                                                                                                     NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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ilarity 20.0%;
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Score 135; DB 3;
Pred. No. 0.00077;
3; Mismatches 176
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 Indels 180;
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RESULT 25
US-09-576-281-8
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Patent No.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/576,281
ATTORNEY/AĞENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 503
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cherry, Joel
TITLE OF INVENTION: LAC
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                    PRIOR APPLICATION DATA:

"APPLICATION NUMBER:
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                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                        405 Lexington Avenue
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Schneider, Palle
Rasmussen, Grethe
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                        5032.200-US
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                                                                                                                                                                                                                                                                   Sequence 2, Application US/08172331B
Patent No. 5480801
GENERAL INFORMATION:
APPLICANT: Wahleithner, Jill A.
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 1: MOLECULE TYPE:
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                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                            STREET: 405 Lexington Avenue CITY: New York
                                      COUNTRY: USA
ZIP: 10174-6401
                                                                              STATE:
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TELEFAX: 212-878-9655
                                                                                                                                    ADDRESSEE:
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 SFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 SHLSSQYVDGLRGPLVIYPKDPHRRLYDVDDEKTVLIIGDWY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 APVGMHIANGMYGLILVEPKE---GLPKVDKEYYVM-QGDFYTKGKYGEQGLQPFDMEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 MPHNVDFHAA-----TGPGGGAEASFT----APGHTSTFSFKA-LQPGLYVYHCAV
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                                                                              New York
                                                                                                                                                                                                                           Wahleithner, Jill A.
Christensen, Bjoern E.
Schneider, Palle
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                                                                                                                                    No. 54808010 No. 5480801disk of No. 5480801th America,
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linear
Floppy disk
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 576 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: LOWNEY Dr., Karen A.
REGISTRATION NUMBER: 31.274
REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 03-DEC-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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TOPOLOGY: linear
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SOFTWARE: Patenti
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VILPKNKCIEFNIKGNSGIPITHPVHLHGH---
                              SIVANGLSGKITVNGNQYESVMPAIALSDQQIANVITYTLNSFGN 483
                                                                                               QEQIKAGKATYDSNCAACHQPDGKGVPNAFPPL------ANSDYLNADHARAA 438
                                                                                                                                                               LGILKVEG-----EENHEIYS-----HKQTDAVYLPEGAPQAIDTQEAPKTPAPANL
                                                                                                                                                                                               QEPDTYWINAPLTNVPNKTAQALLVYEEDRRPYHPPKGPYRKWSVSEAIIKYWNHKHKHG 337
                                                                                                                                                                                                                               --PGDYVL---
                                                                                                                                                                                                                                                               FRFSV--
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                                                                                                                             RGLLSGHGGLKARMIEGSHHLHSRSVVKRQNETTTVVMDESKLVPLEYPGAACGSKPADL
                                                                                                                                                                                                                                                                                          SSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDV--------
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                                                                                                                                                                                                                                                                                                                                                           AI-----ALKAKVGETVRLFVGNGGPNLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  576 amino acids
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SYSTEM: PC-DOS/MS-DOS
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                                                               TFGLNFATGHWMI-NGIPYESPKIPTLLKILTDEDGVTESDFTKEEH---T
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20.2%;
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                                                                                                                                                                                                                                                               EGHKV--TVIAADGVSTKPYQVDAFDILAGQRIDCVVEAN
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- TWDVVQFGN
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RESULT

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RESULT 28
US-09-328-352-8029
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-6003
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                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. BRETON et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
                                                                           NUMBER OF SEQ ID NOS:
SEQ ID NO 8029
LENGTH: 635
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID A
TITLE OF INVENTION: BAUMANNII FOR
                                                                                                                                                                                                                                                                                                Sequence 8029, Application US/09328352 Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6003, Application US/09328352
Patent No. 6562958
  Query Match
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SEQ ID NO 6003
                                                                                                                                                       CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                       ORGANISM: Acinetobacter baumannii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 ---NALKAKVGE-TVRLFVGNGG---PNLTSSFHVIGEIFDKVHFEGGKGENH-----N
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Score 131.5;
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Pred. No. 0.0019;
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Length 635;
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-746-111-5
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US-08-746-111-5
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GENERAL INFORMATION:
                Query Match
Best Local Similarity
     Matches
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                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2183 amino aci
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ginsburg, David APPLICANT: Cui, Jisong
                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Compositions And Methods For Screening TITLE OF INVENTION: Compounds For Anticoagulant Activity
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 06-NO CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Medlen & Carroll, LLP
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70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Californ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 Montgomery Street, Suite 2200
                                                                                                                                            2183 amino acids
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5.0%; Score 130; DB 20.7%; Pred. No. 0.02 tive 46; Mismatches
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                DB 3; Length 2183;
   120;
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 Indels 102;
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 Gaps
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                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/00488
FILING DATE: 2-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL94200321.1
PILING DATE: 9-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: MASS, Clifford J.
REGISTRATION NUMBER: 30,086
REGISTRATION NUMBER: 30,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMA
                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/4" Disk 1.
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: Microsoft Windows SOFTWARE: WordPerfect 8 for Windows CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/687,580B FILING DATE: 20-NOV-1996
SEQUENCE CHARACTERISTICS:
                                                                                          REFERENCE/DOCKET NUMBER: U-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                        ZIP: 10023
COUNTRY: U
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VENTION: Antifungal proteins, DI
VENTION: hosts incorporating sa
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BRES-VLOEMANS, Alexa
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PONSTEIN, Anne Silene
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                                                                          (212) 708 1890
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                                                                                                                                             ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23088
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/074,788; PRIOR APPLICATION NUMBER: US 60/074,788; PRIOR FILING DATE: 1998-02-18; PRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23088
LENGTH. 720
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23088, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                Matches
                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: Marc J.
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                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                              LENGTH: 310
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TYPE: an
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                                           187 MHIANGMYGLILVEPKEGLPKVDKEYYVMQGDFYTKGKYGEQGLQPFDMEKAIREDAEYV 246
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                                                                                              Similarity
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                  MNIAQEKYGPIFA--
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                                                                           4.8%; Score 125.5; DB 4; 22.0%; Pred. No. 0.0022; tive 37; Mismatches 89;
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               ---KYAAMPIEEVAKDEHA---
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                                                                                                           Length
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               -MKMGSRMFATYC 145
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RTTSIHWHGLLQHRNADDDGPAFVTQCPI-VPQASYTYTMPLGDQTGTYWYH---SHLSS
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; TOPOLOGY: li
; MOLECULE TYPE:
US-09-032-315-7
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: ROZEK, CAROL
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                 TELEPHONE: 212-878-9655
                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10174
                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
137 MPHNVDFHAA-----TGPGGGAEASFTAPGHTSTFSFK-ALQPGLYVYHCAVAPVGM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 IYNLSHNQG 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 TDAVYLPEGAPQAIDTQEAPKTPAPANLQEQIKAGKATYDSNCAACHQPDGK-----GVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 QSIETTIL--GGR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 HNIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQ
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                                    17 VLARTVEYNLKISNGKIAPDGVERDATLVNGGYPGPLIFANKGDTLKVKVQNKLTNPDMY
                                                                        86 VKMETVEKVMRLA-----DGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSN---HPDSK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
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                                                                                                                              Similarity
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                                                                                                           4.7%; Score 124; DB 2;
21.4%; Pred. No. 0.0081;
ative 55; Mismatches 124
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                                                                                                             124;
                                                                                                                                            Length 572;
                                                                                                             Indels 112;
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                                                                                                             Gaps
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US-08-993-318A-7
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                                                                                                                                     US-08-993-318A-7
                                                                   Matches
                                                                                Query Match
Best Local
                                                                                                                                                                INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 572 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                   MOLECULE TYPE:
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17
                86 VKMETVEKVMRLA-----DGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSN---HPDSK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10174
                                                                                 Similarity
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VLARTVEYNLKISNGKIAPDGVERDATLVNGGYPGPLIFANKGDTLKVKVQNKLTNPDMY
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Svendsen, Allan
Schneider, Palle
Rasmussen, Grethe
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                                                                 Conservative
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                                                                                4.7%;
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                                                                 55; Mismatches 124;
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                                                                                Score 124; DB 2;
Pred. No. 0.0081;
                                                                                                Length 572;
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                                                                Indels 112;
                                                                Gaps
76
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US-09-399-886-7
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-09-399-886-7
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                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 572 amino acid
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                                                                                                                                                                           FILING DATE: December 18, 195
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: LACCASE MUTANTS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                STRANDEDNESS:
                                                                   TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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Svendsen, Allan
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                               ss: single
linear
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ber 18, 1997
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US-09-396-260-7
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Svendsen,
APPLICANT: Xu, Feng
TITLE OF INVENTION:
                                                                      TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 7:
               SEQUENCE CHARACTERISTICS:
LENGTH: 572 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: """

CITY: New York

"""TE: NY
                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: ROZEK, CARO1
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 27-FEB-
                                                                                                                                                                                                                                                                                                                              SOFTWARE: FABLSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                      TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM CON OPERATING SYSTEM: SOFTWARE: FastSE
STRANDEDNESS:
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/396,260 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRRPYHPPKG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SFDÍLAGQRIDÁV------VEANQEÞDTYWINÁÞLTNVANKTAQALLIÝED 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKT---PAP-ANLQEQIKAGKATYDS 404
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                                                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. 61840150 No. 6184015disk of No.
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                                                                                                                                                                                                                                                                                                                                                                                                        Diskette
                                                                                                                                                                                                                   UMBER: US/09/032,315
27-FEB-1998
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Pred. No. 0.0081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6184015th America,
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US-09-576-281-7
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Peders
             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62776
                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cherry, Joel TITLE OF INVENTION: LAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                 STREET:
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 NCAACHQPDG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 KVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKT---PAP-ANLQEQIKAGKATYDS 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 ----RMSIQGHK-----MTVIAADGVSTKPYQVD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 EIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 QYVDGLRGPLVIYDPKDPHRRLYDIDDEKTVLIIGDWYHTSSKAILATGNITLQQPDS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 HIANGMYG-LILVEPKEGLPKV----DKEYYVMQGDFY-TKGK----YGEQGLQPFDMEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 MPHNVDFHAA-----TGPGGGAEASFTAPGHTSTFSFK-ALQPGLYVYHCAVAPVGM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 RTTSIHWHGLLQHRNADDDGPAFVTQCPI-VPQASYTYTMPLGDQTGTYWYH---SHLSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 VKMETVEKVMRLA-----DGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSN---HPDSK 136
                                                                                                                                                                                                                                                                                                                              10174
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                                                                                                                                                                                                                                                                                                                                                                New
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                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                   405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Svendsen, Allan
Schneider, Palle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rasmussen, Grethe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pedersen, Anders
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                                                                                                                                                                                                                                                                                                                                                                                                      No. 62776110 No.
212-867-0123
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                                  5032.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 124; DB 3;
Pred. No. 0.0081;
                                                                                                                                                                                                                                                                                                                                                                                                      6277611disk of No. 6277611th America
                                                                                                                                                                                                                                        Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -VEANQEPDTYWINAPLTNVANKTAQALLIYED
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Best Local Similarity 21.4
79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09032315 Patent No. 5985818
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Xu, Feng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOPTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59858180 No. 5985818disk of No. 5985818th America,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                     COMPUTER READABLE FORM:
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STRANDEDNESS: si
                                                                                                                                                                                   MEDIUM TYPE:
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REFERENCE/DOCKET NUMBER:
                                                                                 FILING DATE:
                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 QYVDGLRGPLVIYDPKDPHRRLYDIDDEKTVLIIGDWYHTSSKAILATGNITLQQPDS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 RTTSIHWHGLLQHRNADDDGPAFVTQCPI-VPQASYTYTMPLGDQTGTYWYH---SHLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 VLARTVEYNLKISNGKIAPDGVERDATLVNGGYPGPLIFANKGDTLKVKVQNKLTNPDMY 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKT---PAP-ANLQEQIKAGKATYDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKMETVEKVMRLA-----DGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSN---HPDSK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ATINGK-GRFDPDNTPANPNTLYTLKVKRGKRYRLRVINS--SAIASF----
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linear
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                                                                                                                                                                                     Diskette
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                                                                                               US/09/032,315
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5200.200-US
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Pred. No. 0.0081
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US-08-993-318A-1
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08993318A Patent No. 5998353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOR COMPATION OF THE COMPATION OF THE COMPATION OF THE COMPATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                 APPLICANT: Cherry, Joel TITLE OF INVENTION: LAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                STREET: 405
                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                APPLICATION NUMBER: US/08/993,318A FILING DATE: December 18, 1997 CLASSIFICATION: 435
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                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 GHAFLYKFTPAGHAGTFWYH---SHFGTQYCDGLRGPMVIYDDNDPHAALYDEDDENTII 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 VPGQMIRVREGDTIEVQFSN---HPDSKMPHNVDFHA-----ATGPGGGAEASFTAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 VRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDVPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 Q-GDFYTKGKYGEQGLQPFDMEKAIREDAEYVVFNGS---VGALTGE-NALKAKVGE--T
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ew York
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Svendsen, Allan
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Rasmussen, Grethe
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Best Local Similarity
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               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 50
TELECONMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                         APPLICANT: Halkier, Torben P
TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60080290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                              COUNTRY: United ZIP: 10174-6401
                                                                                                                                                    CITY: New Yor)
                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KITVNGNOYESVMPAI----ALSDOQIAN 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YVLVDHAIFRAF-NKGALGILKVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKTPA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDVPGD 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHAFLYKFTPAGHAGTFWYH---SHFGTQYCDGLRGPMVIYDDNDPHAALYDEDDENTII 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHTSTFSF-KALQPGLYVYHCAVAPVGMHIANGMYGLILV----EPKEGLPKVDKEYYVM 215
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                                                                                                                                 New York
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                                                                                                                                                                    405 Lexington Avenue, 64th
                                                                                                                                                                                                                                                                            Brown, Kimberley M.
Kauppinen, Sakari
Halkier, Torben P
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   PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                      No. 6008029disk of 
venue, 64th Floor
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                                                                                                                  America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165;
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                                                                                                                                                                                                                                                           Sequence 1, Application US/09399886
Patent No. 6140092
GENERAL INFORMATION:
APPLICANT: Pedersen, Anders
APPLICANT: Svendsen, Allan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local S
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 9-AUG-1996
                                                                                                                                 CORRESPONDENCE ADDRESS: ADDRESSEE: No. 61400
                                                                                                                                                                    APPLICANT: Cherry, Joel TITLE OF INVENTION: LAC NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                          APPLICANT:
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                                                                                          STREET: 409
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TELEPHONE: 212-878-9655
TO NO:
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CLASSIFICATION:
                                                                       COUNTRY:
                                                          ZIP: 10174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 GHAFLYKFTPAGHAGTFWYH---SHFGTQYCDGLRGPMVIYDDNDPHAALYDEDDENTII 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 VPGQMIRVREGDTIEVQFSN---HPDSKMPHNVDFHA-----ATGPGGGAEASFTAP
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amino acid
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Svendsen, Allan
Schneider, Palle
Rasmussen, Grethe
                                                                                            405 Lexington Avenue
ew York
                                                                           USA
                                                                                                                                 No. 61400920 No. 6140092disk of No. 6140092th America
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Search completed: August 27, 2003, 18:33:21 Job time : 33 secs
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MOLECULE TYPE:
US-09-399-886-1
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4.6%; Score 121.5; DB 3;
Best Local Similarity 23.6%; Pred. No. 0.013;
Matches 92; Conservative 50; Mismatches 165;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
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APPLICATION NUMBER: 08/993,318
FILING DATE: December 18, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 539 amino acids
TYPE: amino acid.
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 212-867-01
TELEFAX: 212-878-9655
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CLASSIFICATION:
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                                                                                      357 RFTINGTAYES--PSVPTLLQIMSGAQSAN 384
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                                                                                                                                                                                                                                                                                271 ---VDNYWIRAQPNKGRNGLAGT-----FANGVNSAILRYAGAANADPTTSA--NPN 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 VPGQMIRVREGDTIEVQFSN---HPDSKMPHNVDFHA-----ATGPGGGAEASFTAP 160
                                                                                                                                        448 KITVNGNQYESVMPAI ---- ALSDQQIAN 472
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                                                                                                                                                                                    PAQLNE-----ADLHALIDPAAPGIPT--PGAAD---VNLRFQLGFS------GG 356
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linear
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OM protein - protein search, using sw model
                                                                                                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on: August 27, 2003, 18:19:41; Search time 84 Seconds (without alignments) 948.580 Million cell updates/sec

Sequence: Title: Perfect score: 1 MSKPTLIKTTLICALSALML.....NKGGQLSADDVAKAKKTKPN 502 US-10-088-045-2

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 10: 11: 12: 13: A_Geneseq_19Jun03:*

| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Query Match Length DB ID	Length	DB	ID	Description
_ :	2626	100.0	- ;	22	AAB67668	Amino acid sequenc
N	2626	100.0	502	22	AAB67669	Amino acid sequenc
w	1388	52.9		24	ABP77627	N. gonorrhoeae ami
4	1034	39.4		23	AA017561	M catarrhalis MCA1
ហ	349	13.3		22	AAU42578	Propionibacterium
6	237	9.0		21	AAY74274	Neisseria gonorrhe
7	237	9.0		24	ABP78130	N. gonorrhoeae ami
80	222	8.5		21	AAY74276	·Neisseria meningit
9	222	8.5		21	AAY74275	Neisseria meningit

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R. solani laccase
C glutamicum prote
Eucalyptus grandis
Tobacco laccase cl
Laccase RSlacl R Coprinus cinereus Tobacco leaf antif Tobacco leaf antif C glutamicum prote Corynebacterium gl Arabidopsis thalia A.altocetigenes me Brassica microspor G. oxydans D-sorbi Herbicidally activ Murine factor V SE Herbicidally activ Rhizoctonia solani Rhizoctonia solani Rhizoctonia solani Rhizoctonia solani Rhizoctonia solani Novel Botrytis cin Laccase RSlac3. R Brassica napus mic Sequence of cytoch Ascorbate oxidase 2-keto-D-gluconate Maize diphenyl N. gonorrhoeae ami ADH complex protei Pseudomonas aerug: Arabidopsis thalia Ascorbate oxidase me C. Glu dehydroge

## ALIGNMENTS

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AAB67668 standard; Protein; 502 AA

WX B X D X A X D A B AAB67668;

11-JUN-2001 (first entry);

Amino acid sequence of a BASB109 polypeptide.

BASB109; bacterial infection; vaccine; genetic immunisation.

Moraxella catarrhalis.

WO200119996-A1.

ZXZXXX 22-MAR-2001.

14-SEP-1999; 99GB-0021691.

14-SEP-2000; 2000WO-EP09035.

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

Thonnard J;

WPI; 2001-257883/26. N-PSDB; AAF55658.

Novel BASB109 polypeptides of Moraxella catarrhalis useful for diagnostic, prophylactic and therapeutic purposes against microbial diseases, preferably bacterial infections

Claim 3;

Page

65;

93pp;

English

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RESULT 2
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Pred. No. 2.9e-227;
Nismatches 0;
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N-PSDB; AAF55657.
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Pred. No. 2.9e-227;
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Matches 265;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 316; 815pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial; infection; vaccine;
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DB; ABZ38597.
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IVPAGGSAIVEFKVDIPGNYTLVDHSIFRAFNKGALGQLKVEGAENPEIMTQKLSDTAYA
                         LIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYL
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for treating or preventing
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Pred. No. 4.7e-116;
3; Mismatches 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seful for the manufacture of gonorrheae infection -
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05-SEP-2000;
05-SEP-2000;
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01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
proteins from Moraxella catarrhalis. These can be used to produce vaccines which protect against M. catarrhalis infection, which can otitis media, respiratory infection, sinusitus, and pneumonia. The present sequence is a protein of the invention.
                                                                                                                                                                                                           05-SEP-
                                                                                                                                                                                                                                                                                                            29-AUG-
29-AUG-
                                                                             Moraxella polypeptide and polynucleotides useful as immunizing a host e.g. humans against disease e.g. c pneumonia, caused by infection of the bacteria
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29-AUG-2000;
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28-AUG-2000;
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                                                              Claim
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antibacterial;
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Best Local
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02-JUN-2000;
07-JUL-2000;
                  Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogen: polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by p. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hyperrosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                        Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris -
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  ö
                                                                                                                                                                                                                                                     SEQ ID No 3773; 1069pp; English
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e J, Zhang
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2000US-208841P.
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     Of P.
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Pred. No. 1.2e-84;
0; Mismatches 0;
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, Carter I
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patient comprises
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are used in
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the prin specification, but was obtained in electronic format directly from WI at fifty.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the arms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                           812
                                                                                                                                                                                            184
                                                                                                                                                                                                                                  706
                                                                                                                                                                                                                                                                                                             650
                                                                                                                                                                                                                                                                                                                                               72 VPPPV--DRDHPAKVVVKMETVEKVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQF
                                                                                                                                                                                                                                                                                                                                                                                     92;
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                           EYVVFNGSVGALTGENALĶAKVGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEG-----
                                                                                                                                                                                          PVGMHIANGMYGLILVEPKEGLPKVDKEYYVMQGDFYTKGKYGEQGLQPFDMEKAIREDA
                                                                                                                                                                                                                                  VNR - - GTMGHSLDFHAGT
                                                                                                                                                                                                                                                                                                          VLPPLMTGRVHRMTLIAQ----ESVQEIAPETTIDAMTYNGRYMAPVIHARIGDEMRVHL
RGNPEGGGCQALDLASAQGGFVEMVFEEPGRYTFVNHS-FVEMERGAKGFIEV
                                                                           DLTMFNGHANQYVFE-PLKARVGERVRIWVLAAGPSRGCSFHVVGTQFDTVFKEGAYTLK
                                                                                                                                                     FMSAHIAAGMFGAVIVPPHD-LPRADREFYLVQSETYLSEHNGAE----VNTAKIANETP
                                                                                                                                                                                                                                                                    SNHPDSKMPHNVDFHAATGPGGGAEASFT-----APGHTSTFSFKALQPGLYVYHCAVA
                               -GKGENHNIQTTLIPAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                               924 AA;
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       13.3%;
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                                                                                                                                                                                                                                  ----VSPTRVMRTIAPGOELDYNFTLHRAGIWLYHCSTA
                                                                                                                                                                                                                                                                                                                                                                                   Score 349; DB 2
Pred. No. 5e-22;
6; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                       121;
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                     34;
   922
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RESULT 6
AAY74274
01-MAY-1998;
31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
02-OCT-1998;
                                                                                                                                                                     Neisseria meningitidis; Neisseria gonorrheae; antigenic; diagnosis; immunogenic; infection;
      (CHIR )
                                    09-OCT-1998;
09-OCT-1998;
                                                                                                  30-APR-1999;
                                                                                                                                               Neisseria gonorrheae
                                                                                                                                                              antibacterial;
                                                                                                                                                                                           Neisseria gonorrheae ORF 007
                                                                                                                                                                                                            21-MAR-2000
                                                                                                                                                                                                                                          AAY74274
                                                                                                                  11-NOV-1999.
                                                                                                                                WO9957280-A2
      CHIRON CORP
                                                                                                                                                                                                                                          standard;
       GENOMIC
                                                                                                                                                                                                            (first
                           98US-0083758

98US-0094869

98US-0098994

98US-0099062

98US-0103749

98US-0103794

98US-0103794

99US-0121528
                                                                                                                                                              gene
                                                                                                  99WO-US09346
                                                                                                                                                                                                                                          Protein;
                                                                                                                                                             therapy
                                                                                                                                                                                            protein sequence
                                                                                                                                                                                             SEQ
                                                                                                                                                                      meningitis; septicaemia;
                                                                                                                                                                              antigen; vaccine;
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RESULT 7
ABP78130
ID ABP7
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Best Local S
Matches 50
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Petersen J,
Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                  Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
         New protein from Neisseria gonorrheae, useful for the manufacture medicament for treating or preventing N. gonorrheae infection -
                                                WPI; 2003-058415/05
N-PSDB; ABZ39100.
                                                                                                                                                                                                                                                                        Antibacterial;
                                                                                                                                                                                                                                                                                                                           07-MAR-2003
                                                                                                                                                                                                                                                                                                                                                     ABP78130
                                                                                                                                                                                                                                                                                                                                                                             ABP78130 standard; Protein;
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                                                                                                                                        12-FEB-2001; 2001GB-0003424
                                                                                                                                                                  12-FEB-2002; 2002WO-IB02069
                                                                                                                                                                                            10-OCT-2002
                                                                                                                                                                                                                      WO200279243-A2
                                                                                                                (CHIR-)
                                                                                                                                                                                                                                                                                                  gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      457
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                                                                                                               CHIRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            NGFMPATAISDADIAAVATYIMNAFDNGGGSVTEKDVKQAKGKK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 180; 1453pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESVMPAIALSDQQIANVITYTLNSFGNKGGQLSADDVAKAKKTK 500
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                                                                                                                                                                                                                                              gonorrhoeae
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, Pizza M, Rappuoli R,
, Venter JC;
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                                                                                     Pizza M,
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                                                                                                                                                                                                                                                                        infection;
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                                                                                      Masignani
                                                                                                                                                                                                                                                                        vaccine;
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                                                                                                                                                                                                                                                                                                                                                                               184
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Pred. No. 3.3e-13;
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Ratti G,
                                                                                                                                                                                                                                                                      gene therapy
                                                                                      Monaci
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Scalato E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 133;
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Scarselli M;
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ARZSULT 8
AAY7427
ID AAY7
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AAY7427
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Also disclosed are the nucleic acid molecules encoding the proteins a antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention.
                                                                                                                                                                                                                                                                                                        01-MAY-1998;
31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigenic; diag
antibacterial;
                           Claim
                                                   Novel Neisserial polypeptides vaccines and diagnostics -
                                                                                           WPI; 2000-062150/05
N-PSDB; AAZ53038.
                                                                                                                                                           Fraser C,
                                                                                                                                                                                                                                                                                                                                                  30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis
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                                                                                                                                   Tettelin
                                                                                                                                                                                                                                                       09-OCT-1998
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                                                                                                                                                                                                                                                                                             02-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 392; 815pp; English
                                                                                                                                                                                      (GENO-)
                                                                                                                                                                                                     CHIR )
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                          2;
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INST GE
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                          Page 181; 1453pp; English
                                                                                                                                 'n,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQKVYESNCIACHGKKGEGRGTAFPPLFRSDYIMNKPHVLLHSMV-KGINGTIKVNGKTY
                                                                                                                                                           Galeotti C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis;
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98US-0103796.
99US-0121528.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunogenic;
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Rappuoli R,
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Pred. No. 5.4e-13;
3; Mismatches 39;
                                                                predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein sequence
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                                                                                                                                                           Hickey
                                                                                                                                               Ratti
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Scalato E,
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                                                                                                                                                              Mora M;
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615,

and

AAY74253 to AAY75941

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AAY74275
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Best Local S
Matches 44
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31-JUL-1998;
02-SEP-1998;
                                                                                                                                                                                                                  Fraser C, G
Petersen J,
Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                          09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis ORF 007 protein sequence SEQ ID NO:46.
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                                                  Novel Neisserial polypeptides predicted vaccines and diagnostics
                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                  (CHIR )
                                                                                                                                   2000-062150/05.
DB; AAZ53037.
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44; Conser
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INST GENOMIC RES.
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J, Pizza M, Rappuoli R,
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llarity 42.7%;
Conservative 1.
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98US-0094869.
98US-0098994.
98US-0099062.
98US-0103749.
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98US-0103796.
99US-0121528.
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Pred. No. 7.3e-12;
4; Mismatches 45;
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Ratti
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                                                                                 be useful antigens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      meningitis; septicaemia;
                                                                                                                                                                                                                                              Masignani V, Mora M;
Scalato E, Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 132;
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Claim 2; Page 180; 1453pp; English.

conversion into he protein sequence for

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Best Local (
The present invention relates to a novel cell membrane-bound 2-keto-D-gluconate dehydrogenase and a method for conversion 2,5-diketo-D-gluconate. The present sequence is the protein a
                                                                                            Base sequence of novel cell membrane-bound 2-keto-D-gluconate dehydrogenase gene and method for conversion into 2,5-diketo-D-gluconate - NoAbstract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                 WPI; 2001-088033/10.
N-PSDB; ABL52917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell membrane bound; 2-keto-D-gluconate dehydrogenase; enzyme;
                                                                Claim 3; Page 9-11; 16pp; Korean.
                                                                                                                                                                                                               Shin YC,
                                                                                                                                                                                                                                                                                                         10-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
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                                                                                                                                                                                                                                            (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.
                                                                                                                                                                                                                                                                          10-SEP-1998;
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                                                                                                                                                                                                               Bahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 AA;
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Best Local S
Matches 97
Cytochrome C gene - comprises specified sequence of 1473 bases which is inserted in host cells and is used to produce cytochrby oxidative fermentation
                                                                                                WPI; 1993-169634/21
N-PSDB; AAQ48234.
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Best Local S
Matches 49
This invention relates to an isolated membrane-bound sorbitol dehydrogenase (SDH) from Gluconobacter oxydans. The invention includes polynucleotides (AAC83153 - AAC83154) encoding the 3 subunits of SDH (AAB35987 - AAB35989). Also included in the invention are two polynucleotide sequences AAC83156 and AAC83157 which contain the subunit coding regions. The sorbitol dehydrogenase polynucleotide sequences are useful for producing L-sorbose from D-sorbitol and for increasing the production of 2-keto-L-gulonic acid by transforming a host cell, especially Gluconobacter with the DNA and selecting the transformed host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of encoded by the cytochrome C gene from Gluconobacter suboxydans IFD 12528 which may be used to give improved prodn. of cytochrome C by oxidative fermentation.
                                                                                                                                                                    Novel membrane-bound sorbitol dehydrogenase nucleic acid molecule isolated from Gluconobacter suboxydans useful for the fermentative production of 2-keto-L-gulonic acid and L-sorbose from D-sorbitol
                                                                                                                                                                                                                           WPI; 2000-687351/67.
N-PSDB; AAC83154.
                                                                                                                                                                                                                                                                     Choi E,
                                                                                                                                                                                                                                                                                               (CHOI/)
(RHEE/)
(LEEE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gluconobacter oxydans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sorbitol dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sorbitol dehydrogenase subunit 2 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB35988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB35988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 13-15; 20pp; Japanese
                                                                                                                                          Claim 6; Fig 8; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                        23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                  23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                              02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L-sorbose production;
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200065066-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 VPEGKNLG---QDDGQTTALLNKGGQGNAGAEVYLHNCAICHMNDGTGVNRMFPPLAGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 LPEGAPQAIDTQEAPKTPAPANLQEQIKAGKATYDSNCAACHQPDGKGVPNAFPPLA-NS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
                                                                                                                                                                                                                                                                                               CHOI E.
RHEE S.
LEE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-GQLSADDVAKAKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVITDDPTSLANVVAFG--GILPPTNSAPSAVAMPGFKNHLSDQEMADVVNFMRKGWGNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DYLNADHARAASIVANGLSGKITVNGNQYESV-MPAIA--LSDQQIANVITYTLNSFGNK
                                                                                                                                                                                                                                                                     Rhee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APGTVSASDIQKLRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 AA;
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                                                                                                                                                                                                                                                                                                                                                        99WO-IB00736
                                                                                                                                                                                                                                                                                                                                                                                  99WO-IB00736
                                                                                                                                                                                                                                                                     Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2-keto-L-gulonic
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Pred. No. 1e-05;
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Best Local
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                                                                                                                                                                The sequence was deduced from a DNA sequence obtd. from a clone isolated from a library prepd. from RNA extracted from the fruit of C. moschata. The DNA can be used to produce the enzyme in high
                                                                                                                              Sequence
                                                                                                                                                                                                                     Disclosure; Fig 1; 8pp; Japanese.
                                                                                                                                                                                                                                                         DNA encoding polypeptide with ascorbate oxidase activity - from Cucuria moschata, used to produce recombinant enzyme:
                                                                                                                                                                                                                                                                                                WPI; 1991-314587/43.
N-PSDB; AAQ14178.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           JP03210182-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cucurbita moshata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ascorbate oxidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR14306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YLNADHARA-ASIVANGLSGKITVNGNQYESV-MPAIA--LSDQQIANVITYTLNSFGNK 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPEGKNLG---QDDGKATALLEAGGKGDAGAEVYLHNCAICHMNDGTGVNRMFPPLAGNP 362
 PG-----GGAEASFTA--PGHTSTFSFKALQPGLYVYHCAVAPVGMHIANGMYGLILVEP 201
                         VEYMFWAPDCNENIVMGINGQFPGPTIRANAGDTVVVELINKLHTEGVVIH----WHGILQ
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ilarity 37.3%;
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                                                -----FGGQVPGQMIRVREGDTIEVQFSN--HPDSKMPHNVDFHAATG 148
                                                                                     6.2%;
                                                                         44;
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                                                                           Score 163; DB 12;
Pred. No. 1.4e-05;
4; Mismatches 130;
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Pred. No. 1e-05;
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                                                                                                    Length 579;
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                        Purified cytochrome c-553 (CO) was isolation from Gluconobacter suboxydans IFO 1258 and partially sequenced. From this information, 32P-labelled oligonucleotide probes were constructed and used too screen a bank of genomic EcoRI fragments from IFO 1258 in vector 13mpl9RP. A plasmid which hybridised strongly contained an approx.

1.5kb fragment which was sequenced. This sequence lacks the N-terminal region which was located from the same source and used to construct a complete gene. The probes used are based on the N-terminal amino acid sequence (KGWGNNA) of peptide I which was isolated following limited hydrolysis of c-553(CO) using arginyl endopeptidase. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                     Plasmid contg. gene for cytochrome C-553 (CO) - and transformed cells useful in high productivity oxidative fermentation, e.g. \epsilon ethanol to acetic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of
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08-JUN-1993
                                                                                                                                                                                                         Disclosure; Fig 1; 39pp; French.
                                                                                                                                                                                                                                                                                               N-PSDB; AAQ36687.
                                                                                                                                                                                                                                                                                                               WPI; 1993-054531/07.
                                                                                                                                                                                                                                                                                                                                           Shimizu T,
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                                                                                                                                                                                                                                                                                                                                                                        (ASAH ) ASAHI KASEI KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytochrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 PQGKKEPFHYDGEINLLLSDWCHQSIHKQEVGLS----SKPIRWIGEPQTILLNGRGQFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTLIPAGGAAITE---FKVDVPGDYV----LVDHAIFRAFNKGALGILKVEGEENHEIY-
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Sequence

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  Query Match
Best Local S
Matches 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                           The invention comprises a method for identifying a compound capable of modulating biofilm formation by bacteria. The method of the invention is useful for identifying a compound capable of modulating biofilm formation by bacteria or modulating bacterial antibiotic resistance. The method of the invention is also useful for diagnosing and treating a subject (especially an immunocompromised human) that is afflicted with a biofilm-associated disease or disorder, such as: cystic fibrosis; AIDS; middle ear infections; acne; periodontal disease; catheter-associated infections; and medical device-associated infections. The present amino acid sequence represents a protein that is used in the invention.
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biofilm formation modulation; biofilm-associated disease; cystic fibrosis; AIDS; middle ear infection; acne; period
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying compound capable of modulating biofilm formation by bacteria/bacterial antibiotic resistance, useful for treatment biofilm associated disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-2001; 2001US-285190P.
24-OCT-2001; 2001US-344142P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-APR-2002; 2002WO-US12532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200285295-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa biofilm formation-related protein #31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Whiteley M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IOWA )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                catheter-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003-075601/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 LPEGAPQAIDTQEAPKTPAPANLQEQIKAGKATYDSNCAACHQPDGKGVPNAFPPLA-NS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIV IOW
HARVARD
                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 115-116; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYLNADHARAASIVANGLSGKITVNGNQYESV-MPAIA--LSDQQIANVITYTLNSFGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APGTVSASDIQKLRTT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-GQLSADDVAKAKKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPEGKNLG---QDDGQTTALLNKGGQGNAGAEVYLHNCAI CHMNDGTGVNRMFPPLAGNP
                                                                                                                   374
5.7%;
llarity 22.0%;
Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bangera MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lory
  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
Score 150; DB 24;
Pred. No. 0.0001;
8; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 162; DB 14;
Pred. No. 1.2e-05;
8; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    medical device-associated infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Greenberg
                                                      Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
  Indels
  100;
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f
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362
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  11;
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Query Match
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Matches 93
                                                                                                                                                            This sequence represents the D-sorbitol dehydrogenase of the invention. Cells transformed with a recontaining DNA encoding the dehydrogenase can be used to produce L-sorbose or 2-keto-L-gula acid as precursor for simple large-scale L-ascorbic acid production
                                                                                                                                                                                                                                                                                                         Gene group for D-sorbitol dehydrogenase, useful for simple large-scale production of L-sorbose or 2-keto-L-gulonic acid precursor for L-ascorbic acid
                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gluconobacter oxydans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G. oxydans
                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishii Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-APR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L-ascorbic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D-sorbitol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY14051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY14051 standard;
                                                                                                                                                                                                                                                                                                                                                                                           1999-302741/25
DB; AAX57911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 -- TAMAAFGKQLNEVDLAAVITYERNAWGNDDGDMVTPKDVVAYKQK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 KAGKATYDSNCAACHOPDGKGVPNAFPPLANSDYLNADHARAASIVANGLSGKITVNGNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 TSSDVIHSWWVPAFAVKRDAIPGFVNEAWTKVDEPGIYRGQCAELCGKDHGFMPIVVD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 LGQDVEYFSNLATPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 VGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQT---TLIPAGGA----
180 CAVAPVGMHIANGMYGLILVEPKEGL-----PKVDKEYYVMQGDFYTKGKYGEQGLQPF
                                                                                                                                                                                                                                                                   9; Page 57-59; 83pp; Japanese
                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUJISAWA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YESVMPAIA--LSDQQIANVITYTLNSFGNKGGQLSADDVAKAKKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARGDKVYHTICAACHQAEGQGMPPMFPALKGSKIVTGPKEHHLEVVFNGVPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKTPAPANLQEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Noguchi Y,
                                                                                                                          478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dehydrogenase; L-sorbose; acid production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-sorbitol dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                           5.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saito Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ဗ
                                      Score 148; DB
Pred. No. 0.000
47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AITEF-----KVDVPGDY------VLVDHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soeda S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2-keto-L-gulonic
                                                           DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yoshikawa
                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ζ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid;
                                                                                                                                                              keto-L-gulonic production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor;
  233
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CHTKPGGAPFAG---GLVIASPMGGIVASNITPDPDTGI--

GKYTEEEFAN-

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RESULT 17
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                      Query Match
Best Local Similarity
Matches 40; Conserv
                                                                       Sequence
                                                                                                                                                     DNA encoding polypeptide having ascorbate oxidase activity derived from Cucumis sativus, and transformants producing polypeptide in high yields
                                                                                                                                                                                                         N-PSDB; AAQ12068
                                                                                                                                                                                                                   WPI; 1991-180924/25.
                                                                                                                                                                                                                                                                              19-SEP-1989;
                                                                                                                                                                                                                                                                                                     19-SEP-1989;
                                                                                                                                                                                                                                                                                                                             08-MAY-1991.
                                                                                                                                                                                                                                                                                                                                                    JP03108485-A
                                                                                                                                                                                                                                                                                                                                                                           Cucumis sativus
                                                                                                                                                                                                                                                                                                                                                                                                   Ascorbate oxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                          Ascorbate oxidase from Cucumis sativus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR12339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR12339 standard;
                                                                                           The DNA is derived from Cucumis sativus and can be used to large amts. of polypeptide having ascorbate activity.
                                                                                                                                Disclosure; Fig 2; 9pp; Japanese.
                                                                                                                                                                                                                                        (TOYM ) TOYOBO KK.
(NAGS ) NAGASE SANGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273
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  101 VEYQFWT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGGP 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDLFPM--DGERIYVNNCAACHGLDGAGAADHFTPSLSSNAVVGAPGADNLIMA--IVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSKLTDEDLHAI-----AAYIRQ-IPKIEDSQAKQPRDRFGVAVQPIVDLQKPKLDRE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKVGETVRLFVG----NGGPNLTSSF---HVIGEIFDKVHFEGGKGENHNIQTTLI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDR --TTNG--HHVLMPGFGPTSDVQRLSDTDVAKLTNYVSGTFGSGDHHVTAQDVKVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSGKITVNGNQYESVMPAIA-----LSDQQIANVITYTLNSFGNKGGQLSADDVAKAK 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANIQEQIKAGKATYDSNCAACHQPDGKGVPNAFPPLANSDYL----NADHARAASIVANG 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILKVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSAYLGGTPLAGWYAPNITPSMNSGIGDWSEDDLVQYLRTGSVPGRAQAAGMMGEAVEHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PAGGAAITEFKVDVPGDYVLVDHAIFRAFNKGALG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMMISWNLLFAGPPPAKGDPQTYSTIERGHYLADAL-----GHCGTCHTPRNFLMGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALRKGIRRDGAHLYPAMPYTAYSEIADTDIHALYVYFMHGVAPLRQDNPKTELKFPFNIR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DMEKAIRED-----LK 262
                                                                       555 AA;
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   501
                                                                                                                                                                                                                                                                              89JP-0244257
                                                                                                                                                                                                                                                                                                     89JP-0244257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 555
                                                                                                                                                                                                                                                                                                                                                                                                   transformant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                  32.5%;
 -----FGGQVPGQMIRVREGDTIEVQFSN--HPDSKMPHNVDFHAATG 148
                                                                                                                                                                                                                                          KPL.
                      16;
                      Score 146.5; DB 1
Pred. No. 0.00039;
6; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide;
                                              DB 12;
                       42;
                                                                                                                                                                                                                                                                                                                                                                                                   activity.
                        Indels
                                              Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------EAPKTPAP 388
                       25;
                                                                                                        obtain
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380
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RESULT 18
AAR20193
ID AAR20
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                                                                                                                                                                                        Matches
                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                            Acetobacter transformed with the sequence encoding this protein can enhance the efficiency of acetic acid fermentation. The ADH comples can be easily extracted from the bacteria and purified and it can be used for the determination of an alcohol.

See also AAQ20383-84, and -86-88.
                                                                                                                                                                                                                                                                                                                                                         Alcohol dehydrogenase complex structural gene - used and enhancing efficiency of acetic acid fermentation transformed acetic acid bacteria
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 4(1-3); 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP03266988-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acetobacter altoacetigenes NH-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alcohol dehydrogenase; acetic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH complex protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR20193;
                                                                                                                                                                                                                                                                                                                                                                                                                                          (NAKA-) NAKANO SUTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR20193 standard; Protein; 467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    1992-019325/03.
300
                                               261 AVF-GGMGD-
                                                                                                                                           149
                                                                                                                                                              184 PVGMHIANGMYGLIL-VEPKEGLPKVDKEYYVMQGDFYTKGKYGEQGL----QPFDM-EK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 KEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149
                                                                                                                 238 AIREDAEYVVFNGSVGALTGENALKAKVGETVR----LFVGNGGPNLTSSFHVIGEIFDK 293
                                                                                                                                                                                        84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         AAQ20384.
GN----YTYDPSTANMLASG----
                     GEENHEIYSHKQTDAVYLPEGAPQAIDTQEAPKTPAPANLQEQIKAGKATYDSNCAACHQ
                                                                 VHFEGGKGENHNIQTTLIPAGGAAITEFKVDVPGDYVLVD--HAIFRAFNKGALGILKVE
                                                                                            AL--DAA----
                                                                                                                                          PLSMRWPLGIWRMMFSPSPKDFTPAPGTDPEIARGDYLVTGP-GHCGACHTPRGFAMQEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGTPWADGTASISQCAINPGETFTYRFVVDKAGTYFYH---GHLGMQRSAGLYGSLIVDP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PG----
                                                                                                                                                                                                                                       467 AA;
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90JP-0042301
90JP-0073440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90JP-0073440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAEASFTA--PGHTSTFSFKALQPGLYVYHCAVAPVGMHIANGMYGLILVEP
                                                                                                                                                                                                   25.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (mol.wt.
                                                                                            -GGPDFLSGGAPIDNWVAPSLRNDPVVGLGRWSEDDIYTFLKSGRIDHS
                                                                                                                                                                                       ; Score 146; DB 13; 
; Pred. No. 0.00033; 
50; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.000).
  -NTASVP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fermentation
                                               -VVAWSTQYFTDDDLHAIAK-YLKSLPPVPPSQ
                                                                                                                                                                                         127;
                                                                                                                                                                                                              Length 467;
                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                        in plasmid for
  GADTYVKECAICHR
                                                                                                                                                                                                                                                                                      ADH complex
nd it can be
                                                                                                                                                                                         72;
                                                                                                                                                                                        Gaps
                       411
                                               299
                                                                     351
                                                                                            260
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  335
                                                                                                                                           207
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RESULT 19
AAW08380
ID AAW08
XX AAW08
AC AAW08
AC AAW08
AC AAW08
AC AAW08
AC AAW08
AC AAW08
AC AAW08
AC AAW08
AC AAW08
AC AAW09
CO Brass
XX Wale
PH 07-JU
XX 07-JU
XX 07-JU
XX WPI;
DR WPI;
DR WPI;
DR N-PSI
XX WPI;
DR N-PSI
XX WPI;
DR N-PSI
XX RECOUNTY
CC A POCOCC TEGIC
CC AA POCOCC CC AAV00
CC TEGIC
CC AA POCOCC CC AAV00
CC AAV01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A polypeptide sequence (AAW08380) was deduced from the coding region contained in a fragment (AAT48863) of Brassica napus microspore specific clone L10. Promoter regions of the L10 gene have been used to develop pollen-specific vectors useful for controlling antisense gene sequences for the prodn. of male
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant molecule for preparation of male sterile plants - used to produce stress resistant plants and for increase in seed yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-052340/05.
N-PSDB; AAT48866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Male sterile plant; hybrid seed; pollen; microspore; oilseed; canola; rape; antisense RNA; stress resistance; herbicide resistance; transgenic plant; crop protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sterile plants and hybrid seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica napus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; Fig 3b(1-4); 224pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WQ9640950-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica napus microspore-specific clone L10 product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW08380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW08380 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          412
                             264
                                                                         157
                                                                                                                    208
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                                                                                                                                                                                                                                                                                             100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 NDGGGVARMFPPLAGNPVVVTENPTSLVNVIAHG--GVLPPSNWAPSAVAMPGYSKSLSA 393
                                                                                                                                                                                                                                                  43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dd,
  KVGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAG---GAAITE
                                                                                                             VDKEYYVMQGDFYTKGKYGEQGLQPF-DMEKAI-REDAEYVVFNGSVGALTGENA--LKA
                                                                                                                                                           CP---IMPGTNYTYHFQPKDQIGSYFYY---PTTGMHRAAGGYGGLRVNSRLLIPVPYAD
                                                                                                                                                                                                    AEASFTAPGHTSTFSFKAL-QPGLYVYHCAVAPVGMHIANGMYGLILVEPKEGLP----K
                                                                                                                                                                                                                                           GVPQQVILINGQFPGPNINSTSNNNVIINVFNNLDEPFLLTWNGIQHRKNCWQDGTPGTM 102
                                                                                                                                                                                                                                                                                       GVEYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPD-----SKMPHNVDFHAATGPGGG
                                                                    PEDDYTVLIGDWYTK---SHTQLKKFLDGGRTIGRPDG--IVINGKSGKGDGSDAPLFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQIANVITYTLNSFGNKG-GQLSADDVAKAKKT 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDGKGVPNAFPPLANSDYLNADHARA-ASIVANGLSGKITVNGNOYESV-MPAI--ALSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQIADVVNFIRTSWGNKAPGTVTAADVTKLRDT
                                                                                                                                                                                                                                                                                                                                                                                                                           559 AA;
Arnison
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0476864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US08692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,
Pd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                  5.6%; Score 146; DB
26.1%; Pred. No. 0.00
tive 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fabijanski SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              559 AA
                                                                                                                                                                                                                                                                                                                                    DB 18;
0.00043;
nes 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laurian RS;
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                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                263
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  RESULT 21
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    AAR06518;
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RESULT 20
AAR13994
ID AAR13
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09-DEC-1991
                                                                                                                                                                                                                            See also
(Updated
                                                                                                                                                                                                                                                                                                                                                       Gene for membrane-bound alcohol dehydrogenase complex - from Acetobacter altocetigenes, used for prodn. of enzyr converting alcohol to acid
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                         membrane-bound ADH complex is a cytochrome c. See also AAQ13580 and AAQ13582-4.
                                                                                                                                                                                                                                                                         This sequence was deduced from the nucleotide sequence from A.altocetigenes MH-24 total DNA. The 44kD subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-1990;
26-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alcohol dehydrogenase complex; cytochrome c; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.altocetigenes membrane-bound
                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 4; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1991-289462/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawamura Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tamaki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acetobacter altocetigenes.
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                                                              322
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                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ13581.
                                                                                                                                          Similarity
                         ESV-MPAI--ALSDQQIANVITYTLNSFGNKG-GQLSADDVAKAKKT
                                                            GADTYVKECAICHRNDGGGVARMFPPLAGNPVVVTENPTSLVNVIAHG--GVLPPSNWAP 379
                                                                                             GKATYDSNCAACHQPDGKGVPNAFPPLANSDYLNADHARA-ASIVANGLSGKITVNGNQY
                                                                                                                                                                                                                             on 25-MAR-2003 to correct PA field.)
SAVAMPGYSKSLSAQQIADVVNFIRTSWGNKAPGTVTAADVTKLRDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takemura
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ilarity 36.4%;
Conservative 21
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                                                                                                                           Score 145.5; DB 12;
Pred. No. 0.00037;
1; Mismatches 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Clone L10 was identified as microspore-specific and critical to pollen formation and function. The promoter sequence may be clor into a plasmid in the anti-sense direction with respect to anoth microspore-specific gene and used to transform Brassica sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybrid seed prodn. fi induced by insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-1989;
02-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                   In addition the plasmid carries a resistance gene to a chemical agent or stress. The sense and anti-sense genes are regulated sy that they are expressed at about the same time as each other. Transfected plants are pollinated and selected according to
                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                        See also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PALA-) PALADIN HYBRIDS
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                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                   GVPQQVILINGQFPGPNINSTSNNNVIINVFNNLDEPFLLTWNGIQHRKNCWQDGTPGTM 102
                                                                                                                                                                                                                           GVEYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPD----SKMPHNVDFHAATGPGGG 152
                                                                                                                                                                                                                                                                                                                        AAQ05749 and
         NQ--EPKDYYMVASSRFLKTVITTTGLLRYEG
                               FKVDVPGDYVLVDHAIFRAFNKGALGILKVEG
                                                                              KVGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAG---GAAITE 320
                                                                                                                            VDKEYYVMQGDFYTKGKYGEQGLQPF-DMEKAI-REDAEYVVFNGSVGALTGENA--LKA
                                                                                                                                                     CP---IMPGTNYTYHFQPKDQIGSYFYY---PTTGMHRAAGGYGGLRVNSRLLIPVPYAD
                                                                                                                                                                           AEASFTAPGHTSTFSFKAL-OPGLYVYHCAVAPVGMHIANGMYGLILVEPKEGLP----K 207
                                                        KPGKTYRVRICNVGVKTSINFRIQNHKMKLVEMEGSHVLQNDYDSLDVHVGQCFGTIVTA
                                                                                                      PEDDYTVLIGDWYTK---SHTQLKKFLDGGRTIGRPDG--IVINGKSGKGDGSDAPLFTL
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                                                                                                                                                                                                                                                 Score 145; DB 11;
Pred. No. 0.00053;
Nismatches 132
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formation of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phytoalexin; resveratrol; animal pest; insect; mite; nematode; microbial pest; phytopathogenic fungus; Fusarium colmorum; septoria nodorum; Cercospora cenescens; Orthoptera; Dermaptera; Pseudocercosporella herpotrichoides; Isoptera; Tarsonemus spp; Pseudocercosporella herpotrichoides; Isoptera; Tarsonemus spp; Panonychus spp; Tetranychus spp; Pratylenchus spp; Globodera spp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYWA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heteroptera spp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laccase;
167
                                                   177
                                                                                                         111 IHVTNN----LQHNGTSIHWHGIRQLGSLEYDGVPGVTQCPIAPGDTLTYKFQATQYGTT
                                                                                                                                                               127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant Botrytis cinerea laccase protein (BcLCC2 converts the phytoalexin resveratrol into fungitoxic for protecting plants against animals and microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botrytis cinerea
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---HYW
                                                   VYHCAVAPVGMHIANGMYGLILVEPKEGLPKVDKEYYVMQGDFYTKGKYGEQGLQP----
                                                                                                                                                                                                                     WYDVTPNTGVTREY - -
                                                                                                                                                                                                                                                                                                                               STVFTALTALFAQASATAIPAVRSPLAPRQSTTASCAN--SATSRSCWGEY----SIDTN
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                                                                                                                                                               VQFSNHPDSKMPHN---VDFHAATGPGG
                                                                                                                                                                                                                                                                      APEVPP--PVDRDHPAKVVVKMETVEKVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIE
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SHFSLQYADGLFGPLII ---NGPATADYDEDV---
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Pred. No. 0.00
57; Mismatches
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RESULT 23
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17-SEP-1993;
03-DEC-1993;
22-DEC-1993;
                                                                                                          WPI; 19
                                                                                                                                                                                                                                                                                        23-MAR-1995
                                                                                                                                                                                                                                                                                                                                      Rhizoctonia solani
                                                                                                                                                                                                                                                                                                                                                              depolymerization.
                                                                                                                                                                                                                                                                                                                                                                        RSlac3; laccase; lignin;
                                  Claim 6; Page 44-46; 78pp; English.
                                                                                                                                            Christensen BE,
                                                                                                                                                                    (NOVO)
                                                                                                                                                                                                                                                                 13-SEP-1994;
                                                                                                                                                                                                                                                                                                               WO9507988-A1
                                                                                                                                                                                                                                                                                                                                                                                                  Laccase RSlac3.
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14-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR72328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR72328 standard;
             ₽.
                                                         neutral Rhizoctonia laccase(s) and corresp. nucleic acids - used industrially for polymerising lignin, lignosulphate(s) phenolic cpds. and for oxidising dyes.
                                                                                                         1995-131356/17.
DB; AAQ86526.
              solani
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lani RS22 (IMI CC 358730) cDNA library was so
The DNA insert of a plasmid from an isolated
                                                                                                                                                                    NOVO NORDISK BIOTECH NOVO-NORDISK AS.
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93US-0122827.
93US-0162827.
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                                                                                                                                            Schneider
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Best Local S
Matches 103
                                                                                        Key
Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequenced to reveal a novel gene, RSlac3 (given in AAQ86526), encoding a laccase (AAR72328) optimally active at pH 6.0-8.5. Recombinant laccase was expressed in E. coli. (Updated on 25-MAR-2003 to correct PN field.)
 Peptide
                      Binding-site
                                                                                                                                Rhizoctinia
                                                                                                                                                      protein
                                                                                                                                                                                                                  07-AUG-1997
                                             Binding-site
                                                                     Binding-site
                                                                                                                                                                                          Rhizoctonia
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                                                                                                                                                   copper oxidase; laccase; enzyme engineering;
ein engineering; lignin depolymerisation; dye oxidation
                                                                                                                                                                                                                                                                                                                                                                                                                                               382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103;
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                                                                                                                                                                                                                                                                                                                          IHLHGH-----VFDIVKSLGGTPN
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                                                                                                                                solani.
                                                                                                                                                                                         solani laccase isozyme
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217..226
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                                                          /note=
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                                                                                  note=
                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.4%;
                                                          "possible
                                                                                "Type I copper site ligand"
                                                                                                                                                                                                                                                                                                                                                                                                                                             -APKTPAPANLQEQIKAGKATYDS----NCAACHQPDGKGV
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Pred. No. 0.0011;
0; Mismatches 216;
            copper site ligand
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                                                          copper site
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Best Local
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                                                                                                       alter e.g. its specific activity or pH-activity profile or to improve expression yields. The mutant laccase is prepd. by site-directed mutagenesis of the rs14 gene [16317] and expression in host cells. The mutation may be a deletion, insertion or pref. a substn. of one or more amino acids at a location no greater than 12 Angstroms, pref. no more than 2.5 Angstroms, from the Type I copper site. The mutant enzyme can be used e.g. for the polymerisation of depolymerisation of flighlins, oxidation of dyes, or polymerisation of phenolic or aniline cpds. present in liquids, e.g. for the treatment of fruit juices.
                                                                                                                                                                                                                         New mutant blue copper oxidase enzymes - having activities to wild-type enzymes, used for e.g. (de)polymerisation or oxidation of dyes
                                                                                                                                                                                                                                                                                                                                                  13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
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NOVO
                                                                                                                                                                                                                                                                                                                   01-SEP-1995;
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                                                                                          Sequence
                                                                                                                                                                                          Rhizoctonia solani laccase isozyme 4 (AAW16301) can be engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
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DB; AAT63317.
          117
                                                          103;
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                                         59
                         8
                                                                  Similarity
IRVREGDTIEVQFSNH----PDSKMPHNVDFH-----AATGPGGGAEASFTAP-----GHTS
                                         LPVIDAIVTHAPEVPPPVDRDHPAKVVVK--METVEKVMRLADGVEYQFWTFGGQVPGQM 116
                          LPLLAAVST --
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                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          "preferred site
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0; Mismatches
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Pred. No.
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R285 region o
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of ascorbate
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  IHLHGH---
                                     LNSFGNKGGQLSADDVAKAKKTKPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Y-----TKGKYGEQG---LQPFDMEKAIREDAEYVVFNGSVGALTGENALKAKVGETV
                                                                                                                   PNAFPPLANSDYLNADHARAASIVANGLSGKITVNGNQYESVMPAIALSDQQIANVITYT
                                                                                                                                                           AIGTAVVEENVHALINPGAPGGSAPADVSLNLAIGRSTVDGILRFTFNNIKYEAP----
                                                                                                                                                                                                                                           AGORYSVIVEANOTAANYWIRAPMTVAGAGTNANLDPTNVFAVLHYEGAPNAEPTTEQGS
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    ---VFDIVKSLGGTPN
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RESULT 25 AAW76310

AAW76310 standard; protein; 529 AA

C AAW76310;

08-JAN-1999 (first entry)

Rhizoctonia solani (I) laccase protein.

Laccase; variant; oxidisation; dye transfer inhibition; bleaching; denim; lignin modification; paper strengthening; phenol polymerisation; hair dye; waste water treatment.

Rhizoctonia solani.

WO9838287-A1.

03-SEP-1998.

23-FEB-1998; 98WO-DK00070

28-FEB-1997; 97DK-0000222

(NOVO ) NOVO-NORDISK AS

Svendsen A, Xu F;

WPI; 1998-495393/42.

New variants of Coprinus and related laccases with increased oxidation potential - or altered pH optimum, or mediator or oxygen-hydroxide ion pathways, useful for oxidation, for inhibiting dye transfer and in bleaching textiles, especially as detergent additive

Disclosure; Pages 124-125; 147pp; English

C The present sequence represents a laccase protein. The specification describes active laccase variants (see AAW76282, AAW76296-99 and AAW76316-17) having increased oxidation potential, altered pH optimum. altered mediator and/or altered oxygen/hydroxide ion pathway. The

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RESULT 26
AAW60878
ID AAW60
XX AAW60
XX O9-NO
XX O9-NO
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Matches 103;
                                     Misc-difference
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t; bleaching.
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                                                                                                  Location/Qualifiers
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                        /note=
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                                             "variant may have Ala, Val, Leu, Phe, Met, Gly, Ser, Thr, Cys, T Gln, Asp, Glu, Lys, Arg or His Phe or His) at this position"
        "variant may have Al
Phe, Trp, Gly, Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specifically to oxidise substrates, to for bleaching textiles, specifically deni lignin modification, strengthening paper, dyeing of hair and textiles and waste
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Mismatches 216;
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Matches 103
                                                                                                                                                               are based on the previously unknown three-dimensional structure of C. cinereus laccase. Amino acid residues identified as being cimportant to protein stability are identified and altered to improve stability. The variants are typically obtained by cutagenesis of laccase DNA and expression in a host cell. Variants are preferably modified within 15 (especially 10 or 5) Angstrom C are preferably modified within 15 (especially 10 or 5) Angstrom C of a copper ion in the three-dimensional structure of the laccase. For R. solani laccase variants, preferred substitutions are one or more of M128F/H, Y137F, Y129F, Y171F or M78F/V/I/L/Q. The stabilised laccase variants can be used in detergent additives, for dye transfer inhibition in detergents, in bleaching of textiles (in particular denim), for lignin modification, paper strengthening, phenol polymerisation, hair dyeing and in waste water treatment.
                                                                                                                                                                                                                                                                                                                            This is a laccase enzyme of Rhizoctonia solani. The invention relates the design of new variants of Coprinus-like laccases (see AAW60874-79, AAW60925 and AAW62591-03); the R. solani lacc. shows 64.8% homology to C. cinereus laccase. The modifications
                                                                                                                                                                                                                                                                                                                                                                                                               New laccase variants with improved stability - having changes based on Coprinus laccase structure, used for oxidation, dye transfer inhibition or bleaching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cherry JR,
Svendsen A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-1997;
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                                                                                                                                           Sequence
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                        117
                                                                                            103;
                                                                                                                                                                                                                                                                                                                                                                                        13; 147-148; 168pp; English
                                                                     59 LPVIDAIVTHAPEVPPPVDRDHPAKVVVK--METVEKVMRLADGVEYQFWTFGGQVPGQM 116
                                             æ
                                                                                                        Similarity
ITANKGDTLRINVTNQLTDPSMRRATTIHWHGLFQATTADEDGPAFVTQCPIAQNLSYTY
                     IRVREGDTIEVQFSNH----DSKMPHNVDFH----AATGPGGGAEASFTAP-----GHTS
                                                                                                                                           529
                                                                                             Conservative
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96DK-0001449
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Phe, Trp, Gly, Ser, Thr, Cy
Gln, Asp, Glu, Lys, Arg or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "variant
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Asp,
Val,
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, Asp, Glu, Lys,
) at this positio
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at this
                                                                                           Score 141; DB 19;
Pred. No. 0.0011;
0; Mismatches 216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       t may have Ala, Val
rp, Gly, Ser, Thr,
sp, Glu, Lys, Arg o
al, Ile, Leu or Gln
                                              PAFAAVRNYKFDIKNVNVAPDGFQRSIVSVNGLVPGTL
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Leu or Gln)
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vr His
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r. Cys,
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Cys,
H;
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Tyr,
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net,
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Met,
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This invention describes novel mutant Rhizoctonia solani laccase enzymes modified to exhibit altered characteristics (e.g. pH activity profile) relative to the wild-type enzyme. The mutant enzymes have a number of commercial and industrial applications. For example, they may be used for the polymerization of lignin (both Kraft and liganosulfates) in solution to produce high molecular weight lignin. They may also be used for the situ depolymerization of lignin in Kraft pulp to produce low molecular
                                                                                                                                        08-FEB-2000
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                                                                                                             Claim 3; Column 31-34; 43pp; English.
                                                                                                                                                                                                                                                      (FENG/) FENG X.
(BERK/) BERKA R M.
(WAHL/) WAHLEITHNER J
                                                                                                                                                                                                                                                                                                               30-AUG-1996;
                                                                                                                                                                                                                                                                                                                                         09-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     depolymerization; phenol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laccase; mutant; lignin polymerization; Kraft; liganosulfate;
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)B; AAZ24235.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y-----TKGKYGEQG---LQPFDMEKAIREDAEYVVFNGSVGALTGENALKAKVGETV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNAFPPLANSDYLNADHARAASIVANGLSGKITVNGNQYESVMPAIALSDQQIANVITYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGG-----AAITEFKVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YHTPAPVLEKQMFSTNNTALLSPVPDSGLINGKGRYV-----GGPAVPRSVINVKRGKRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laccase isozyme 4 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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IHLHGH
                                 LNSFGNKGGQLSADDVAKAKKTKPN
                                                                     --SLPTL-----
                                                                                                       PNAFPPLANSDYLNADHARAASIVANGLSGKITVNGNQYESVMPAIALSDQQIANVITYT
                                                                                                                                           AIGTALVEENLHALINPGAPGGSAPADVSLNLAIGRSTVDGILRFTFNNIKYEAP----
                                                                                                                                                                                                                 AGQRYSVIVEANQTAANYWIRAPMTVAGAGTNANLDPTNVFAVLHYEGAPNAEPTTEQGS
                                                                                                                                                                                                                                                     VPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQE---
                                                                                                                                                                                                                                                                                           RLRVINASAIGSFTFSI ----
                                                                                                                                                                                                                                                                                                                         RLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGG-----AAITEFKVD
                                                                                                                                                                                                                                                                                                                                                                                                 Y-----TKGKYGEQG----LQPFDMEKAIREDAEYVVFNGSVGALTGENALKAKVGETV
                                                                                                                                                                                                                                                                                                                                                                                                                                    EIPLRG-QTGTMWYH---AHLASQYVDGLRGPLVIYDPNDPHKSRYDVDDASTVVMLEDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITANKGDTLRINVTNQLTDPSMRRATTIHWHGLFQATTADEDGPAFVTQCPIAQNLSYTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRVREGDTIEVQFSNH----DSKMPHNVDFH----AATGPGGGAEASFTAP-----GHTS
                                                                                                                                                                             -----APKTPAPANLQEQIKAGKATYDS-----NCAACHQPDGKGV
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                                                                   --LKILANNASNDADFTPNEHTIVLPHNKVIELNITGGADHP
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RESULT 28
AAG93026
ID AAG93
 AAG93026 standard;
 Protein;
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26-SEP-2001 (first

C glutamicum protein fragment SEQ ID NO: 6780

Coryneform orm bacterium; acid synthesis synthesis. amino acid synthesis; vitamin; saccharide;

Corynebacterium glutamicum

EP1108790-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAH68245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2000; 2000EP-0127688
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323 GIFPLTALAVGKDDRAFAVIRTAGGQAPRPDVDFPELSSTGLLLSSLKPADRALLPEGTP
                                  329
                                                                                                     274
                                                                                                                                  212 HNGRMGMGGHGQMMHGTPDRVLGGDVGDVMYPHYLINGRIPRAHRTFEARPGDKARLRFI
                                                                                                                                                                     238
                                                                                                                                                                                                    156
                                                                                                                                                                                                                                      186
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                                                                                                                                                                                                                                                                                                        129
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                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                                                                                                                                                                                                                                                                                                                         15 LSALMLSGCSNQADKAAQPKSSTVDAAAKTANADNAASQEHQGELPVIDAIVTHAPEVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                 YVLVDHAIFRAFNKGALGILKVEGEENHE---
                                                                                               GNGGPNLTSSFHVI--GEIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDVP---GD
                                                                                                                                                                                                                                                                                                                                                                     PVDRDHPAKVVVKMETVEKVMRL-----ADGVEYQFWTFGGQVPGQMIRVREGDTIEVQ 128
                                                                                                                                                                                                   GLQLDRGLHAPLIIRDPQDAEDQDVEWTIVLDDWVD----GIQGTPDDELDKLTGMGSGD
                                                                                                                                                                                                                                  GMHIANGMYGLILVEPKEGLPKVDKEYYVMQGDFYTKGKYGEQGLQPFDMEK-----
                                                                                                                                                                                                                                                                       ITNELPESTSIHWHGIALHNAADGVPGMTQDPIEPGESFSYVFEVPHGGTYFYH---SHT
                                                                                                                                                                                                                                                                                                   FSNH-PDSKMP--HNVDFHAATGPGGGAEASFTAPGHTSTFSFKALQPGLYVYHCAVAPV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent
                                                                                                                                                                                                                                                                                                                                     PSLRPTPTPTALGEPTVRRTLTARPLSLDIGGIEAKTWGYVSDTGDAAIEATAGDVLQVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO: 6780; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mizoguchi H, Ando
Senoh A, Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000JP-0159162.
2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Office.
                                                                -FKVALGGHRMTVTHTDGFPVQPWETESIYLSMGE----RVDVEVILGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.4%;
19.0%;
                                                                                                                                                                  -AIREDAEYVVFNGSVGAL-----TGENALKAKVGETVRL-FV
                                                                                                                                                                                                                                                                                                                                                                                                        -----TGAVAACTSDPGPAAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 140.5; DB Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S, Hayash
Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174;
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                             ----IYSHKQTDAVYLPEGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
 382
                                                                322
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RESULT 29 AAB16365

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                                                                                                                                                                                                                                                                                       (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:COA ligase (4CL), coniferol glucosyl transferase (CGT), coniferon beta-glucosidase (CBG), caffeic acid methyl transferase, caffeoyl COA methyl transferase, caffeoyl COA methyl transferase, caffeoyl COA methyl transferase, caffeoyl COA methyl transferase, commerate COA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol cylucosyl transferase, flavanoid hydroxylase, and isoflavone reductase, which are involved in the lignin biosynthetic pathway. The polynucleotides can be used for modulating lignin content, lignin composition and the structure of a plant, especially eucalyptus and pine species, and for modifying the activity of an enzyme involved in lignin content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any corganism and for PCR amplification. The lignin content can be efficiently modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to AAB16449 represent polynucleotide and protein sequences used in the
                                                                                                                                                                                    Matches
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:CoA ligase (4CL),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and structure
                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-OCT-1998;
14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant; lignin;
Pinus radiata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Page 151-152; 213pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-317962/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bloksberg LN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eucalyptus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB16365 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes isolated polynucleotides and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200022099-A1
                                                                                                                                                                                                     Local
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                                                                                                                                                                                                     Similarity
MHIANGMYGLILVEPKEGL----PKVDKEYYVMQGDFYTKGKYG---
                                    KYNVTIHWHGIRQLRTGWADGPAYITQCPI-QPGQSYVYNFTITGQRGTLLWHAHI----
                                                                      PHNVDFH-----AATGPGGGAEASFTAPGHTSTFSFKAL-QPGLYVYHCAVAPVG
                                                                                                                                             RDHPAKYVVKMETVEKVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPDSKM 137
                                                                                                           RNYTFNVVMKNTT----RLCS--SKPIVTVNGMFPGPTLYAREDDTVLVRVSN----RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   grandis diphenol oxidase protein sequence SEQ ID NO:291.
                                                                                                                                                                                                                                                             326 AA;
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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99US-0143811.
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                                                                                                                                                                                  5.2%; Score 136.5;
20.9%; Pred. No. 0.00
tive 46; Mismatches
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                                                                                                                                                                                                     .0014;
                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                    129;
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                    Length
 -EQGLQPFDME
                                                                                                                                                                                    93;
 236
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RESULT 30
AAW43448
AAC AAW43
AXX AAW43
AXX TODAG
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            This sequence represents a full length tobacco laccase (an oxidoreductase acting on diphenols) encoded by the clone pTL-3. The complete protein has a calculated molecular weight of 61.9 kD and a pI of 10.08. The protein has a putative signal sequence of 22 amino acids, leaving a 535 amino acid protein of molecular weight 509.4 kD. The mature protein contains 12 putative N-glycosylation sites (Asn-Xaa-Ser/Thr) and also contains 2 potential copper ion binding sites. The gene sequence was isolated from a cDNA library from tobacco leaves using a probe derived from the sequence of the sycamore (Acer pseudoplatanus) laccase gene. The gene can be used to transform plant cells for producing transgenic plants having a reduced or altered lignin content, for improved digestibility of forage crops, for paper manufacture. Plants with increased lignin content may have better resistance to parasites.
                                                                                                                                                                                                                                                                                                                                                      Modifying lignin biosynthesis in plants with gene encoding laccase mRNA - or its anti-sense complement, especially for crops used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tobacco; laccase; oxidoreductase; probe; hybridisation; sycamore; transgenic plant; digestibility; forage crop; paper manufacture;
                                                                                                                                                                                                                                                                                               Claim 19; Page 32-35; 72pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV01596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Faye L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lignin;
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                                                                                                                                                                                                                                                                                                                                  and for paper production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CENT NAT RECH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEENHEIYSHKOTDAVYLPEG----APQAIDTQEAPKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQTTNALISTDQSSGKYMVAASPFMDSPIAVDNMTATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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23..557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kiefer-Meyer
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AAR72318
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17-SEP-1993;
03-DEC-1993;
22-DEC-1993;
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N-PSDB; AAQ86524
                  WPI; 1995-131356/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
14-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR72318;
                                                         Christensen BE,
                                                                                              (NOVO)
                                                                                                                                                                                                                                                                                               23-MAR-1995
                                                                                                                                                                                                                                                                                                                                      WO9507988-A1
                                                                                                                                                                                                                                                                                                                                                                           Rhizoctonia solani
                                                                                                                                                                                                                                                                                                                                                                                                                  depolymerization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR72318
                                                                                                                                                                                                                                                          13-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laccase RSlac1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 AAITEFKVDVPGDYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 YYVMQGDFYTKGKYGEQGLQPFDMEKAIRE------DAEYVVFNGSVG-----AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 I-QPGQNYVYNFTITGQRGTLFWHAHI----LWLRATVHGAIVILPNLGVPYPFPKPNHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47
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                                                                                              NOVO NORDISK
NOVO-NORDISK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSKKYPAKVPKKIDHSLFFTVGLGINPCPTCKQGNGSRVVASVNNVTFVMPTVALLQAHF
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(first entry)
                                                                                                                                                     93US-0122230.
93US-0122827.
93US-0162827.
93US-0172331.
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                                                         Schneider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -FGTKG
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AS.
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                                                         שֻ
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Pred. No. 0.0031;
8; Mismatches 16
                                                                                                                   INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTEAVINEAIKSGLAPNVSDAHTI--NGHPGPVSNCAS
                                                         Wahleithner
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                                                         JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19;
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430

247 372 286

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157

211

102

17; 156

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RESULT 32
AAW62501
ID AAW62
XX AAW62
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Best Local S
Matches 107
                                                     aetergent;
                                                                   Coprinus laccase-like
                                                                                                                        8661-AON-60
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a probe based on consensus sequ
RS1ac1 gene given in AAQ86524 w.
(AAR72318) optimally active at
expressed in E. coli
                          Rhizoctonia
                                                                                                                                                   AAW62501;
                                                                                                                                                                             AAW62501 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neutral Rhizoctonia laccase(s) and corresp. used industrially for polymerising lignin, l phenolic cpds. and for oxidising dyes.
                                                                                                                                                                                                                                             449 VILPKNKCIEFNIKGNSGIPITHPVHLHGH-----TWDVVQFGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Page
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                                                                                                                                                                                                                                                                                                                                                                                                           QEPDTYWINAPLTNVPNKTAQALLVYEEDRRPYHPPKGPYRKWSVSEAIIKYWNHKHKHG
                                                                                                                                                                                                                                                                     SIVANGLSGKITVNGNQYESVMPAIALSDQQIANVITYTLNSFGN
                                                                                                                                                                                                                                                                                                 VLDL----TFGLNFATGHWMI-BGIPYESPKIPTLLKILTDEDGVTESDFTKEEH---T
                                                                                                                                                                                                                                                                                                                           QEQIKAGKATYDSNCAACHQPDGKGVPNAFPPL-----ANSDYLNADHARAA
                                                                                                                                                                                                                                                                                                                                                    RGLLSGHGGLKARMIEGSHHLHSRSVVKRQNQTTTVVMDESKLVPLEYPGAACGSKPADL
                                                                                                                                                                                                                                                                                                                                                                         LGILKVEG-----EENHEIYS-----HKQTDAVYLPEGAPQAIDTQEAPKTPAPANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRFSV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDV----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AILASGNITRORPVSATINGK-GRFDPDNTPANPDTLYTLKVKRGKRYRLRVINSSEIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHLSSQYVDGLRGPLVIYDPKDPHRRLYDVDDEKTVLIIGDWY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APVGMHIANGMYG-LILVEPKE---GLPKVDKEYYVM-QGDFYTKGKYGEQGLQPFDMEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                       --PGDYVL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI-----REDAEYVVFNGSVGALTGEN-----ALKAKVGETVRLFVGNGGPNLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTTSIHWHGLLQHRNADDDGP-----SFVTQCPIVPRESYTYTIPLDDQTGTYWYH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLARTVEYGLKISDGEIAPDGVKRNATLVNGGYPGPLIFANKGDTLKVKVQNKLTNPEMY
                                                     bleaching.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576 AA;
                            solani
                                                                                            solani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 E. coli.
25-MAR-2003
                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-33;
 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMI CC 358730) genomic library was screened with consensus sequences of known laccases. The n in AAQ86524 was isolated; it encoded a laccase ally active at pH 6.0-8.5. Recombinant laccase was
                                                                                            (IV)
                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.2%;
20.4%;
                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78pp; English.
                                                                   enzyme;
                                                                                              laccase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---EGHKV--TVIAADGVSTKPYQVDAFDILAGQRIDCVVEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       correct PN field.)
                                                                                                                                                                             575
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                                                                   enzyme
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                                                               engineering;
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lignosulphate(s)
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                                                                  enzyme
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                                                                  stability;
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Cherry JR,
                                      C. cinereus laccase. Amino acid residues identified as being important to protein stability are identified and altered to improve stability. The variants are typically obtained by mutagenesis of laccase DNA and expression in a host cell. Variants are preferably modified within 15 (especially 10 or 5) Angstrom of a copper ion in the three-dimensional structure of the laccase. For R. solani laccase (II) variants, preferred substitutions are one or more of W411F/H, Y125F, Y134F, Y126F, Y170F or M78F/V/I/L/O. The stabilised laccase variants can be used in detergent additives, for dye transfer inhibition in detergents, in bleaching of textiles (in particular denim), for lignin modification, paper strengthening,
                                                                                                                                                                                                          This is a laccase enzyme of Rhizoctonia solani. The invention relates the design of new variants of Coprinus-like laccases (see AAW60874-79, AAW60925 and AAW62501-03); this R. solani lacc shows 59.7% homology to C. cinereus laccase. The modifications are based on the previously unknown three-dimensional structure
                                                                                                                                                                                                                                                                                                                                 New laccase variants with improved stability - have changes based on Coprinus laccase structure, used oxidation, dye transfer inhibition or bleaching
                          phenol polymerisation,
                                                                                                                                                                                                                                                                                                        Claim
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19-DEC-1996;
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575 AA;
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96DK-0001449.
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                          hair dyeing and
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Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laccase; variant; oxidisation; dye transfer inhibition; denim; lignin modification; paper strengthening; phenol hair dye; waste water treatment.
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New variants of Coprinus
                                                   WPI; 1998-495393/42
                                                                                                       Svendsen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVANGLSGKITVNGNQYESVMPAIALSDQQIANVITYTLNSFGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -PGDYVL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILPKNKCIEFNIKGNSGIPITHPVHLHGH----
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and related laccases with increased
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Pred. No. 0.0044;
3; Mismatches 176;
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polymerisation;
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Matches 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oxidation potential - or altered pH optimum, or mediator or oxygen-hydroxide ion pathways, useful for oxidation, for ind dye transfer and in bleaching textiles, especially as detergadditive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Pages 129-131; 147pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 5.1%;
Similarity 20.0%;
05; Conservative 6
                             IVANGLSGKITVNGNQYESVMPAIALSDQQIANVITYTLNSFGN
                                                                 LDL
                                                                                                EQIKAGKATYDSNCAACHQPDGKGVPNAFPPL-----
                                                                                                                                 GLLSGHGGLKARMIEGSHHLHSRSVVKRONETTTVVMDESKLVPLEYPGAACGSKPADLV
                                                                                                                                                                  GILKVEG----
                                                                                                                                                                                                   EPDTYWINAPLTNVPNKTAQALLVYEEDRRPYHPPKGPYRKWSVSEAIIKYWNHKHKHGR
                                                                                                                                                                                                                                                                  RFSV-----EGHKV--TVIAADGVSTKPYQVDAFDILAGQRIDCVVEANQ
                                                                                                                                                                                                                                                                                                 SFHVIGEIFDKVHFEGGKGENHNIQTTLIPAGGAAITEFKVDV---------
                                                                                                                                                                                                                                                                                                                                ILASGNITRQRPVSATINGK-GRFDPDNTPANPDTLYTLKVKRGKRYRLRVINSSGIASF
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ILPKNKCIEFNIKGNSGIPITHPVHLHGH-----
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                                                               TFGLNFATGHWMI-NGIPYESPKIPTLLKILTDEDGVTESDFTKEEH--
                                                                                                                                                              -EENHEIYS-----HKQTDAVYLPEGAPQAIDTQEAPKTPAPANLQ
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Pred. No. 0.0054;
3; Mismatches 17
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   -TWDVVQFGN
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                                                                                                  ----ANSDYLNADHARAAS
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RESULT 34
ABB91862
ID ABB91
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ABB91862 standard; Protein; 541 Ş

ABB91862;

31-MAY-2002 (first entry)

Herbicidally active polypeptide SEQ ID NO

Herbicidal; plant; agriculture; herbicide

Arabidopsis thaliana.

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RESULT 35
AAG90799
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Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
         AAG90799
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                             AAG90799 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; SEQ ID NO 1073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tietjen
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                                                                                                                                           AIDTQEAPKTPAPANLQEQIKAGKATYDSNCAACHQPDGKGVPNAFPPLANSDYLNADHA
                                                                                                                                                                                                                          LKAKVGETVRLFVGNGGPNLTSSFHVIGEIFDKVHFEGGKGENHNIQTTL----IPAGGA
                                                                                                                                                                                                                                                                    --- PKVDKEYYVMQGDFYTKGKYGEQGLQ-PFDMEKAIREDAEYVVFNGSVG-ALTGENA
                                                                                                                                                                                                                                                                                                             GPGGGAEASFTAPGHTSTFSFKAL-QPGLYVYHCAVAPVGMHIANGMYGLILVEPKEGL-
                                                                                                                                                                                                                                                                                                                                                      GVEYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPDS------KMPHNVDFHAAT
                                                                                                                                                               VTVLVTLKAPVKDYFIVASTRFTKPILTTTGILSYQGSKIRP--SHP-----LPIGPTY
                                                                                                                                                                                 AITEFKVDVP-GDYVLVDHAIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLPEGAPQ
                                                                                                                                                                                                                                               VPYPKPDADFTLLVSDWY---KMGHKELQRRLDSSRALPPPDGLLINGASKGLVFTGQH-
                                                                                                                                                                                                                                                                                                                                 GVPQQVILINGQFPGPPIEGVTNNNIVVNVINKLDEPFLITWNGIKQRKMSWQDGVLGTN
                                                                                NRTFVLANGRAMINGKLRYTVNRVSYVNPATPL
                                                                                                 RAASIVANG---LSGKITVNGNOYESVMPAIAL
                                                                                                                                                                                                                                                                                        CP-----IQPKSSWTYHFQLKDQIGTYAY---FASTSMHRASGAFGALNVNQRSVIF
                                                                                                                                                                                                      ----GKIYRFRISNVGISTSINFRIQGHMMTLVEVEG----SHTLQEVYESLDIHVGQS
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                                                                                                                                                                                                                                                                                                                                                                                                                    541 AA;
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                                                                                                                        MKQARTIRLNLTANAA---RPNPQG
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; Pred. No. 0.0068;
49; Mismatches 17
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Best Local
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Tateishi
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                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17;
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotides derived from Coryneform bacteria, mutation point of a gene, measuring expression of a gene expression profile or pattern of a gene and identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from the ean Patent Office.
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                                          EYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNL----TSSFHVIG-----EIFD
                                                                                           LAGMIIVE-DEATDKLDLPREYGVDDIPLVLMDHRFLEDGSLDEEDLP--DLGLLGDTPT
                                                                                                                                        MYGLILVEPKEGLPKVD--KEYYV------MQGDFYTKGKYGEQGLQPFDMEKAIREDA
                                                                                                                                                                                                                                                                                                                                                                                                                             KAAQPKSSTVDAAAKTANADNAASQEHQGE---LPVIDAIVTHAPEVPPPVD--RDHPAK
ANGITNAHFDATTRRVRFRVLNGSNMRFY-----NLAFSDTRTFQVIASDSGLLDEPQD
                                                                                                                                                                                       MKLPAIADGGPHSPIGPGQTWSPTWTVANDAATLWYHPHTHGL-----TGLHAYRG
                                                                                                                                                                                                                                   -KMPHNVDF--HAATGPGGGAEASFTAPGHTSTFSFKALQPGLYVYHCAVAPVGMHIANG
                                                                                                                                                                                                                                                                                     VHFALEAQTGESQILPDVTTKTWGFNGTHLGPTLVVKKGDDVHVDVINNLDEMTTVHWHG
                                                                                                                                                                                                                                                                                                                               VVVKMETVEKVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSNHPDS-----
                                                                                                                                                                                                                                                                                                                                                                              KGAGVLAATVVGAQVLVACSSDDVRGYGGEPRTLPI------PPADLGTREGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        511 AA;
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Senoh A, Ik
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da M, Ozaki A;
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                          N-PSDB;
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                                                                                                    Schroeder H,
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                                                                                                 Zelder O,
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                                                                                                    Haberhauer G;
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                                                                                                                                                                                                                                                                                                                                                                       CC C. glutamicum HA genes (I) can be used in vectors for expression in host CC cells and production of fine chemicals, such as, an organic acid, CC proteinogenic or nonproteinogenic amino acid (preferred), purine or CC primidine base, nucleoside, nucleotide, lipid, saturated or unsaturated fatty acid, diol, carbobydrate, aromatic compound, vitamin, cofactor, CC polyketide or enzyme. The amino acids produced can be lysine, glutamine, CC glutamate, alanine, aspartate, glycine, serine, threonine, methionine, CC tyrosine, valine, leucine, isoleucine, arginine, proline, histidine, CC tyrosine, phenylalanine, or tryptophan. The fine chemical production can be modulated. The presence of (I) or HA proteins encoded by then are CC used for diagnosing the presence or activity of Corynebacterium or CC used as markers for genetically engineered Corynebacterium or CC used as markers for genetically engineered Corynebacterium or CC used as markers for genetically engineered Corynebacterium or CC different control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
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                                                            132
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                                                                                                                                                                                                                                                                           Similarity
   NLDEMTTVHWHGMKLPAIADGGPHSPIGPGQTWSPTWTVANDAATLWYHPHTHGL-----
                                                                                                                                                                               PPVD--RDHPAKVVVKMETVEKVMRLADGVEYQFWTFGGQVFGQMIRVREGDTIEVQFSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ť
                                                                                                                     PPADLGTREGSSVHFALEAQTGESQILPDVTTKTWGFNGTHLGPTLVVKKGDDVHVDVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                environmental conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 373-374; 712pp;
                                                                                                                                                                                                                                                                                                                                                                       497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF71357 encode the Corynebacterium glutamicum homeostasis ion (HA) proteins given in AAB79023 to AAB79242. The um HA genes (I) can be used in vectors for expression in ho
                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                        5.0%;
                                                            - KMPHNVDF - - HAATGPGGGAEASFTAPGHTSTFSFKALQPGLYVYHC
                                                                                                                                                                                                                                           45:
                                                                                                                                                                                                                                        Score 131; DB
Pred. No. 0.00
45; Mismatches
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                                                                                                                           standard; Protein;
                                                                                                                                                                                                                         KTPAPANLQEQIKAGKATYDSNCAACHQPDGKGVPNAFPPLANSDYLNADHARAA
                                                                                                                                                                                                                                                    GMSDSFQ----LLTITGPSD
                                                                                                                                                                                                                                                                                                                                                                  --DLGLLGDTPTANGITNAHFDATTRRVRFRVLNGSNMRFY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVAPVGMHIANGMYGLILVEPKEGLPKVD--KEYYV-----
                                                                                                                                                                                               NTFSINDLQMDMQRVDVVIDHD-----QPEVWIVTN--
                                                                                                                                                                                                                                                                                AIFRAFNKGALGILKVEGEENHEIYSHKQTDAVYLP-----
                                                                                                                                                                                                                                                                                                          ASDSGLLDEPQDRTTLAIGPGERWEIVVELEP--GEDVTLESVGFEDNYGVPDDEFVPDF
                                                                                                                                                                                                                                                                                                                                    G----EIFDKVHFEGGKGENHNIQTTLIPAGGAAIT-----
                                                                                                                                                                                                                                                                                                                                                                                           PFDMEKAIREDAEYVVFNGSVGALTGENALKAKVGETVRLFVGNGGPNL----TSSFHVI
                                                                                                                                                                                                                                                                                                                                                                                                                        ----TGLHAYRGLAGMIIVE-DEATDKLDLPREYGVDDIPLVLMDHRFLEDGSLDEEDLP
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                                                                                                                                                                                                                                                      -DAAQAPALPGVLVKSTEPDVIDATERTFIM
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Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;

pathway;
promoter;

genetic mapping;

Arabidopsis thaliana protein fragment

SEQ ID NO:

67862

18-OCT-2000

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Arabidopsis t EP1033405-A2.  06-SEP-2000.  25-FEB-1999; 05-MAR-1999; 05-MAR-1999; 07-MAR-1999; 06-APR-1999; 06-APR-1999; 07-APR-1999; 08-APR-1999; 09-APR-1999; 0													
thaliana.  thaliana.  2000EP-0301439.  99US-0123180. 99US-0125788. 99US-0126264. 99US-0126264. 99US-0127462. 99US-0130871. 99US-0131449. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132486. 99US-01332407. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-0134768. 99US-013467. 99US-0139457. 99US-0139457. 99US-0139458. 99US-0139458. 99US-0139453. 99US-0139453. 99US-0139453. 99US-0139453. 99US-0139453. 99US-0139463. 99US-0139463. 99US-0139750. 99US-0139899. 99US-0139899. 99US-0139899. 99US-0139899. 99US-0139899. 99US-0139899. 99US-0139899. 99US-0139899. 99US-0139899.													
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99US-0140823 99US-0141287 99US-0142154 99US-0142154 99US-0142390 99US-0142390 99US-0142390 99US-0142390 99US-0142390 99US-0143624 99US-0144085 99US-0144085 99US-0144332 99US-0144331 99US-0144332 99US-0144332 99US-0144332 99US-0144332 99US-0144332 99US-0144332 99US-0144333 99US-0145086 99US-0145086 99US-0145086 99US-0145218 99US-0145218 99US-0145218 99US-0145218 99US-0145386 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0149723 99US-0149723 99US-0149723 99US-0149723 99US-0149929 99US-0149929 99US-0151066 99US-0151066 99US-0151066 99US-0151303 99US-0151303													

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                                                                                                                                                                                                                          Similarity
                                                                                                                                                           HPD-----SKMPHNVDFHAATGPGGGAEASFTAPGHTSTFSFKAL-QPGLYVYHCAVA 183
                                                                                                                                                                                              AKVVVKME-----TVEKVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSN
               VEGEENHEIYSHKQTDAVYLPEG-----
                                  MEGSHVLQNDYDSLDVHVGQCYGTILTANQEAK----
                                                                    LGRPDG--ILINGKSGKGDGSDAPLFTLKPGKTYRVRICNVGLKTSLNFRIQNHKLKLVE
                                                                                     I-REDAEYVVFNGSVGALTGENA--LKAKVGETVRLFVGNGGPNLTSSFHVIGEIFDKVH 295
                                                                                                                        PVGMHIANGMYGLILVEPKEGLP----KVDKEYYVMQGDFYTKGKYGEQGLQPF-DMEKA 238
                                                                                                                                          NLDEPFLLTWNGIQHRKNCWQDGTPGTMCP---IMPGTNYTYHFQPKDQIGSYFYYPSTA 131
                                                   FEGGKGENHNIQTTLIPAG---GAAIT---EFKVDVPGDYVLVDHAIFRAFNKGALGILK 349
                                                                                                                                                                             ATVVVRAEDPYFHHVWNVTYGTVSPL-
                                                                                                        MHRSAGGFGGLRVNSRLLIPVPYADPEDDYTVLIGDWYTK---SHTQLKKFLDSGRT
                                                                                                                                                                                                                 Conservative
----GKGPASSQLPPGPVGWAWSLNQFRSFRWNLTASAARPNPQGSYHYGKIN
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99US-0153758
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Pred. No. 0.012;
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                                                                                                                                                                             -GVPQQVILINGQFPGPNVNSTSNNNVIINVFN
                                                                                                                                                                                                                               DB 21;
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                                 DYYMVASSRFLKSVITTTGLLR
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                 -APQAIDTQEAPKTPAPAN
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RESULT 38
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                                                                                                                                                                                       Matches
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Best Local (
                                                                                                                                                                                                                                                                               The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                  organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tietjen K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herbicidal; plant; agriculture; herbicide
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                                                                                                                                                                                                                                                                      useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FARB )
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 239 I-REDAEYVVFNGSVGALTGENA--LKAKVGETVRLFVGNGGPNLTSSFHVIGEIFDKVH
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                                                    184 PVGMHIANGMYGLILVEPKEGLP----KVDKEYYVMQGDFYTKGKYGEQGLQPF-DMEKA
                                                                                                        132 HPD-----SKMPHNVDFHAATGPGGGAEASFTAPGHTSTFSFKAL-QPGLYVYHCAVA
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                                                                                                                                                             82 AKVVVKME------TVEKVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQFSN
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                                                                                                                                                                                                     Similarity
                           ---MHRSAGGFGGLRVNSRLLIPVPYADPEDDYTVLIGDWYTK---SHTQLKKFLDSGRT
                                                                                NLDEPFLLTWNGIQHRKNCWQDGTPGTMCP---IMPGTNYTYHFQPKDQIGSYFYYPSTA
                                                                                                                                   ATVVVRAEDPYFHHVWNVTYGTVSPL--GVPQQVILINGQFPGPNVNSTSNNNVIINVFN
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                                                                                                                                                                                       184;
                                                                                                                                                                                                               Length 554;
                                                                                                                                                                                       Indels
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                                                                                                                                                                                       118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences
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  295
                             185
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RESULT 39
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                                              The present invention describes transgenic mice (I) and (II) containing modifications in the factor V gene, where (I) expresses an activated protein C (APC) resistant factor V and (II) lacks the ability to express wild-type factor V. The transgenic animals (I) and (II) are useful for screening compounds with anticoagulant activity. Methods from the present invention, and the transgenic animals, are also useful in providing models for human thrombophilia. These models are useful in providing insight into the basic regulatory mechanisms of blood coagulation and pathogenesis of human thrombosis. In addition, factor V null transgenic mice, especially pregnant females may be used as a model system to test in utero gene replacement therapy protocols. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6066778-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activated protein thrombophilia.
                                                                                                                                                                                                                Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine; factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB03533;
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                                                                                                                                                                                                                                                                                                                                                                              ONMI ) UNIV
                                                                                                                                                                                                                                                    w transgenic mice expressing activated d factor V null transgenic mice useful models for human thrombophilia and as
                                                                                                                                                                                                                                        therapy protocols
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)B; AAA60446.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGRPDG--ILINGKSGKGDGSDAPLFTLKPGKTYRVRICNVGLKTSLNFRIQNHKLKLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEGEENHEIYSHKQTDAVYLPEG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEGGKGENHNIQTTLIPAG----GAAIT----EFKVDVPGDYVLVDHAIFRAFNKGALGILK 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VANGLSGKITVNGNOYESV----MPAIALSDQQIANVITYTLNSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITRTIKLVNTQGKVDGKLRYALN-----
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                                                                                                                                                                                                                Fig
                                       murine factor V,
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C resistant fa
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                                                                                                                                                                                                             English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor V;
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                                     protocols. is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; APC; anticoagulant;
thrombosis; screening;
                                                                                                                                                                                                                                                    protein C resistant factor V for screening anticoagulants, models for testing in utero
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                                       in an example
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RESULT 40
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Best Local S
Matches 70
         The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins an antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention.
                                                                                                                         Disclosure; Page 410; 815pp; English
                                                                                                                                                                                                                                                                                                                                10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                  Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial; infection; vaccine; gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGHSFIYGRRHEDTLTLFPMRGESVT-VTMDNVGTWML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVIWNYAPVIPANMDKIYRSQHLDNFSNQIGKHYKKVIYRQYEEETFTKRTDNPSIK---
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for treating or
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                                                                                                                                                 gonorrheae,
preventing
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Pred. No. 0.
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                                                                                                                                                 useful for the manufacture N. gonorrheae infection -
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                                                                                    proteins and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                    441 VANGLSGKITVNGNQYE--SVMPAIA----LSDQQIANVITYTLNSFGNK 484
                                                                                                                                                                                               323 VDVPGDYVLVDHAIFRAFNK-GALGILKVEGEENHEIYSHKQTDAVYLPEGAPQAIDTQE 381
                                                                                                    394 ---- KGKDTLHKHAIEGFNTMPAKGGRGDLSDDEVKAAVDYMVNOSGGK 438
                                                                                                                                                                                                                                                                                               294 LHIMTAYV-----WGLSNKDGKAPVKKAEPAPAAEPAPSAPAEAAQAASEAKPAAAEPK 347
                                                                                                                                                                                                                                                                                                                                                                                               244 DKGQGIQGLGPNLT------DDVWLWGGTQKSIIETITNGRSSQMPAWGHFLDKDK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                           277 ------GPNLTSSFHVIGEIFDKVHFEGGKGEN-----HNIQTTLIPAGGAAITEFK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 POAKQIAQNIENTYCIQCHGSDAKGSKGFPNLTDSDWLWGGDPDKIHETIEKGRVATMPA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 PVGMHIANGMYGLILVE-----PKEGLPKVDKEYYVMQGD-----FYTKGK----- 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 WGPALGEEG-----VKDVAHYVMSLSKPKGQYDEERAARGQALFSGPPANCFTCHG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 ----YGEQGLQPFDMEKAIREDAEYVV-FNGSVGALTGENALKAKV---GETVRLFVGNG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439 AA;
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OM protein -, nucleic search, using frame_plus_p2n model 92: September 5, 2003, 05:17:53 ; Search time 407 Seconds (without alignments) 3329.528 Million cell updates/sec

Title: Perfect score: US-10-088-045-2 2626

MSKPTLIKTTLICALSALML... ....NKGGQLSADDVAKAKKTKPN 502

Scoring table: Xgapop 10.0, Ygapop 10.0, Fgapop 6.0, Delop 6.0, BLOSUM62 . . . Xgapext Ygapext Fgapext Delext

Total number of hits satisfying chosen parameters:

5105512

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2552756 seqs, 1349719017 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10 Listing first 45 summaries 100%

Command line parameters:

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-Q-/Ggn2_1/USPTO_Spool/US10088045/runat_04092003_083141_3908/app_query.fasta_1.647
-DB=N_Geneseq_19Jun03_-QFMT=fastap_-SUFFIX=ring_-MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits_-START=1 -END=-1 -MATRIX=blosum62 -TRANS=hunan40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct_-THR_MAX=100 -THR_MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=pto_-NORM=ext_-HEAPSIZE=500_-MINLEN=0 -MAXLEN=200000000
-MODE=LOCAL -OUTFMT=pto_-NORM=ext_-HEAPSIZE=500_-MINLEN=0 -MAXLEN=200000000
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-DEV_TIMEOUT=120_-WARN_TIMEOUT=30_-THREADS=1_-XGAPDF=10_-XGAPEXT=0.5_-FGAPOP=6
-PGAPEXT=7_-YGAPOP=10_-YGAPEXT=0.5_-DELOP=6_-DELEXT=7 -MODEL=frame+ p2n.model -DEV=xlh

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Database : N_Geneseq_19Jun03:*
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| SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT: *
| SIDS1/gcgdata/geneseq/geneseq/geneseqn-embl/NA2001B.DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-em

/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

## Result ŏ 1388 1346.5 158.5 158.5 152.5 152.5 152.5 152.5 152.5 146.5 141 140.5 140.5 140.5 136.5 Score 1034 Match 2007 4403765 4411529 5187 1125 349980 1437668 349980 837096 Length 309400 349980 37337 12893 1404 342 1437 1479 4830 4830 2064 1437 7919 1533 B Ħ AAH68534 ABZ13870 AAA68115 AAI99682 AAX57912 ABT14589 AAQ48234 ABA96893 AAC83154 AAQ14178 AAZ53033 AAQ36687 AAF21608 AAF26419 AAZ53037 AAA81536 ABZ38597 AAH68245 AAH68527 AAC83156 ABA96894 AAZ53034 AAS5951 AAA81490 Description Gene encoding asco Gluconobacter oxyd DNA encoding Gluco N. meningitidis pa M catarrhalis MCAl Nucleotide sequenc Nucleotide sequenc Genomic fragment # Rhizoctonia solani R. solani laccase Laccase gene RSlac C glutamicum codin Corynebacterium gl A.altocetigenes me Ascorbate oxidase Pseudomonas aerugi ADH complex struct G. oxydans D-sorbi Mycobacterium tube Sorbitol dehydroge Cytochrome C gene. Gluconobacter oxyd Neisseria gonorrhe Sequence encoding Neisseria meningit Neisseria meningit Neisseria meningit N. meningitidis B Neisseria meningit N. meningitidis pa N. gonorrhoeae nuc Propionibacterium Neisseria meningit Neisseria gonorrhe Neisseria meningit Eucalyptus grandis rabidopsis thalia 2-keto-D-gluconate glutamicum codin glutamicum codin glutamicum codin meningitidis gonorrhoeae

ALIGNMENTS

RESULT 1 AAF55657 CDS Moraxella catarrhalis. AAF55657; AAF55657 standard; DNA; 1506 BP. Nucleotide sequence of a BASB109 polypeptide. 11-JUN-2001 (first entry): /*tag= Location/Qualifiers

BASB109; bacterial infection; vaccine; genetic immunisation; ss.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel BASB109 polypeptides of Moraxella catarrhalis useful for diagnostic, prophylactic and therapeutic purposes against microbial diseases, preferably bacterial infections
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                                                            HisLysGlnThrAspAlaValTyrLeuProGluGlyAlaProGlnAlaIleAspThrGln
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                                            CACAAACAAACAGACGCTGTCTATCTGCCAGAGGGTGCCCCACAAGCAATTGATACCCAA
                                                                                                  AACAAAGGGGCATTGGGCATACTTAAGGTGGAAGGTGAAGAAATCATGAGATTTATTCA
                                                                                                                  AsnLysGlyAlaLeuGlyIleLeuLysValGluGlyGluGluAsnHisGluIleTyrSer
                                                                                                                                                                         PheLysValAspValProGlyAspTyrValLeuValAspHisAlaIlePheArgAlaPhe
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                                                  The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets comprises Moraxella catarrhalis nucl
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The present invention describes the full length genome of CC Neisseria meningitidis B (NMB). The sequences in AAF21613 represent fragments of the NMB genomic sequence, as the CC sequence was too long to go in a record on its own it was split into 8 csequences which overlap each other at the beginning and end of each compared to go in a record on its own it was split into 8 csequences which overlap each other at the beginning and end of each compared to go in a record on its own it was split into 8 csequence by 49980 by (i.e. the last 49980 bp of AAF21607 are repeated at the beginning of AAF21607, the last 49980 bp of AAF21544 is repeated at the beginning of AAF21608, and so on). AAF21545 to AAF21598 encode the CC Neisseria proteins given in AAB58550 to AAB58593, and AAF21598 to of CC AAF21606 represent PCR primers which are used in the exemplification of CC the present invention. The NMB genome and fragments from it have cantibacterial activity, and can be used in vaccines and gene therapy. CC Neisseria mucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection CC proteins can be used in compositions for treating or preventing the computers. Computers, computer memory, computer storage medium or computer CC databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more offercive in vaccines than the outer membrane norteins currently are
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                                                                          effective in vaccines than the outer membrane proteins currently
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Sequence 349980 BP; 87189 A; 93501 C; 84627 <u>ი</u> 84663 T; 0 other;

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Percent Similarity:
Best Local Similarity:
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Masignani V, Galeott
Rappuoli R, Pizza M;
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30-APR-1999;
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 80 HisProAlaLysValValValLysMetGluThrValGluLysValMetArgLeuAlaAsp
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CC proteins from Neisseria genomic sequences. AAA81431 to AAA81244
CC represent specifically claimed Neisseria meningitidis genomic DNA
CC sequences; AAA81260 to AAA81303 and AAB25620 to AAA81254
CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to
CC AAA81259 and AAA81304 to AAA81331 represent PCR primers used in the
CC isolation of Neisseria meningitidis DNA sequences; and AAA81254 to
CC AAA81452 represent Neisseria meningitidis DNA sequences; and AAA81224 to
CC CAAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
CC sequences, which are all used in the exemplification of the present
CC invention. The nucleic acid sequences, protein sequences, and antibodies
CC degainst them, can be used in the manufacture of a composition. The
CC medicament) for treating, preventing or diagnosing infection due to
CC medicament) for treating, preventing or diagnosing infection due to
CC medicament) for treating, preventing or diagnosing infection due to
CC medicament of vaccines against Meningococcus B; against all serotypes;
CC and/or against all pathogenic Neissariae. Identified proteins could
CC be components of vaccines against Meningococcus B; against all serotypes;
CC from the bacterium will also facilitate production of biological probes,
CC meningococcus B vaccines have failed mainly due to make efficacious
CC meningococcus B vaccines have failed mainly due to antigen tolerance.
CC Multivalent vaccines have also been tried but none have successfully
CC overcome antigenic variability. The provision of further, complete
CC exposed proteins that may be presumed targets for the immune system and
CC which are not antigenically variable or at least more conserved than
CC other more variable regions.
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227065 C; 205215 G; 197280 T; 2 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins an antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New protein from Neisseria gonorrheae, useful for the manufacture medicament for treating or preventing N. gonorrheae infection
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             TCCAACAATCCTTCTACCGTTCCGCACAACGTCGACTTCCACGCCCAACCGGTCAG
                                                                                GlyGlnValProGlyGlnMetIleArgValArgGluGlyAspThrIleGluValGlnPhe
                                                                                                                                                                                 CCCGAAGTACCTCCCGCAATCGACCGCCGACTATCCTGCCAAAGTACGCGTAAAAATGGAA
                                                                                                                                                                                                  ProGluValProProProProAlAspArgAspHisProAlaLysValValValLysMetGlu
                                                                                                                                                                                                                                                           AlaAlaSerGlnGluHisGlnGlyGluLeuProValIleAspAlaIleValThrHisAla
                                                                                                                                                                                                                                                                                                                                                           ATGATTGCTTCCTTATTCGCATTGGCCGCCTGCGGC--
                                SerAsnHisProAspSerLysMetProHisAsnValAspPheHisAlaAlaThrGlyPro
                                                                                                                                              ThrValGluLysValMetArgLeuAlaAspGlyValGluTyrGlnPheTrpThrPheGly 109
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KW Neisse
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composition can be used as a medicament for in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                                                                                     proteins from Neisseria genomic sequences. AAA8145 to AAA82114 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA8120 to AAA8130 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences, and AAA81322 to AAA81452 represent Neisseria meningitidis MRB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleotide sequences of Neisseria meningitidis which used in the diagnosis and treatment of N. meningitidis infections, for example, N.gonorrhoea -
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Ratti G, Scarselli
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Sequence 7919 BP; 2282 A; 1729 Ç 1972 G; 1936 T; 0 other;

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Best Local Similarity:
                                            US-10-088-045-2 (1-502) x AAA81536
                                                                               Query Match:
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            GluLeuProValI1eAspAlaI1eValThrHisAlaProGluValProProProValAsp
GAACTGCCCGTTATCGATGCGGTTACCACCCACGCTCCCGAAGTGCCTCCTGCAATCGAC
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CGCGACTACCCCGCCAAAGTCCGCGTAAAAAATGGAAAACCGTCGAAAAAAACCATGACCATG

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ProHisAsnValAspPheHisAlaAlaThrGlyProGlyGlyGlyAlaGluAlaSerPhe 157 CGCGTACGCGAAGGCGATACGGTTGAAGTGGAATTTTCCAACAATCCTTCTTCTACCGTT ArgValArgGluGlyAspThrIleGluValGlnPheSerAsnHisProAspSerLysMet 137 GAAGACGGTGTGGAATACCGCTACTGGACATTTGACGGCGACGTTCCGGGCCCGTATGATC AlaAspGlyValGluTyrGlnPheTrpThrPheGlyGlyGlnValProGlyGlnMetIle

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ThrAlaProGlyHisThrSerThrPheSerPheLysAlaLeuGlnProGlyLeuTyrVal 177

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11-SEP-2000;

11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunizing pneumonia,
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P-PSDB; AAO17561.
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                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide and polynucleotides useful as vaccine g a host e.g. humans against disease e.g. otitis mu, caused by infection of the bacteria
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     Sequences AAS59506-AAS59804 represent DNA molecules encoding Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and onverved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the protein
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02-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris -
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18574

CGTGGCAATCCGGAAGGTGGCGGCTGCCAAGCCCTCGACCTGGCCAGCGCCCAGGGCGGT 18633

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Alignment Scores: Pred. No.:
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09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
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31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
                                                           AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54576 and AAZ54576 and AAZ54716 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, annibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention
                                Sequence
                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis; Neisseria gonorrheae; antigenic; diagnosis; immunogenic; infection;
                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                      vaccines
                                                                                                                                                                                                                                              Novel Neisserial polypeptides
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Tettelin H,
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   Pizza M, Rappuoli R,
   Venter JC;
                                                       used
                                 B₽;
                                                                                                                                                                                                                                  diagnostics
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98US-0099062.
98US-0103749.
98US-0103794.
98US-0103796.
99US-0121528.
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98US-0094869
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                                                      protocols
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Length:
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Ratti
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Scalato E,
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                       07-MAR-2003
                                                                                                                                                                                                                                                                                                                                                         ABZ39100;
                                                                           Disclosure; Page 392; 815pp;
                                                                                            New protein from Neisseria gonorrheae, medicament for treating or preventing !
                                                                                                                                                                                                                  12-FEB-2002;
                                                                                                                                                                                                                                                         WO200279243-A2
                                                                                                                                                                                                                                                                           Neisseria gonorrhoeae.
                                                                                                                                                                                                                                                                                                Antibacterial;
                                                                                                                                                                                                                                                                                                                  N. gonorrhoeae nucleotide sequence
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                                                                                                                                                                                              12-FEB-2001; 2001GB-0003424
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                                                                                                                                                                          (CHIR-)
                                                                                                                          2003-058415/05.
DB; ABP78130.
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                                                                                                                                                                                                                                                                                                                                                                            standard;
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9.03%
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                               gene therapy;
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                                                                                              N. gonorrheae infection -
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The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the mucleic acid molecules encoding the proteins antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid

and

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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                 02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
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                                            (CHIR )
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31-JUL-1998;
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Fraser C,
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                                            CHIRON CORP.
INST GENOMIC
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; infection; meningitis; septicaemia;
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Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
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Tettelin
                                         Neisseria meningitidis ORF 007 partial DNA sequence SEQ ID NO:45
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09-OCT-1998;
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                          CTGCACAGCATGGTCAAAGGCATCAACGGTACAATCAAAGTCAACGGCAAAACCTACAAC
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The present invention describes methods of obtaining immunogenic CC proteins from Neisseria genomic sequences. AAAB1453 to AAAB2144 CC represent.specifically claimed Neisseria meningitidis genomic DNA CC sequences; AAAB1260 to AAAB1303 and AAB25620 to AAB2563 represent CC Neisseria DNA sequences and their corresponding proteins; AAAB1254 to CAAAB1259 and AAAB1304 to AAAB1321 represent PCR primers used in the CC isolation of Neisseria meningitidis DNA sequences; and AAAB1322 to AAAB1452 represent Neisseria meningitidis Men Bolynucleotide ORF CC sequences, which are all used in the exemplification of the present CC invention. The nucleic acid sequences, protein sequences, and antibodies composition can be used in the manufacture of a composition. The CC spainst them, can be used in the manufacture of a composition can be used as a medicament (or in the manufacture of a composition can be used as a medicament of in the manufacture of a composition can be used as a medicament of in the manufacture of a composition can be used as a medicament of a gainst the components of vaccines against Meningococcus B; against all pathogenic Neissariae. Identification of sequences; and/or against all pathogenic Neissariae. Identification of sequences, from the bacterium will also facilitate production of biological probes, CC particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. CC will transpared to a sequences may provide an opportunity to identify secreted or surface ce sequences may provide an opportunity to identify secreted or surface.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 1561-1565; 1760pp; English.
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                                                                                                                                                                                                                                                                                                    US-10-088-045-2 (1-502)
                                                                                                                                                                                                    Percent Similarity:
Best Local Similari
                                                                                                                                                                                                                                                                   Alignment Scores
                                                                                                                                                                                                                                                                                                                                   sequences which overlap each other at the beginning and end of each consequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of AAF21607, the last 49980 bp of AAF21544 is repeated at the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the consistency of AAF21608, and so on). AAF21545 to AAF21588 encode the present proteins given in AAB58550 to AAB58593, and AAF21589 to AAF21608 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. One isserial activity, and can be used in vaccines and gene therapy. One isserial bacteria or as a diagnostic reagent for detection the to Neisserial bacteria or of antibodies which binds to the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria or of antibodies raised to Neisserial bacteria. Computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are considered in a second to the other proteins currently used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes the full length genome of Neisseria meningitidis B (NMB). The sequences in AAF21644 and AAF21607 to AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis B full length frames are used to detect, treat and
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08-OCT-1999;
                                                                                                                                                                                                                                                                                                Sequence 349980
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                                             321 PheLysValAspValProGlyAspTyr---
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C, Mora M,
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Rátti G,
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Scarlato V,
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RESULT 16
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           WPI; 2000-318079/27
                                     Frazer CM, Hickey E, Peterson
Masignani V, Galeotti C, Mora
Rappuoli R, Pizza M;
                                                                                                                                                                                                                                                                                                                                        N. meningitidis B full length genome
                                                                                                                          09-OCT-1998;
30-APR-1999;
                                                                                                                                                                                                                                                                                   antigen; vaccine; diagnosis; infection; antibacterial; identification;
Meningococcus B; MenB; ds.
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                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2000
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                                                                                                                                                                    08-OCT-1999;
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                                                                                                                                                                                                                                                        Neisseria meningitidis.
                                                                                              (CHIR ) CHIRON CORP.
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                                                    Tettelin H,
Ratti G, S
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                                                    H, Venter
Scarselli
                                                                                                                                                                                                                                                                                                               genome; immunogenic;
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                                                    Scarlato V;
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Isolated nucleotide sequences of Neisseria meningitidis which used in the diagnosis and treatment of N. meningitidis infectiother Neisserial infections, for example, N.gonorrhoea infection can be and

Claim 7; Page 866-1272; 1760pp; English.

Neisseria DNA sequences and their corresponding proteins; ApaB1254 to AAAB1259 and AAAB1304 to AAAB131 represent PCR primers used in the cisotration of Neisseria meningitidis DNA sequences; and AAAB1322 to AAAB1452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The medicament for treating, preventing or diagnosing infection due to medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious williant also been tried but to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences, AAA81260 to AAA81303 and AAB25620 to AAB25663 represent The present invention describes methods of obtaining more variable regions g immunogenic to AAA82414

Sequence 1437668 BP; 344338 A; 353206 C; 385074 G; 355045 T; 5 other

Ş 밁 Ś 밁 á Ś 밁 S 밁 밁 밁 á 밁 Ś Percent Similarity: Best Local Similarity: US-10-088-045-2 (1-502) x AAA81490 (1-1437668) Query Match: Alignment Scores: ŏ. AAAGTGTACGAATCCAACTGCGTCGCCTGCCACGGCAAAAAGGGCGAAGGCCGCGGAACC 748041 GlnGluAlaProLysThrProAlaProAlaAsnLeuGlnGluGlnIleLysAlaGlyLys 399 CTGATTTTTGTTAATCCACTATACTACTGATTCGGCAAAAAAATCTTTCACCCGCTACGC 748233 TACGGCGTTGCCTCGCCTTG-CCGTACTATTTGTACTGTCTGCGGCTTCGTCGCCTTATC 7482 GGACAACAACATCAAGTGCAA-------CCTTATAGTGGATTAAATTTAAACCAG TyrLeuProGlu---GlyGluAsnHisAsnIleGlnThrThrLeuIleProAlaGlyGlyAlaAlaIleThrGlu AlaThrTyrAspSerAsnCysAlaAlaCysHisGlnProAspGlyLysGlyValProAsn 419 AGCATCATGACAAAA-----ValGluGlyGluGluAsnHisGluIleTyrSerHisLysGlnThr-----AspAlaVal 367 ValLeuValAspHisAlaIlePheArgAlaPheAsnLysGlyAlaLeuGlyIleLeuLys PheLysValAspValProGlyAspTyr----------AAAATCAACAACAAGGTTTCAAACATGAAGGAAACACCAATGAACACAACC 748182 2.18e-06 222.00 43.44% 28.96% 8.45% Length:
Matches:
Conservative:
Mismatches: Gaps: Indels: -GlyAlaProGlnAlaIleAspThr 379 1437668 64 32 84 42 GGGCAA 748101 349 329 748352

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AlaPheProProLeuAlaAsnSerAspTyrLeuAsnAlaAspHisAlaArgAlaAlaSer 439

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RESULT 17
AAZ53034
ID AAZ53
XX AAZ53
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                                                                                                                                                                                                                                          Fraser C, Ga.
Petersen J,
AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to
                                                                                                                                                                                                                                                                                                                                            09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
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31-JUL-1998;
02-SEP-1998;
                                                                                                                                      Claim
                                                                                                                                                             vaccines
                                                                                                                                                                       Novel Neisserial polypeptides
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, Pizza M, Rappuoli R,
, Venter JC;
                                                                                                                                                         diagnostics
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RESULT 18
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                                                             02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
                                                                                                                                                                                                                                      Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
                   (CHIR )
                                                                                                                    01-MAY-1998;
31-JUL-1998;
                                                                                                                                                                                                                     Neisseria meningitidis.
                                                                                                                                                      30-APR-1999;
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98US-0103794.
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99US-0121528.
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98US-0099062.
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RESULT 19
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Best Local Similarity:
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   Хeу
                                    Unidentified
                                                               2,5-diketo-D-gluconate;
                                                                   Cell membrane bound; 2-keto-D-gluconate 2,5-diketo-D-gluconate; gene; ds.
                                                                                                                2-keto-D-gluconate dehydrogenase coding
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                                                                                                                                                  16-JUL-2002
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Tettelin H,
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                               tTyrGly-----
                                                                 TGCCGACGGCATCGGGCCTTACAGCGAAGCTGAATTTTCGCAGGCGGTACGCCATGGCGT
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31-JUL-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                     AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54576 and AAZ54576 and AAZ54710. The PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the
                                                                                                                                                                                                                                   presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                     Sequence 342
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               Purified cytochrome c-553 (CO) was isolation from Gluconobacter suboxydans IFO 1258 and partially sequenced. From this information, 32P-labelled oligonuclectide probes were constructed and used to screen a bank of genomic EcoRI fragments from IFO 1258 in vector 13mp19RF. A plasmid which hybridised strongly contained an approx. 1.5kb fragment which was sequenced. This sequence lacks the N-terminal region which was located from the same source and used to construct a complete gene. The probes used are based on the N-terminal amino acid sequence (KGWGNNA) of peptide I which was isolated following limited hydrolysis of c-553 (CO) using arginyl endopeptidase. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                    Plasmid contg. gene for cytochrome C-553 (CO) - and transformed cells useful in high productivity oxidative fermentation, e.g. ethanol to acetic acid
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                                                                                                The sequence is that of a cytochrome C gene from Gluconobacter suboxydans IFO 12528 which may be used to give improved prodn. cytochrome C by oxidative fermentation.
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Best Local Similarity:
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The invention relates to a sorbitol dehydrogenase (SDH) Gluconobacter oxydans (referred to as Gluconobacter subspecification) and the gene encoding it. The sorbitol d
                                                     Claim 11; Page 10; 18pp; Korean
                                                                                  Sorbitol
                                                                                                                                    Choi US,
                                                                                                                                                                                                                                                                                              Gluconobacter
                                                                                                                                                                                                                                                                                                                                                             Gluconobacter oxydans sorbitol dehydrogenase subunit 2 DNA,
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                                                                                                           WPI; 1999-608154/52
                                                                                                                                                                                         26-FEB-1997;
                                                                                                                                                                                                                                           26-OCT-1998.
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                                                                                                                                                                                                                                                                                                                        coenzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               967 CTGAACAAGGGTGGCCAGGGCAACGCAGGTGCGGAAGTCTATCTGCACAACTGCGCCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 LeuProGluGlyAlaProGlnAlaIleAspThrGlnGluAlaProLysThrProAlaPro
                                                                                                                                                               KOREA
                                                                                                                                                                                                                                                                                                                       dehydrogenase;
PQQ dependent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gly---GlyGlnLeuSerAlaAspAspValAlaLysAlaLysLysThr
                                                                                dehydrogenase of Gluconobacter suboxydans and
                                                                                                                                    Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCACCGGGAACCGTGTCCGCTTCCGATATCCAGAAGCTGCGCACGACG 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCGTCATTACCGACGATCCGACGTCGCTCGCCAATGTCGTAGCCTTCGGT-----GGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCTCCGACCAGGAGATGGCCGATGTCGTGAACTTTATGCGCAAGGGCTGGGGCAACAAC 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprises 3 subunits of 75 kD, 50 kD and 29 kD, utilises coenzyme has a haem group. The present sequence represents DNA encoding the 50 kD subunit (subunit 2) of Gluconobacter oxydans sorbitol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 ValGlyMetHisIleAlaAsnGlyMet----------TyrGly 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity:
                                                                                                                                                                                                                                                                                    LysAlaLysValGlyGluThrValArg-LeuPheValGlyAsnGlyGlyProAsnLeuTh
             CGGTGGCATGGCTGACGTGGCCTACAGCACCCAGCACTGGACCGACGACGATCTGCA
                                                                                                                    laspHisalaIle-----PheargalaPheasnLysGlyAlaLeuGly-----
                                                                                                                                                               alleThrGluPheLysValAspValProGlyAspTyrValLeu-------Va
                                                                                                                                                                                                        uGlyGlyLysGlyGluAsnHisAsnIleGlnThrThrLeuIleProAlaGlyGlyAlaAl 317
                                                                                                                                                                                                                               CAAGAGCATCTCCGATCCGGAAGTGGCGCGTGGCGAATACCTC-----GTGAATGGCCC
                                                                                                                                                                                                                                                  rSerSerPheHis-----ValIleGlyGluIlePheAspLysValHisPheGl
                                                                                                                                                                                                                                                                                                                   AA-GCCGGTCGCCCTTCAGAACAAGCAGCCGGACATCTCCTGGCCGATGAACATGCGCTG
                                                                                                                                                                                                                                                                                                                                        GlyAla-----
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                                 rHisLysGlnThrAspAlaVal---Tyr-LeuProGluGlyAlaProGlnAlaIleAspT
                                                                                                CGACAACTGGATTGCTCCCAGCCTGCGTAGCAATAGCGACACGGGTCTGGGTCGCTGGTC
                                                                                                                                           GCAGGTCAAGGGCTATACGGCCAAGGACGGCAACGCTTACCTCTCCGGTGGCGCACCGAT
                                                                                                                                                                                     AGGCCATTGTGGCGAGTGTCATACG----
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                                                                            ----IleLeuLysValGluGlyGluGluAsnHisGluIleTyrSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
This invention relates to an isolated membrane-bound sorbitol dehydrogenase (SDH) from Gluconobacter oxydans. The invention polynucleotides (AAC83153 - AAC83154) encoding the 3 subunits
                                           Claim
                                                                                                           P-PSDB;
                                                                                                                      WPI;
                                                                                                                                         Choi E,
                                                                                                                                                                         (CHOI/)
                                                                                                                                                                                                         23-APR-1999;
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Novel membrane-bound sorbitol dehydrogenase nucleic acid molecule isolated from Gluconobacter suboxydans useful for the fermentative production of 2-keto-L-gulonic acid and L-sorbose from D-sorbitol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gluconobacter oxydans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sorbitol dehydrogenase; SDH; Gluconobacter oxydans; D-sorbitol; L-sorbose production; 2-keto-L-gulonic acid; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sorbitol dehydrogenase subunit 2 DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC83154 standard;
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6; Fig 8; 96pp; English.
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RHEE
                                                                                                                                     AAB35988.
                                                                                                                                                                                                    Rhee S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AAB35987 - AAB35989). Also included in the invention are two polymucleotide sequences AAC83156 and AAC83157 which contain the subunit coding regions. The sorbitol dehydrogenase polymucleotide sequences are useful for producing L-sorbose from D-sorbitol and for increasing the production of 2-keto-L-gulonic acid by transforming a host cell, especially Gluconobacter with the DNA and selecting the transformed host cell. Note: An additional 66 DNA sequences (fragments of the SDH subunit genes) encoding fragments of SDH are specifically claimed, however these sequences are not given separately in the specification but are included in sequences AAC83156 and AAC83157.
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DNA encoding polypeptide with ascorbate oxidase activity from Cucuria moschata, used to produce recombinant enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence was obtd. from a clone isolated from from RNA extracted from the fruit of C. moschata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
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                                                                                                                                                                                                                                                                                       568
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 118
                            325
                                                        751
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                      ValProGlyAspTyrVal-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HisThrSerThrPheSerPheLysAlaLeuGlnProGlyLeuTyrValTyrHisCysAla 181
GCCGACGGTAATTACGTCCAACCATTTTACACCTCCGACATCGACATTTATTCCGGCGAG
                                                                                                               CCCAAAAAGACTTACAGGATAAGAATT---
                                                                                                                                          GlyGluIlePheAspLysValHisPheGluGlyGlyLysGlyGluAsnHisAsnIleGln
                                                                                                                                                                                                                                                        ---SerValGlyAlaLeuThrGlyGluAsn----AlaLeuLysAlaLysValGlyGlu
                                                                                                                                                                                                                                                                                    CCTATTCGTTGGATCGGTGAGCCTCAAACCATACTCTTAAATGGAAGAGGGCAGTTCGAT
                                                                                                                                                                                                                                                                                                            AlaIleArg-----GluAspAlaGluTyrValValPheAsnGly-------
                                                                                                                                                                                                                                                                                                                                                                       PheTyrThrLysGlyLysTyrGlyGluGln---GlyLeuGlnProPheAspMetGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                               LysGluGlyLeuProLys------ValAspLysGluTyrTyrValMetGlnGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---GGTCATTTGGGAATGCAAAGATCGGCAGGGTTATATGGATCTTTGATAGTGGATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValAlaProValGlyMetHisIleAlaAsnGlyMetTyrGlyLeuIleLeuValGluPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAACGTTCTTCTACAATTTCACTGTTGATAACCCTGGGACGTTTTTCTATCAT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGAĞĞAACTCCGTGGGCTGATĞĞCACTĞCTTCCATCTCCCAGTGTĞCTATTAACCCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProGly-----
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                                                     ACCACTGCTTTAGCGGCCCTCAACTTTGCCATTGGGAATCACCCATTGTTGGTGGTAGAA
                                                                                ThrThrLeuIleProAlaGlyGlyAlaAlaIleThrGlu-----PheLysValAsp
                                                                                                                                                                                               ThrValArgLeuPheValGlyAsnGlyGlyProAsnLeuThrSerSerPheHisValIle
                                                                                                                                                                                                                             TGTTCAATTGCAGCTAAATACGACAGTAATTTAGAGCCATGTAAACTAAAAGGAAGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATAAGCTCCACACTGAAGGTGTCGTCATTCAC-----TGGCATGGAATTTTGCAA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asn----
                                                                                                                                                                                                                                                                                                                                           TGGTGCCATCAAAGTATTCATAAACAAGAAGTTGGTCTTAGC------TCCAAA
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                         -----LeuValAspHisAlaIlePheArgAlaPhe
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The DNA can be
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                                                                                             US-10-088-045-2 (1-502) x ABA96894 (1-4830)
                                                                                                                                                                                                                                                         Gluconobacter oxydans (referred to as Gluconobacter suboxydans in the specification) and the gene encoding it. The sorbitol dehydrogenase comprises 3 subunits of 75 kD, 50 kD and 29 kD, utilises coenzyme PV has a haem group. The present sequence represents DNA encoding all subunits of the Gluconobacter oxydans sorbitol dehydrogenase of
                                                                                                                                                                                                                      Sequence 4830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gluconobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gluconobacter oxydans sorbitol
                                                                                                                                                                                                                                               the invention
                                                                                                                                                                                                                                                                                                                       The invention relates to a sorbitol dehydrogenase (SDH) from
                                                                                                                                                                                                                                                                                                                                               Example; Page 14-18; 18pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                         Sorbitol
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-608154/52
                                                                                                                                                                                                                                                                                                                                                                                                                         Choi US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KR98069057-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sorbitol dehydrogenase; SDH; subunıt 1; subunıt 2; subunıt 3; Gluconobacter suboxydans; coenzyme PQQ dependent; haem group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA96894;
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                                                                                                                                                                                    No.:
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CCTAACGGCGAATTCCTC--
                                               dehydrogenase of Gluconobacter suboxydans and gene thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATTCCGTCTCGAAA---TTACCCÁCTTCTCCGCCGCGGAAÁCCCCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCTACTCCGTCCTCATCACCACCGACCAAAACCCCATCGGAGAACTACTGGGTCTCCGTC
                     ProValIleAspAlaIleValThrHisAlaProGluValPro----
                                                                      LysThrAlaAsn-----AlaAspAsnAlaAlaSerGlnGluHisGlnGlyGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluGlyAlaProGlnAlaIleAspThrGlnGluAlaProLysThrProAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry
                                                                                                                                                                                                                      BP; 1071 A; 1424
                                                                                                                                                                                                                                                                                                                                                                                                                       SG,
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                                                                                                                                                                                                                      C; 1350 G; 985 T; 0 other;
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                                                                                                                                                                       Length:
Matches:
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- AACGTCCCTCAGGGTTCGGTTGCGCCT
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3399 AA-GCCGGTCGCCCTTCAGAACAAGCAGCCGGACATCTCCTGGCCGATGAACATGCGCTG
               TGAAGACGACATTGCCGAGTTCCTGAAG---AGCGGCCGTATCGACCATTCTGCCGTCTT 3784
                                                                                                                       lAspHisAlaIle-----PheArgAlaPheAsnLysGlyAlaLeuGly-----
                                                                                                                                                                                               alleThrGluPheLysValAspValProGlyAspTyrValLeu----
                                                                                       CGACAACTGGATTGCTCCCAGCCTGCGTAGCAATAGCGACACGGGTCTGGGTCGCTGGTC
                                                                                                                                                                                                                                                                                                            CAAGAGCATCTCCGATCCGGAAGTGGCGCGTGGCGAATACCTC-----GTGAATGGCCC
                                                                                                                                                                 GCAGGTCAAGGGCTATACGGCCAAGGACĠĠĊAACGCTTACĊŤĊTCCGGTGGCGCACCGAT
                                                                                                                                                                                                                                         AGGCCATTGTGGCGAGTGTCATACG--
                                                                                                                                                                                                                                                                      uGlyGlyLysGlyGluAsnHisAsnIleGlnThrThrLeuIleProAlaGlyGlyAlaAl 317
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                                                                                                                                                                                                                                                                                                                                                      rSerSerPheHis----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCCGTAAGGGTÄTCCGCAAGGÄCGGCGCGCGACGGTTTATCCGGCCCATGCCGTATCCTGAG 3338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetGluLysAlaIleArgGluAsp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCGAAGAT----- TTCACGAAGGCG---- 3278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCAACATCACGCCTGACCCGAAATACGGTATCGGCAAC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACGGCCAGCCTTTTGCTGGTGGTCTGGAGATCAAGAGCCCGATCGGCACGATCTACTCC 3212
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                                                 ------IleLeuLysValGluGlyGluGluAsnHisGluIleTyrSe
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                          Novel membrane-bound sorbitol dehydrogenase nucleic acid molecule isolated from Gluconobacter suboxydans useful for the fermentative production of 2-keto-L-gulonic acid and L-sorbose from D-sorbitol
                                                                                                                                                                                              (CHOI/)
(RHEE/)
(LEEE/)
                                                                                                  WPI; 2000-687351/67.
P-PSDB; AAB35987, AAB35988.
                                                                                                                                                           Choi E,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sorbitol dehydrogenase; SDH; Gluconobacter oxydans; D-sorbitol; L-sorbose production; 2-keto-L-gulonic acid; ds.
                                                                                                                                                                                                                                                                      23-APR-1999;
                                                                                                                                                                                                                                                                                                        23-APR-1999;
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                                                                                                                                                                                              CHOI E.
RHEE S.
LEE E.
                                                                                                                                                         Rhee S,
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                                                                                                                                                           Lee
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Claim 16; Fig 8; 96pp; English

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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to an isolated membrane-bound sorbitol dehydrogenase (SDH) from Gluconobacter oxydans. The invention includes polymucleotides (AAC83153 - AAC83154) encoding the 3 subunits of SDH (AAB35987 - AAB35989). Also included in the invention are two polymucleotide sequences AAC83156 and AAC83157 which contain the subunit coding regions. The sorbitol dehydrogenase polymucleotide sequences are useful for producing L-sorbose from D-sorbitol and for increasing the production of 2-keto-L-gulonic acid by transforming a host cell, especially Gluconobacter with the DNA and selecting the transformed host cell. Note: An additional 66 DNA sequences (fragments of the SDH subunit genes) encoding fragments of SDH are specifically claimed, however these sequences are not given separately in the specification but are included in sequences AAC83156 and AAC83157.
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                                                             CTCGAAGAT----TTCACGAAGGCG--
                                                                                               MetGlnGlyAspPheTyrThrLysGlyLysTyrGlyGluGlnGlyLeuGlnProPheAsp
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Best Local Similarity:
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                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                         This invention describes novel DNA sequences (I) that encode iron or CC heavy metal transporters (II). The invention also describes (I) a CC recombinant expression vector (III) containing (I); (2) prokaryotic or CC eukaryotic cells (III) transformed with (I) or (III); (3) production of CC (II) by culturing (III); (4) (partial) expression products (IV) of (I) CC and synthetic proteins or peptides with the same sequences; (5) CC antibodies (Ab) specific for (IV); (6) hybridoma cells that produce CC monoclonal Ab; and (7) transgenic plants that contain (III). The iron or CC heavy metal transporters encoded by (I) transport heavy metal ions across CC cell walls and regulate homeostasis of trace elements. (I), and their CC fragments are useful for: (1) expression of (II); (2) as probes and CC primers for detection, isolation and amplification of full length cDNA CC sequences; and (3) producing transgenic plants. (III) are used to promote CC growth, development and yield of plants, particularly Leguminosae, CC cells that express the iron or heavy metals injurious to CC plants. They also improve homeostasis of iron and trace elements. Host CC cells that express the iron or heavy metal transporters take up heavy CC metals which improves soil quality and protect plants against pollutants CC from the soil improves soil quality and protect plants against pollutants
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                                           AlaLeuGlyIleLeuLysValGluGlyGluGluAsnHisGluIleTyrSerHisLysGln
                                                                                                                             AspValProGlyAspTyrValLeuValAspHisAlaIlePheArgAlaPheAsnLysGly
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was obtained in electronic format directly ov/sequence.html?DocID=6294328B1. P; 758565 A; 1449983 C; 1444602 G; 758379 T	ricting. If the sequence data for this patent did not form part of the professions.	M. tuberculosis and has valuable application in the fields of cuberculosis genetics, epidemiology, patient treatment and epidemic	tirst strain at positions in the complete t correspond to positions that differ in the tuberculosis strains CDC 1551 (AAI99683) and		Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.	Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ -	WPI; 2001-647261/74.	Fleischmann RD, White OR, Fraser CM, Venter JC;	(GENO-) INST GENOMIC RES.	24-JUN-1998; 98US-0103840.	24-JUN-1998; 98US-0103840.	25-SEP-2001.	US6294328-B1.	Mycobacterium tuberculosis.	Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds.	Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.	15-JAN-2002 (first entry)	AAI99682;	SULT 30 (199682/c AA199682 standard; DNA; 4411529 BP.	942894 GGCACCATGGCCAAGTACGACTGGACAATCAACGGGGAACCCTACAGCACGACCAATCCA 942835	o d	6GTCACCTTGGGC 94	uAspAlaAspHisAlaArgAlaAlaSerTleValalalanen 443		404 SerAsnCysAlaAlaCysHisGlnProAsnGlvIvsGlvValDroAsnAlaBhaBroBro	0 10	GlnGluGlnIleLysAlaGlyLysAlaThrTyrAsp 403	ه د	364 ThrAspAlaValTyrLeuProGluGlyAlaProGlnAlaIleAspThrGlnGlnAlaPro

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GCGTTCCGCATCGCGCTGGCCGGGCATTCGATGACGGTCACCCACACCGACGGTTACCCCA 943287
                          ThrSerSerPheHisValIleG|yGluIlePheAspLysValHisPheGluGly-----
                                                        TTTAAGGCCAAGCCTGGCCAGCGAATCCGGATCATCAACAGCGCCGCCGACACC
                                                                                  LeuLysAlaLysValGlyGluThrValArgLeuPheValGlyAsnGlyGlyProAsnLeu
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                                                    Gane group for D-sorbitol dehydrogenase, large-scale production of L-sorbose or 2-precursor for L-ascorbic acid
This sequence encodes
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                                                                                                                                                                    (FUJI ) FUJISAWA
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                          21; Page 60-62;
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                                                                                                                                       Noguchi Y,
                                                                                                                                                                                                                                                                                                                                      acid
                                                                                                                                                                                                                                                                                                                                                    dehydrogenase; L-sorbose; 2-keto-L-gulonic
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the D-sorbitol dehydrogenase of
                        83pp; Japanese
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-gulonic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention. Cells transformed with a vector containing DNA encoding the dehydrogenase can be used to produce L-sorbose or 2-keto-L-gulonic acid as precursor for simple large-scale L-ascorbic acid production.
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erValGlyAlaLeuThrGlyGluAsnAla--
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                                                                                                                                                                                                               tTyrGlyLeuIleLeuValGluProLysGluGlyLeuProLysValAspLysGluTyrTy 213
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                           heAspMetGluLysAlaIleArgGluAsp------
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                                                                                                                                                                                                                                                                                                                                                                                                                                             the invention is also useful for diagnosing and treating a subject (especially an immunocompromised human) that is afflicted with a biofilm-associated disease or disorder, such as: cystic fibrosis; AIDS; middle ear infections; acne; periodontal disease; catheter-associated infections; and medical device-associated infections. The present DNA
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1125 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises a method for identifying a compound capable of modulating biofilm formation by bacteria. The method of the invention is useful for identifying a compound capable of modulating biofilm formation by bacteria or modulating bacterial antibiotic resistance. The method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying compound capable of modulating bacteria/bacterial antibiotic resistance, u biofilm associated disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Whiteley
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(HARD )
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24-OCT-2001;
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lAspLysGluTyrTyrValMetGlnGlyAspPheTyrThrLysGlyLysTyrGlyGluGl
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                                                                                                                                            CACCGGCTACCAGTGGAAGTGGCAGTACAAGTACCTGGG-----
                                                                                                                                                                                                      CACCCTGAT --
                                                        IleAlaAsnGlyMetTyrGlyLeuIleLeuValGluProLysGluGlyLeuPro-LysVa
                                                                                                               LysAlaLeuGlnProGlyLeuTyrValTyrHisCysAlaValAlaProValGlyMetHis
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacteria and purified and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The gene encodes a protein of mol. wt. ca. 44.000. Acetobacter transformed with the sequence can enhance the efficiency of acetic transformetation. The ADH complex can be easily extracted from the bacteria and purified and it can be used for the determination of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 4(1-3); 21pp; Japanese
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P-PSDB; AAR20193.
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eTyrThrLysGlyLysTyrGlyGluGlnGlyLeu------
                                                                                                                                        TGGGGTGAAGCCGGTCGCGCAGCCGGACAAGCAGCCGGACATCTCCTGGCCCCTTGTCCAT
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                                      TTCGCCGAAGGACTTCACGCCGGCGCCAGGCACGGATCCTGAAATCGCACGTGGCGATTA
                                                                                        GCGCTGGCCGCTGGG
                                                                                                                                                                 ProGlyHisThrSerThrPheSerPheLysAlaLeuGlnProGlyLeuTyrValTyrHis
                                                                                                                                                                                          TCCCTCCTTCTCGCGCATGACGAAGGAAGACATGCAGGCGCTGTATGCGTACTTCATGCA
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                                                                                                              CysAlaValAlaProValGlyMetHisIleAlaAsnGlyMetTyrGlyLeuIleLeuVal
                                                                                                                                                                                                                                                                                              CACGAACATCACACCGGACCCGACCTACGGTATCGGTCGCTACACCTTCGCCGAATTCGA
                                                                                                                                                                                                                                                                                                                                                 CCATGGACAGTCGTACGCAGGCGGGCTTGAAATCAAGAGCCCGATCGGTACGATCTACTC
                                                            -GluproLysGluGlyLeuproLysValAspLysGluTyrTyrValMetGlnGlyAspPh
                                                                                                                                                                                                                                                                      -SerLysMetPro----
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             -GlnProPheAspMe
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RESULT 34
AAQ13581
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DT 25-MA
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DT 09-DE
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AC ALCoh
KW alcoh
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ACeto
 Acetobacter altocetigenes.
                                   alcohol dehydrogenase cytochrome c; ss.
                                                                                                                         25-MAR-2003
09-DEC-1991
                                                                                      A.altocetigenes membrane-bound
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                                                                                                                                                                                                                                                                                      TACGGCTGCGGATGTTACCAAGCTGCGCGACACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGCCGCTGGTCCGAGGATGACATCTACACCTTCCTGAAGTCCGGCCGTATCGACCACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGACAACTGGGTCGCGCCGAGCCTGCGCA------ACGATCCTGTCGTTCGTCT 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               laLeuThrGlyGluAsnAlaLeuLysAlaLysValGlyGluThrValArgLeuPheValG
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                                                     complex;
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                                                   carboxylic acid production;
                                                                                      ADH 44kD sub-unit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mixture was used to transform E.coli JM109. Probes were designed based on the N-terminal amino acid sequence of the 72kD subunit of the ADH complex isolated from A. altoacetigenes (see AAQ13582-Q13584). Fragments encoding the 44kD (cytochrome c) ADH subunit were identified using anti-44kD subunit antibodies in a Western blot. The gene was sequenced. Various experiments suggested that the coding sequence is located immediately downstream of the gene encoding the 72kD sub-unit. See also AAQ13580. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from Acetobacter altocetigenes, converting alcohol to acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total DNA was prepared from A.altocetigenes MH-24, digested with PstI and SmaI and ligated to PstI-SmaI cleaved pUC18. The ligation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 23-24 and Fig 4; 36pp; English.
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26-FEB-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for membrane-bound alcohol dehydrogenase complex - Acetobacter altocetigenes, used for prodn. of enzym
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NAKANO
                                                   CysAlaValAlaProValGlyMetHisIleAlaAsnGlyMetTyrGlyLeuIleLeuVal
                                                                                                                      ProGlyHisThrSerThrPheSerPheLysAlaLeuGlnProGlyLeuTyrValTyrHis
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                                                                                                                                                                                                                                                                    ---SerLysMetPro--------HisAsnValAspPheHisAlaAla 146
                                                                                                                                                                                                                                                                                                                                        PheSerAsnHis-----ProAsp----
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                    GCGCTGGCCGCTGGG----
                                                                                      TGGGGTGAAGCCGGTCGCGCAGCCGGACAAGCAGCCGGACATCTCCTGGCCCCTTGTCCAT
                                                                                                                                                            TCCCTCCTTCTCGCGCATGACGAAĞĞAAGACATGCAĞĞCĞCTGTATGCGTACTTCATGCA
                                                                                                                                                                                                                                  CGAAGCCGTGCGATGGTATCCGCAAGGACGGTTCCACGCTGTATCCGGCCATGCCGTA
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                    -CATCTGGCGCATGAT--
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Conservative:
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Ascorbate oxidase from Cucumis sativus
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                                                                                                                                         uSerAlaAspAspValAlaLysAlaLysLysThr 499
                                                                                                                                                                                      nIleAlaAsnValIleThrTyrThrLeuAsnSerPheGlyAsnLysGly---GlyGlnLe
                                                                                                                                                                                                                                      nGlyAsnGlnTyrGluSerVal---MetProAlaIle-----AlaLeuSerAspGlnGl
                                                                                                                                                                                                                                                               GAACCCGACCTCGCTGGTGAACGTGATTGCGCATGGT----
                                                                                                                                                                                                                                                                                                             CGGTGGTGGCCCGCATGTTCCCCGCCGCTGGCAACCCGGTTGTCGTGACCGA
                                                                                                                                                                                                                                                                                                                               pGlyLysGlyValProAsnAlaPheProProLeuAlaAsnSerAspTyrLeuAsnAlaAs
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                                                                                                                   TACGGCTGCGGATGTTACCAAGCTGCGCGACACG
                                                                                                                                                                GATTGCTGATGTGGTCAACTTCATCCGCACCAGCTGGGGCAACAAGGCGCCCCGGCACCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The DNA is derived from Cucumis sativus and can be used large amts. of polypeptide having ascorbate activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 9pp; Japanese
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(NAGS ) NAGASE SANGYO KPL.
                                 202 LysGluGly 204
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AAH66018
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European batent of fice.
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Tateishi
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                                                                                                                                                                                                                                                         Sequence 1533
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03-AUG-2000;
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                                                                                                                                                                                                                AlaGlyGlyAlaAlaIleThr-----
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Claim 3; Page 370-372; 712pp; English
                  nucleosides, nucleotides,
or enzymes -
                        New isolated Corynebacterium glutamicum nucleic acid for production modulation of production of fine chemicals such as amino acids, nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitami
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E-1041378.
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                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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glutamate, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, or tryptophan. The fine chemical production can be modulated. The presence of (I) or HA proteins encoded by then are used for diagnosing the presence or activity of Corynebacterium diphtheriae. (I) can be used to map the C. glutamicum genome or can be used as markers for genetically engineered Corynebacterium or Brevibacterium. The HA proteins encoded by the (I) are used to maintain homeostasis in C. glutamicum or help the microorganism to adapt to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and adaptation (HA) proteins given in AAB79023 to AAB79242. The C. glutamicum HA genes (I) can be used in vectors for expression in host cells and production of fine chemicals, such as, an organic acid, proteinogenic or nonproteinogenic amino acid (preferred), purine or pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated fatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor, polyketide or enzyme. The anino acids produced can be lysine, glutamine, alanine apartters of acids produced can be lysine, glutamine,
different environmental conditions.
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Sequence 1614 BP; 336 A; 421 C; 493 ດ 364 H 0 other;

0.00399 142.00 33.72% 22.86% 5.41%

Length:
Matches:
Conservative:
Mismatches:

1614 · 99 47 178 109 20

Indels:

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211 GluTyrTyrVal--
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                                                  TTGGCGGGGATGATCATTGTGGAA----GATGAAGCAACAGACAAGCTGGATCTGCCACGC
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    CCACCAGCAGATTTAGGTACGCGTGAGGGATCTAGC

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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                   Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
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Query Match: DB:

Percent Similarity: Best Local Similarity:

5.43 142.00 33.72% 22.86% 5.41%

Matches: Conservative: Mismatches: Indels:

349980 99 47 178 109 20

Length:

Alignment Scores:

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Novel polynucleotides der:
mutation point of a gene,
expression profile or pati
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Tateishi
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Senoh A, Ikeda M,
                                                                                                                                        derived from Coryneform bacteria, for identifiene, measuring expression of a gene, analysing pattern of a gene and identifying homologous
                                                                                                                                                                                       S, Hayashi M,
Ozaki A;
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                                                                                                                                          gene
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Disclosure; SEQ ID NO: 7062; 246pp + Sequence Listing; English

mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office. The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. Tare useful for identifying the mutation point of a gene derived from present These മ

Sequence 349980 BP; 79725 A; 90426 Ç 98918 G; 80911 T; 0 other

밁 Ş 밁 Ş 밁 Ś 문 8 뭐 Ş 밁 Ş 밁 Ś á 밁 US-10-088-045-2 (1-502) x AAH68527 101746 TGGTCACCAACGTGGACTGTGGCCAATGATGCAGCCACTTTGTGGTACCACCCGCACACT 101805 101626 101566 101506 101470 101422 101362 173 ProGlyLeuTyrValTyrHisCysAlaValAlaProValGlyMetHisIleAlaAsnGly 84 66 49 29 ATGAAGTTGCCGGCGATTGCTGATGGTGGTCCGCACTCACCGATCGGGCCTGGGCAGACG ---LysMetProHisAsnValAspPhe-----HisAlaAlaThrGlyProGlyGlyGly GACGTCCACGTTGATGTGATAAACAATTTGGATGAAATGACCACTGTGCACTGGCATGGC 101685 ThrIleGluValGlnPheŞerAsnHisProAspSer-----AAGACGTGGGGTTTCAATGGCACTCATTTGGGGCCCGACGTTGGTGGTGAAGAAAGGTGAT GlnPheTrpThrPheGlyGlyGlnValProGlyGlnMetIleArgValArgGluGlyAsp GTGCACTTTGCCCTGGAGGCTCAGACTGGGGAGAGTCAGATTTTGCCGGATGTCACAACG ValValValLysMetGluThrValGluLysValMetArgLeuAlaAspGlyValGluTyr 103 ValThrHisAlaProGluValProProProValAsp-----ArgAspHisProAlaLys TCAGATGATGTGCGTGGTTATGGGGGAGAGCCGCGGACGTTGCCTATT----AsnAlaAlaSerGlnGluHisGlnGlyGlu-----LeuProValIleAspAlaIle AAAAGGGCCCGGGGTGCTGGCAGCAACGGTGGTGGGTGCTGCTGGTGGTGGCGTGTTCC 101421 LysAlaAlaGlnProLysSerSerThrValAspAlaAlaAlaLysThrAlaAsnAlaAsp AlaGluAlaSerPheThrAlaProGlyHisThrSerThrPheSerPheLysAlaLeuGln (1-349980) -CCACCAGCAGATTTAGGTACGCGTGAGGGATCTAGC 101745 123 83 65 48 192 101625 101565 101505 135 101469

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                                                                                                                  protein engineering; lignin depolymerisation; dye
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                                Location/Qualifiers
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transl_except= pos:1135..1137:_aa:Lys/
                                                                                                                                                                                                                                                                     DNA;
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                                                                                                                                 engineering;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The rs14 gene (AAT63317) encoding Rhizoctonia solani laccase isozyme 4 (AAW16301) can be subjected to site-directed mutagenesis in order talter e.g. the specific activity or pH-activity profile of the enzyme, or to improve expression yields. The mutation is a deletion, insertion or pref. a substr. of one or more amino acids at a location no greater than 12 Angstroms, pref. no more than 2.5 Angstroms, from the Type I copper site. The mutant enzyme is expressed in transformed host cells for use e.g. in the polymerisation or depolymerisation of lignin, oxidation of dyes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 6A-D; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activities to wild-type enzymes, used for e.g. (de)polymerisation or oxidation of dyes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mutant blue copper oxidase enzymes - having different activities to wild-type enzymes, used for e.g. lignin
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P-PSDB; AAW16301.
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GlyGlyGlyAlaGluAlaSerPheThrAlaPro-----
                                                                                               AspSerLysMetProHisAsnValAspPheHis-----
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                                                                                                                                                                                                                                                                  -----CCCGCCTTTGCTGCCGTCCGCAACTATAAGTTCGACATCAAGAACGTCAATGTC
                                                                                                                                                                                                                                                                                                 AspHisProAlaLysValValValLys-----MetGluThrValGluLysValMetArg
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                                                                 AGTATGCGTCGTGCCACAACGATTCATTGGCATGGATTGTTCCAAGCTACTÁCCGCCGAC
                                                                                                                                 ATCACGGCCAACAAGGGTGACACCTTGCGCATTAATGTCACGAATCAACTCACGGACCCT
                                                                                                                                                               IleArgValArgGluGlyAspThrIleGluValGlnPheSerAsnHis------Pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrPheSerPheLysAlaLeuGlnProGlyLeuTyrValTyrHisCysAlaValAlaPro 184
ATCGTATTGCCACACAATAAAGTTATCGAGCTCAATATCACCGGAGGTGCAGACCACCCT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysThrProAlaProAlaAsnLeuGlnGluGlnIleLysAlaGlyLysAlaThrTyrAsp 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspAlaValTyrLeuProGluGlyAlaProGlnAlaIleAspThrGlnGlu------
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                                                              SerValMetProAlaIleAlaLeuSerAspGlnGlnIleAlaAsnValIleThrTyrThr
                                                                                                                             TTGAAGATTTTTGGCAAACAATGCGAGCAATGACGCCGATTTCACGCCAAATGAGCACACT
                                                                                                                                                                                                                                                                                                                      ProAsnAlaPheProProLeuAlaAsnSerAspTyrLeuAsnAlaAspHisAlaArgAla
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Best Local Similarity:
Query Match:

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Matches:
Conservative:
Mismatches:
Indels:

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RESULT 40
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                                                                                                     This invention describes novel mutant Rhizoctonia solani laccase enzymes condified to exhibit altered characteristics (e.g. pH activity profile) crelative to the wild-type enzyme. The mutant enzymes have a number of commercial and industrial applications. For example, they may be used for the polymerization of lignin (both Kraft and liganosulfaces) in solution of tignin eight lignin. They may also be used for the in situ depolymerization of lignin in Kraft pulp to produce low molecular eight lignin. They may also be used for the in compounds in liquids (for example juice may be treated with the enzyme to accelerate precipitation of the phenolic compounds in the juice to stabilize it). Additionally, it may be used to decolorize dyes and dye precursors by oxidation. The mutant laccase enzymes exhibit different characteristics to those of the wild-type enzyme. In particular, they may exhibit an altered phenolic set relative to the wild-type oxidase or altered specific activities. Additionally, they be produced in large quantities. This sequence encodes the method of the produced in large quantities. This sequence encodes the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutant Rhizoctonia laccase enzymes useful for the polymerization depolymerization of lignin - % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1
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(BERK/) BERKA R M.
(WAHL/) WAHLEITHNER
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381	AspAlaValTyrLeuProGluGlyAlaProGlnAlaIleAspThrGlnGlu 3	365	Ş
924	CGTGCACCAATGACCGTTGCAGGAGCCGGAACCAATGCAAACTTGGACCCCACCAATGTC 9	865	밁
364	LeuGlyIleLeuLysValGluGluAgnHisGluIleTyrSerHisLysGlnThr 3	345	8
864	GCTGGACAACGCTACTCTGTCGTTGAAGCCAAACCAAAC	. 805	망
344	ValProGlyAspTyrValLeuValAspHisAlaIlePheArgAlaPheAsnLysGlyAla 3	325	Ś
804	GTCATTGAGGCCGATGGGATCCTGCACCAGCCCTTGGCTGTTGACAGCTTCCAGATTTAC	745	문
324	LeuileProAlaGlyGlyAlaAlaIleThrGluPheLysValAsp 3	310	Ş
744		727	망
309	GlnThrThr	290	ð
726	GCTTGCGCGTAATCAACGCTTCTGCTATCGGGTCGTTTACCTTTTCGATC	676	밁
289	gLeu	270	ð
575	GGCGGTCCCGCAGTTCCCCCGGTCAGTAATCAACGTAAAACGTGGGAAACGATAT 6	622	망
269	GlySerValGlyAlaLeuThrGlyGluAsnAlaLeuLysAlaLysValGlyGluThrVal 2	250	Ş
521	CTCTCTCTGTTCCGGACTCGGGTCTTATCAATGGCAAAGGGCGCTATGTG 6	571	밁
249	LeuGlnProPheAspMetGluLysAlaIleArgGluAspAlaGluTyrValValPheAsn 2	230	S
570	TACCATACTCCGGCACCCGTTCTAGAAAAGCAAATGTTCTCGACTAATAACACCGCTCTG 5	511	망
229	Tyr 2	220	ð
510	CCACACAAGTCGCGCTACGACGTGGATGATGCGAGCACAGTAGTCATGCTTGAGGACTGG 5	451	망
219		202	ð
150	CTTGCGAGTCAATATGTCGATGGATTGCGAGGCCCTTTGGTCATCTATGATCCAAACGAC 4	391	밁
201	ValGlyMetHisIleAlaAsnGlyMetTyrGlyLeuIleLeuValGluPro 2	185	8
390	GAGATCCCATTGCGCGGCCAAACAGGAACCATGTGGTATCACGCCCAT 3	343	밁
184	ThrPheSerPheLysAlaLeuGlnProGlyLeuTyrValTyrHisCysAlaValAlaPro 1	165	ş
342	GAGGATGGCCCCGCATTCGTCACGCAATGCCCTATTGCGCAAAATTTGTCCTATACATAC	. 283	В
164	GlyGlyGlyAlaGluAlaSerPheThrAlaProGlyHisThrSer 1	150	ð
282	AGTATGCGTCGCCACAACGATTCATTGGCATGGATTGTTCCAAGCTACTACCGCCGAC 2	223	밁
149	AspSerLysMetProHisAsnValAspPheHisAlaAlaThrGlyPro 1	134	Ş
222	ATCACGGCCAACAAGGGTGACACCTTGCGCATTAATGTCACGAATCAACTCACGGACCCT	163	밁
133	IleArgValArgGluGlyAspThrIleGluValGlnPheSerAsnHisPro 1	117	ठ
162	GCTCCCGATGGCTTTCAGCGCTCTATCGTCTCCGTCAACGGTTTAGTTCCTGGCACGTTG 1	103	문
116		97	Ş
102	13	. 49	망
96	AspHisProAlaLysValValValLysMetGluThrValGluLysValMetArg 9	79	S
4 6	CTACCTTTGCTCGCTGCGGTCTCAACC		문 4
5	eàlabroGlivValbroBroBroValbanbro	7. O C C C C C C C C C C C C C C C C C C	
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	1327 GGTGGTACCCCGAAC 1341		DЬ
	LysThrLysProAsn 502	498	Ş
CTC 132	ATCCATCTCCACGGCCATGTGTTTGATATCGTCAAATCA	1285	밁
Lys 497	LeuAsnSerPheGlyAsnLysGlyGlyGlnLeuSerAlaAspAspValAlaLysAlaLys 497	478	ρ
CCT 128	ATCGTATTGCCACACAATAAAGTTATCGAGCTCAATATCACCGGAGGTGCAGACCACCCT 128	1225	밁
Thr 477	SerValMetProAlaIleAlaLeuSerAspGlnGlnIleAlaAsnValIleThrTyrThr 477	458	Ş
ACT 122	TTGAAGATTTTTGGCAAACAATGCGAGCAATGACGCCGATTTCACGCCAAATGAGCAC	1165	밁
3lu 457	AlaSerIleValAlaAsnGlyLeuSerGlyLysIleThrValAsnGlyAsnGlnTyrGlu 457	438	Q.
116	TCGTTGCCCACGCTC	1150	밁
Ala 437	ProAsnAlaPheProProLeuAlaAsnSerAspTyrLeuAsnAlaAspHisAlaArgAla 437	418	Q
114	GGGATTCTTAGGTTCACATTTÄÄTAACATCAAGTACGAGGCTCCT	1105	뫄
Val 417	SerAsnCysAlaAlaCysHisGlnProAspGlyLysGlyVal 417	404	Q V
SAT 110	GGCGGCTCCCGCAGACGTTTCCCTCAATCTTGCAATTGGGCGCAGCACAGTT	1045	문
Asp 403	LysThrProAlaProAlaAsnLeuGlnGluGlnIleLysAlaGlyLysAlaThrTyrAsp	384	8
CCG 1044	GCTATCGGTACTGCACTCGTTGAAGAGAACCTCCATGCGCTCATCAACCCCTGGCGCTCCG	985	뮹
Pro 383	Alapro	382	Ş
AGT 984	TTTGCCGTÀTTGCACTACGAGGGAGCGCCCAACGCCGAACCCACGACGGAACAAGGCAGT 984	925	밁

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Perfect score:
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seq length: 2000000000
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Sequence 4, Appl. Sequence 76, App. Sequence 14, App. Sequence 8, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 2, Appl. Sequence 1, Appl. Sequence 31, App. Sequence 84, App.	equence 11, equence 7, equence 7, equence 7, equence 14,	equence 12, equence 12, equence 12, equence 1, equence 4,	equence 34 equence 4, equence 4, equence 16	equence 46 equence 48 equence 10 equence 2,	equence 3, equence 3, equence 45 equence 46	equence 5, equence 4, equence 4, equence 4,	equence equence equence	equence 26 equence 26 equence 26 equence 26	equence 170 equence 170 equence 170	equence 6, equence 6,	equence 2, equence 6, equence 6,	equence 4, equence 71	equence 4, equence 4,	equence 4,	equence 14, equence 2, equence 4.	equence 28	equence 9, equence 11	Sequence 5, Appl. Sequence 5, Appl. Sequence 2, Appl. Sequence 10, App.
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US-09-433-428D-40
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APPLICANT: Zheng, Jian
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION UNDBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 40
LENGTH: 33
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                                                                                                                                                                                                                                      Sequence
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APPLICANT:
APPLICANT:
APPLICANT:
             APPLICANT: CLAVEL, FRANCOISE
APPLICANT: BORMAN, ANDREW
APPLICANT: QUILLENT, CAROLINE
APPLICANT: GUETARD, DENISE
APPLICANT: MONTAGNIER, LUC
APPLICANT: MONTAGNIER, LUC
APPLICANT: DONJON DE SAINT-MARTIN, JACQELINE
APPLICANT: COHEN, JAQUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
TITLE OF INVENTION: SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES:
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US-08-533-298-17

US-08-449-657-3

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; ORGANISM: Staphylococcus epidermidis US-09-134-001C-2971
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                                                                                         PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2971
LENGTH: 172
                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                     Sequence 2971, Application US/09134001C Patent No. 6380370
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: POT/FR 95/01

PILING DATE: 20-OCT-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9412554

PILING DATE: 20-OCT-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9502526

PRIOR DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:
ANDER: MAGNET DATA:
ANDER: 03-MAR-1995
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TOPOLOGY: line
MOLECULE TYPE: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REGERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
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Pred. No. 43;
0; Mismatches
  Score 7;
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  4.
Length 172;
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                                                                                                                                                                                                                                              SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 28
LENGTH: 180
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                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC
FILE REFERENCE: BB-1126
CURRENT APPLICATION NUMBER: US/09/173,300
CURRENT FILING DATE: 1998-10-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 US 60/094,190 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEC ID NOS: 33142
                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/063,423 EARLIER FILING DATE: 1997 October 28
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Falco, Saverio C
APPLICANT: Hitz, William D.
                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Triticum aestivum
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                                                                                     KVEGEEN 355
                                                      KVEGEEN 64
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100.0%; Pred. No. 69;
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100.0%; Pred. No. 68;
ive 0; Mismatches
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LENGTH: 180
TYPE: PRT
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 410, Application US/08311731A Patent No. 6583266
                                                                              TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 4.
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TYPE: linear
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                                                                                                                                                                                                         APPLICATION NUMBER: US/08/311
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                         MOLECULE TYPE: pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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ORGANISM: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 MSKPTLI 125
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BER: US 60/074,788
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Query Match
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Best Local Similarity
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                                                                                                                                 ; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-631-7
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TITLE OF INVENTION: Nucleic Acid Encoding M. Tuberculosis ALGU Protein FILE REFERENCE: 0342/1C587US1APPEND
CURRENT APPLICATION NUMBER: US/09/082,920C
CURRENT FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 60/035,391
EARLIER FILING DATE: 1997-01-16
NUMBER OF SEQ ID NOS: 9
SOPTWARE: F8ECSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 224
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Best Local Similarity 100.0%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/214,631
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: ECT/CA97/00473
EARLIER FILING DATE: 1997-07-04
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER FILING DATE: 1996-07-05
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLICOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: TYROSINE KINASES
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.23USWO
                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 13
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                                148 GPGGGAE 154
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   74
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   GPGGGAE 80
                                                                   Conservative
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k; Pred. No. 87;
0; Mismatches
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Pred. No.
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                                                                                                Length 233;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
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RESULT 10
US-08-299-567-5
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                                                                                                                                                                       Sequence 2, Application US/08240124
Patent No. 5516658
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/299
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPAX: 914-345-7721
TELEPAX: 914-345-7721
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APPLICANT: Davis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: RECEPTOR HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York COUNTRY: U.S.A. ZIP: 10591-6707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 777 Old CITY: Tarrytown
                      STATE:
COUNTRY:
                                                         STREET:
                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                      SEATTLE
                  WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 amino acids
                                                     E: IMMUNEX CORPORATION
51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Regeneron Pharmaceuticals, Inc. 777 Old Saw Mill River Road
  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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100.0%; Pred. No. 87;
ative 0; Mismatches
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5. 87;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPB: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                  SOFTWARE: Microsoft Wo CURRENT APPLICATION DATA: APPLICATION NUMBER: US FILING DATE: 30-MAY-19
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08
FILTED TAREST
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APPLICATION NUMBER: 1
FILING DATE: 30-AUG-
                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 0:
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
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APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
          PRILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft Word for Apple, Version 5.1a CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/240,124
                                                                                                                                                                                             COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                     CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                  UMBER: US/08/453,943
30-MAY-1995
30-AUG-1993
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                                                                  US 08/161,132
                                                                                                  US 08/240,124
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; Pred. No
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Best Local Similarity 100.0%;
Matches 7; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,124
FILING DATE: 03-DEC-1993
PRIOR APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US.08/109,745
FILING DATE: 20-AUG-1993
APTORNEY/AGENT INFORMATION:
NAME: SESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOPTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,121
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MEDIUM TYPE: Floppy
COMPUTER: Apple Maci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                   TELECOMMUNICATION INFORMATION:
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TELEPHONE: (206)
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5. 5969110
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CERRETTI, DOUGLAS P.
FENTION: CYTOKINE THAT BINDS THE CELL SURPACE
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                     (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KATHRYN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4%; Score 7;
100.0%; Pred. No.
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INFORMATION FOR SEQ ID NO:

N

SEQUENCE CHARACTERISTICS

ENGTH:

238 amino acids

; MOLECULE TYPE: protein US-09-057-121-2

Length 238;

TOPOLOGY:

amino acid

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Query Match
Best Local Similarity
Marches 7; Conserve
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US-09-358-734-2
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                     NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
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                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BECKMANN, M. P. APPLICANT: CERRETTI, DOUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 5. CITY: SEATTLE
                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/109,745 FILING DATE: 20-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/358,734 FILING DATE:
                                                                                                                                                                                                                          TELEPHONE:
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148 GPGGGAE 154
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                                                                                                                                amino acid
                                                                                                    TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 UNIVERSITY STREET
                             Conservative
                                                                                                                                                                                                         (206) 233-0644
                                                                                                                     linear
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                                                                                                                                                                                                                          (206) 587-0430
                                           1.4%;
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CYTOKINE THAT BINDS THE CELL SURFACE
RECEPTOR HEK
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                          ; Score 7; DB 3
%; Pred. No. 89;
0; Mismatches
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Pred. No.
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                                        DB 3;
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                                                       Length 238;
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27792
LENGTH: 300
TYPE: PRT
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                                                                                         US-08-821-872-2
                                                                                                         RESULT 17
                                                                                                                                                                                                                                                                                                          ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27792
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                             Sequence 2, Application US/08821872A Patent No. 6204004 GENERAL INFORMATION:
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SEQ ID NO 22061
LENGTH: 262
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Best Local (
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APPLICANT: Kaper, James B APPLICANT: Jarvis, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 107196.136
                                                                                                                                                               195 ARAASIV 201
                                                                                                                                                                                                435 ARAASIV 441
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7; Conservat
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VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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1998-07-27
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100.0%; Pred. No. 96;
tive 0; Mismatches
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0; Mismatches
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FILE REFERENCE: Seq. ID NO. 62040044 Ref:
CURRENT APPLICATION NUMBER: US/08/821,872A
CURRENT FILING DATE: 1997-03-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 312
TYPE: PRT
ORGANISM: Escherichia coli
US-08-821-872-2
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Best Local Similarity
Marches 7; Conserva
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US-09-134-001C-4439
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US-09-171-5178-11
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          GENERAL INFORMATION:
APPLICANT: LYNN DOUGETTE-Stamm et al
APPLICANT: LYNN DOUGETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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SEQ ID NO 11
LENGTH: 312
TYPE: PRT
ORGANISM: Escherichia coli
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Best Local Similarity
Matches 7; Conserv
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APPLICANT: Finlay, B. Brett
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SEQ ID NO 4439
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APPLICANT: Stein, Markus
TITLE OF INVENTION: PATHOGENIC ESCHERICHIA COLI ASSOCIATED PROTEIN
FILE REFERENCE: 07422/01901
CURRENT APPLICATION NUMBER: US/09/171,517B
CURRENT FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: PCT/CA97/00265
PRIOR FILING DATE: 1997-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/015,999
PRIOR FILING DATE: 1996-04-23
NUMBER OF SEQ ID NOS: 15
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100.0%; Pred. No.
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Pred. No.
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lo. 1.1e+02;
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o. 1.1e+02;
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RESULT 21
US-08-931-668-9
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US-09-154-874-9
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APPLICATION NUMBER: 08/931,66i

FILING DATE: SEPTEMBER 17, 19;

FILING DATE: SEPTEMBER 17, 19;

ATTORNEY/AGENT INFORMATION:

NAME: MAJARIAN, WILLIAM R.

REGISTRATION NUMBER: 41,173

REFERENCE/DOCKET NUMBER: BB-11

TELECOMMUNICATION INFORMATION:

TELEPAN: 302-973-0164

INFORMATION FOR SEQ. ID NO: 9:

INFORMATION FOR SEQ. ID NO: 9:
Sequence 9, Application US/08931668
PATCHI NO. 6521433
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FADER, GARY M.
TITLE OF INVENTION: CDNA SEQUENCES FROM SOYBEAN THAT ENCODE TITLE OF INVENTION: ACTIVITIES ASSOCIATED WITH ISOFLAVONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/09154874 Patent No. 6054636
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE MICROSOFT WORD VERSION 7.0A.
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1007 MAKE
CITY: WILMINGTON
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                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                        107 GALGILK 113
                                                                                                                                                                                      343 GALGILK 349
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1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNITED STATES OF AMERICA
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BER 17, 1997
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                                                                                                                                                                                                                     Mismatches
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No. 1.2e+02;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09154874
Patent No. 6054636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity 100.0%;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
APPLICATION NUMBER: 08/931,668
FILING DATE: SEPTEMBER 17, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: DISKETT
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FADER, (
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                                                                                                                                                                                                                                                                                                      STREET: 1007 MARK
CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: MAJARIAN, WILLIAM R. REGISTRATION NUMBER: 41,173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
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                                                                                                     CLASSIFICATION:
                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                   E: E. I. DU PONT DE NEMOURS AND COMPANY
1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: E. I. DU PONT DE NEMOURS AND COMPANY 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                  FADER, GARY MICHAEL
VENTION: ISOFLAVONE BIOSYNTHETIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                       UNITED STATES OF AMERICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/931,668
                                                                                                                                    US/09/154,874
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o. 1.2e+02;
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Patent No. 6521433
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                                                                                                                                                                                                           TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                        NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1
TELECOMVUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                            SEQUENCE CHARACTERISTICS LENGTH: 327 amino aci
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TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 327 amino acids
                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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107 GALGILK 113
                             343 GALGILK 349
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Similarity 100.0%;
7; Conservative (
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1007 MARKET STREET
                                                                                                                                                                              327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNITED STATES OF AMERICA
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                       IBM PC COMPATIBLE
SYSTEM: MICROSOFT WORD FOR MICROSOFT WORD VERSION 7.0A
                                                                                                                                                                                                                                                                                                                                                                                                                                       DISKETTE, 3.50 INCH
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                                                                         100.0%;
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s; Pred. No. 1.2
0; Mismatches
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o. 1.2e+02;
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RESULT 24 US-09-252-991A-21843

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US-08-886-886-2
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SEQ ID NO 21843
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: 1998-07-27
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Katz,
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 6016.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/01
FILING DATE: 02-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
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APPLICANT: Davies, Julian E.
TITLE OF INVENTION: COENZYME A DISULFIDE REDUCTASE,
TITLE OF INVENTION: AND INHIBITORS THEREOF USEFUL AS ANTIMICROBIAL
TITLE OF INVENTION: AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CITY: Abbott Park
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100.0%; Pred. No.
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US-09-296-284-26
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                                                                                                ; ORGANISM: Gluconobacter suboxydans US-09-296-284-26
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; SEQ ID NO 26
; LENGTH: 442
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Best Local Similarity 100.0%;
Matches 7; Conservative (
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LENGTH: 438
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Matches 7; Conservative (
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                                                                                                                                                                                          TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes TITLE OF INVENTION: and Methods of Use Thereof FILE REFERENCE: 1533.0870000 CURRENT APPLICATION NUMBER: US/09/296,284A CURRENT FILING DATE: 1999-04-22 NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: Modified Phytases
CURRENT APPLICATION NUMBER: US/09/044,718
CURRENT FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
PRIOR FILING DATE: 1997-03-25
                                                                                                                                                                                                                                                                                          APPLICANT: Choi, Eui-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
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SOFTWARE: PatentIn V
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APPLICANT: WYSS, Markus
TITLE OF INVENTION: MODI
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                                                                                                                                TYPE: PRT
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465 LSDQQIA 471
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TOMSCHY, Andrea
van LOON, Adolphus
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                              1.4%; Score 7; DB 3; Ler
100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
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| 100.0%; Pred. No.
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CURRENT APPLICATION NUMBER: US/09/044,718
CURRENT FILING DATE: 1998-03-19
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PRIOR FILING DATE: 1997-03-25
NUMBER OF SEQ ID NOS: 82
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                                                                                                                                                                                                                             ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
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                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/868,435
                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Van Loon,
APPLICANT: Mitchell,
TITLE OF INVENTION: 1
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                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                  COUNTRY: U
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WYSS, Markus
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340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                United States of America
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               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,757
FILING DATE: 18-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Van Loon, APPLICANT: Mitchell,
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LOCATION:
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                                                                                                               CLASSIFICATION:
                                                                                                                                   FILING DATE:
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REFERENCE/DOCKET NUMBER: Case Docket 9339
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GY: linear
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Mitchell, David
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Pred. No. 1.6e+02
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NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 466 amino acid

466 amino acids

TELECOMMUNICATION INFORMATION:

TELEPHONE:

(201)

235-2363

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                                                                                                                  ; LENGTH; 478
; TYPE: PRT
; ORGANISM: Gluconobacter suboxydans
US-09-296-284-5
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                                                           Matches
                                                                      Query Match
Best Local Similarity
                                                                                                                                                                            SOFTWARE:
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09296284A Patent No. 6204040
                                                                                                                                                                                                     APPLICANT: Choi, Eui-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase,
TITLE OF INVENTION: and Methods of Use Thereof
FILE REFERENCE: 1533.087000
CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
RUMBER OF SEQ ID NOS: 87
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LOCATION: 120
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OTHER INFORMATION: /note="potential N-glycosylation site"
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401 LSDQQIA 407
                          465 LSDQQIA 471
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                                                        Conservative
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100.0%; Pred. No
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                                                                      Score 7; Pred. No.
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o. 1.6e+
                                                                         DB 3;
o. 1.6e
                                                                      .6e+02;
                                                                                  Length 478;
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Best Local Similarity
Thes 7; Conserve
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US-08-836-620A-18
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                                                                                                                                                                                                                                                                                                               Patent No. 5891674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/08836620A Patent No. 5958710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 08-MAY-1996 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: GB 96055500.

PRILING DATE: 15-MAR-1996,
PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: GB 9607532.0
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 08-SEP-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Orphan receptor NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                    TILE OF INVENTION:
                                                                                                          ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: am:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
 APPLICATION NUMBER:
                                                                                                                                                      CITY: Palo Alto
                                                                                                                                                                        STREET:
                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
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                                                                                                                                                                      3174 Porter Drive
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                                                                                                                          USA
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Conservative (
                                                         IBM Compatible
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                                                                           Diskette
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                                                                                                                                                                                                                                                   Purvi
                                                                                                                                                                                                                                    INSULIN RECEPTOR TYROSINE KINASE SUBSTRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 7; DB:
100.0%; Pred. No. 1.
1ve 0; Mismatches
US/08/878,563A
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hes 0;
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RESULT 34
US-09-270-117-3
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GENERAL INFORMATION:
APPLICANT: Hilman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
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Best Local Similarity 100
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                      TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 521 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: DiaKette
COMPUTER: IBM Compatil
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                          FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,563
                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS: Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: line
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IMMEDIATE SOURCE:
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LIBRARY: GELL
ONE: 1203820
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                       STRANDEDNESS:
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                                                                                                                   TELEPHONE:
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         ss: single
linear
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SYSTEM: DOS
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100.0%; Pred. No. 1.
ative 0; Mismatches
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45. 1.8e+02;
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RESULT 35
US-08-878-563A-1
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                                         Query Match
Best Local Similarity 100.0%, F
Matches 7; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 31.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/878,563A FILING DATE: Filed Herewith PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hillman, Je
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: INSULIN RECEPTOR TYROSINE KINASE SUBSTRATE NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.0%;
nes 7; Conservative
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CLONE: 1203820
                                                                                                                                 LIBRARY: BRSTI
CLONE: 918158
                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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317 KAAOPKS 323
                            29 KAAQPKS 35
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0; Mismatches
                                                                        Score 7;
Pred. No.
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                                                            Mismatches
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5. 1.8e+02;
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                                                            Indels
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RESULT 36 US-09-270-117-1

Sequence 1, Application US/09270117 Patent No. 6265550

GENERAL INFORMATION:

APPLICANT:

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Best Local Similarity
Thes 7; Conserva
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US-09-328-352-5771
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// ORGANISM: Acinetobacter baumannii
US-09-328-352-5771

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                                                                                                                                       GENERAL INFORMATION:
APPLICANT: GATY L. BYCCHOR et al.
APPLICANT: GATY L. BYCCHOR et al.
TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5771
LENGTH: 539
                                              Query Match
Best Local
                                 Matches
                                                                                                                                                                                                                                                                                                         Sequence 5771, Application US/09328352 Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shah, Purvi
TITLE OF INVENTION: INSULIN RECEPTOR TYROSINE KINASE SUBSTRATE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 534 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: BRSTI
CLONE: 918158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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257 GENALKA 263
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                              Similarity 7; Conserv
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                                              100.0%;
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US-09-252-991A-20407
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SEQ ID NO 19164
LENGTH: 616
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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PRIOR FILING DATE: 1998-02-18.
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20407
GENERAL INFORMATION:
APPLICANT: Marc J.
TITLE OF INVENTION:
                                                    Sequence 26100, Appearent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT: Marc J.
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
Rubenfield et al.

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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FILE REFERENCE: 107196.136
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26100
LENGTH: 727
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26100
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps O;

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Search completed: August 27, 2003, 18:46:11
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TITLE OF INVENTION: Human Proteins and cDNAs thereof
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FILING DATE: 2000-02-10
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, LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-890-688-140
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PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR PPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PPLICATION NUMBER: GB 00/236,359
PRIOR PILING DATE: 2000-10-04
PRIOR PPLICATION NUMBER: PCT/US01/00666
PRIOR PPLICATION NUMBER: PCT/US01/00667
PRIOR PPLICATION NUMBER: PCT/US01/00667
PRIOR PPLICATION NUMBER: PCT/US01/00667
PRIOR PPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PRICALING DATE: 2001-01-30
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                                                                          SOFTWARE: Annomax Sequence Listing SEQ ID NO 44403 LENGTH: 71 TYPE: PRT
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Best Local :
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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                                                                                                                                                                              NUMBER OF SEQ ID NOS: 49117
FEATURE:
OTHER INFORMATION: MAP TO AC005015.2
                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                              FILLING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
ADDITANT
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US FILING DATE: 2000-06-3
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
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5. US20020048763A1
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Hanzel, David K.
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09/774,203
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UMBER: ***
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Pred. No.
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Best Local
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                                                TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO: 100: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER
                                                                                                                                                                                     APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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DONJON DE SAINT-MARTIN, JACQELINE
COHEN, JAQUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE
                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 27-Dec-2001 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                    NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/817,441
FILING DATE: 31-AUG-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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STRANDEDNESS: single
                  TYPE: amino acid
                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                             FILING DATE: 20-OCT-1994
                              LENGTH: 104 amino acids
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BORMAN, ANDREW
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FETAL LIVER, SIGNAL = 0.78
ADULT LIVER, SIGNAL = 0.8
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APPLICANT: Niewenholzen, Nicolaas
APPLICANT: Higgins, Colleen M.
FITLE OF INVENTION: Compositions Isolated from Plant Cells
FITLE OF INVENTION: Compositions Isolated from Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/28,986
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
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        APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILLING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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SEQ ID NO 13774
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APPLICANT:
APPLICANT:
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Best Local Sin
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SOFTWARE: FastSEQ for Windows Version 4.0
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7; Conserva
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HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 15; Length 156; Pred. No. 1.2e+02; 0; Mismatches 0; Indels
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Pred. No.
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o. 82;
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APPLICANT: M56malu, Geraldine
APPLICANT: M56malu, Geraldine
TITLE OF INVENTION: DLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.23USWO
CURRENT APPLICATION NUMBER: US/10/138,787
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
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LENGTH: 180
TYPE: PRT
ORGANISM: Triticum aestivum
US-10-027-450-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                         SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/10138787
Publication No. US20020172984A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Best Local :
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SOFTWARE: Microsoft Word Version 7.0A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/027,450
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/063,423
PRIOR FILING DATE: 1997 October 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Falco, Saverio Carl
APPLICANT: Hitz, William D.
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: .Holland, Sacha
APPLICANT: Mbamalu, Gera
APPLICANT: Pawson, Tony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC
FILE REFERENCE: BB-1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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ORGANISM: Homo sapiens
                      TYPE: PRT
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Local Similarity 100.0%;
ies 7; Conservative (
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o. 1.4e+02;
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Best Local Similarity
7; Conserve
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US-09-904-954-2
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                                                                                                                                                                                                                                               TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/240,124

FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/114,426

FILING DATE: 30-AUG-1993

APPLICATION NUMBER: US 08/109,745

FILING DATE: 20-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: SEESE, KATHRYN A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2814-C

TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/904,954
FILING DATE: 12-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                          MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BECKMANN, M. P.
CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
RECEPTOR HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                 148 GPGGGAE 154
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78 GPGGGAE 84
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OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: <Unknown>
                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: WASHINGTON
                                                                                                                                                                                                                                  LENGTH: 238 amino acids
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                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 UNIVERSITY
                                                                                                                                                                                                                                                                                                         (206) 233-0644
                                                               1.4%; but
100.0%; Pr
                                                                    Score 7; DB 9; Pred. No. 1.7 0; Mismatches
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To. 1.7e+0
                                                                                       DB 9; Ler
o. 1.7e+02;
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                                                                                                      Length 238;
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RESULT 9 US-10-241-220-72

; Sequence 72, Application US/10241220

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; ORGANISM: Homo Sapien
US-10-241-220-72
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                                                           Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                              SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 5155
LENGTH: 278
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
5-09-738-626-5155
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Best Local Similarity
Matches 7; Conserv
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SEQ TD NO 72
LENGTH: 238
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                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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262 RLADGVE 268
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                             96 RLADGVE 102
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YOKOI, HARUHIKO
TATEISHI, NAOKO
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Polakis, Paul
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ANDO, SEIKO
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                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIROSHI
                                                                               1.4%; Score 7;
100.0%; Pred. No.
                                                                 0
                                                                 Mismatches
                                                                               DB 10;
o. 2e+02;
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o. 1.7e+02;
                                                                                               Length 278;
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14202
LENGTH: 300
Ş
                                                                                                                              ; LENGTH: 312
TYPE: PRT
; ORGANISM: Escherichia coli
US-09-967-347-11
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                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/967,347
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 09/171,517
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: PCT/CA97/00265
PRIOR FILING DATE: 1997-04-23
PRIOR APPLICATION NUMBER: 60/015,999
PRIOR APPLICATION NUMBER: 60/015,999
PRIOR FILING DATE: 1996-04-23
PRIOR FILING DATE: 1996-04-23
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                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09967347 Patent No. US20020115829A1
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Best Local Similarity
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APPLICANT: Donnenberg, Michael S.
APPLICANT: Lai, Li-Ching
TITLE OF INVENTION: PATHOGENIC ESCHERICHIA COLI ASSOCIATED PROTEIN ESPA
FILE REFERENCE: 482112.401D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Finlay, B. Brett
APPLICANT: Kenny, Brendan
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490 ADDVAKA 496
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Stein, Markus
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                                                                  1.4%; Score 7; 1
100.0%; Pred. No.
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00.0%; Pred. No. 2.2e+02;
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187 ADDVAKA 193

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US-10-092-947A-37
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Patent No. US20010011131A1
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SOFTWARE: Patentin warn'
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CURRENT APPLICATION NUMBER: US/10/092,947A
CURRENT FILING DATE: 2002-12-27
PRIOR APPLICATION NUMBER: US 60/274,650
PRIOR FILING DATE: 2001-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WOLFF, Anne M
APPLICANT: APPEL, Karen
APPLICANT: PETERSEN, Jes
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA;
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                                                      REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Jr., Malcolm
APPLICANT: Chang, Steven Chao-Huan
TITLE OF INVENTION: CARTILAGE-DERI
TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                    TELEFAX:
                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/730,772 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                  CLASSIFICATION:
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PETERSEN, Jesper F
POULSEN, Ulla
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                                      619-235-0176
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                                              Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative
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                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 436 amino acid
                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NIH099.001APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
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                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 619-235-8550 •
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CARTILAGI
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, M
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OPERATING SYSTEM:
SOFTWARE: FastSE(
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                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                              TYPE: amino acid
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                              148 GPGGGAE 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Luyten, Frank P.
Moos, Jr., Malcolm
Chang, Steven Chao-Huan
NVENTION: CARTILAGE-DERIVED MORPHOGENETIC
                                                                                                                                                                                                              436 amino acids
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                                                                                                                                                                                                                                                                                  619-235-0176
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o. 3e+02;
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5. 3e+02;
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US-10-062-848-2

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TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: Modified Phytases
CURRENT APPLICATION UNDER: US/10/062,848
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/044,718
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
PRIOR APPLICATION NUMBER: EP 97810175.6
PRIOR APPLICATION NUMBER: EP 97810175.6
PRIOR PILING DATE: 1997-03-25
INUMBER OF SEQ ID NOS: 82
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
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TYPE: PRT
; ORGANISM: Aspergillus terreus
US-10-062-848-2
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/151,933
PRIOR FILLING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: US 08/781,986
PRIOR FILLING DATE: 1997-01-03
PRIOR APPLICATION NUMBER: US 08/956,171
PRIOR APPLICATION NUMBER: US 60/009,861
PRIOR APPLICATION NUMBER: US 60/009,861
PRIOR APPLICATION NUMBER: US 60/009,861
PRIOR FILLING DATE: 1996-01-06
                                                                     Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides FILE REFERENCE: P8560 CURRENT APPLICATION NUMBER: US/09/925,637 CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US00/23773
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APPLICANT: PASAMONTES, LI
APPLICANT: TOMSCHY, Andre
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE:
                                                                                                                                                                                            LENGTH: 439
TYPE: PRT
301 RAASIVA 307
                                  436 RAASIVA 442
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WYSS, Markus
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0; Mismatches (
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Pred. No.
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                                                                                                               Length 439;
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RESULT 20
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US-10-062-848-15
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TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: MODIFIED PHYTASES
FURRENT APPLICATION UNMBER: US/10/062,848
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION UNMBER: 09/044,718
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION UNMBER: EP 97810175.6
PRIOR FILING DATE: 1997-03-25
NUMBER OF SEQ ID NOS: 82
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                                                                                                                                                                                                                                                 SEQ ID NO 15
LENGTH: 450
TYPE: PRT
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Publication No. US20030092155A1
GENERAL INFORMATION:
APPLICANT: KOSTREWA, Dirk
APPLICANT: FASAMONTES, Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 20
LENGTH: 439
TYPE: PRT
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                                                                                                                                   Matches
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Best Local
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Best Local Similarity
Matches 7; Conserv
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CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: PCT/US00/23773
PRIOR FILING DATE: 2000-08-31
PRIOR PPLICATION NUMBER: 60/151,933
PRIOR PPLICATION NUMBER: 60/151,933
PRIOR PILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 74
                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.1
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TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: PB515P1
                                                                                                                                   Local Similarity
mes 7; Conserv
                                                         235
                                                                                           487 QLSADDV 493
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                                                       QLSADDV 241
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WYSS, Markus
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van LOON, Adolphus
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No. US20030049648A1
                                                                                                                                 Conservative 0;
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100.0%; Pred. No. 3e+02;
                                                                                                                                 1.4%; Score 7; DB 15; 1
100.0%; Pred. No. 3.1e+02
ive 0; Mismatches 0
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US-09-843-250-24
Sequence 24, Application US/09843250
Publication No. US20030022335A1
GENERAL INFORMATION:

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RESULT 21
US-10-278-481-18
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SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/843,250 CURRENT FILING DATE: 2001-04-26 PRIOR APPLICATION NUMBER: PCT/US99/25079 PRIOR FILING DATE: 1999-10-26 PRIOR APPLICATION NUMBER: US 60/105,575 PRIOR FILING DATE: 1998-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
APPLICANT: KAR
                                                                                                NAME: GUSTAFSSON, Ja:
INFORMATION FOR SEQ ID NO: 18:
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                                                                                                                                    APPLICATION NUMBER: GB 9607532.0 FILING DATE: 11-APR-1996 APPLICATION NUMBER: GB 9609576.5 FILING DATE: 08-MAY-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,481
FILING DATE: 23-OCC-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,057
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KARO BIO AB
TITLE OF INVENTION: Orphan receptor

NUMBER OF SEQUENCES: 19
STREET: c/o Center for Biotechnology and Department
of Medical Nutrition, Karolinska Nutrition, Karolinska
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 PAKVVVK 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: Sweden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Huddinge
                                                       LENGTH: 518 amino acids
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                                                                                                                                                                                                                                             PPLICATION NUMBER: GB 9518272.1
TILING DATE: 08-SEP-1995
PPLICATION NUMBER: GB 9605550.4
TILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                          ILING DATE: <Unknown>
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100.0%; Pred. No. 3.1e+02;
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; ORGANISM: Streptomyces avermitilis US-10-156-761-14029
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FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR TILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14029
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US-10-156-761-14029
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CURRENT FILING DATE: 2002-08405
PRIOR APPLICATION NUMBER: US 60/315,775
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: EP 01119003.0
PRIOR APPLICATION NUMBER: EP 01119003.0
PRIOR FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
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Best Local Similarity 100.
....hes 7; Conservative
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Matches 7; Conservative
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LENGTH: 519
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APPLICANT:
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APPLICANT: Mueller, Stefan
TITLE OF INVENTION: Method for Identifying Substances Which Positively
TITLE OF INVENTION: Influence Inflammatory Conditions
FILE REFERENCE: 0652.2340001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jung,
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                    IPPLICANT: OMURA, SATOSHI
LENGTH: 549
TYPE: PRT
                                                                                                                                                                                                                     PPLICANT: ISHIKAWA, JUN
PPLICANT: HORIKAWA, HIROSHI
PPLICANT: SHIBA, TADAYOSHI
PPLICANT: SAKAKI, YOSHIYUKI
PPLICANT: HATTORI, MASAHIRA
PPLICANT: HATTORI, MASAHIRA
PPLICANT: NOVEL POLYNUCLEOTIDES
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100.0%; Pred. No. 3.5e+02;
lve 0; Mismatches 0;
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US-10-156-761-9578
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                                                                                                                                                       Sequence 9578, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
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LENGTH: 611
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Best Local
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                                                                                                     APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
09-815-242-12111
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                      APPLICANT:
                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
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                                    APPLICANT:
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            PPLICANT: IKEDA HARUO
PPLICANT: ISHIKAWA, JUN
PPLICANT: HORIKAWA, HIROSHI
PPLICANT: SHIBA, TADAYOSHI
PPLICANT: SAKAKI, YOSHIYUKI
PPLICANT: HATTORI, MASAHIRA
PPLICANT: HATTORI, MASAHIRA
PPLICANT: HATTORI, MASAHIRA
REFERENCE: 249-262
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7; Conserve
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Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                         Conservative
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100.0%; Pred. No.
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Pred. No. 3.7e+02;
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o. 4.1e+02;
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RESULT 27 US-09-882-227-308

Sequence 308, Application US/09882227 Publication No. US20030158396A1 GENERAL INFORMATION:

APPLICANT: Kleanthous, Harold APPLICANT: Al-Garawi, Amal

Miller,

Charles

APPLICANT:

Tomb, Jean-Francois

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                                                                                                                                             ; FEATURE:
, NAME/KEY: MOD RES
; LOCATION: (737)
; OTHER INFORMATION: Thr or Pro
US-09-995-587A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; SEQ ID NO 9578
LENGTH: 724
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9578
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SEQ ID NO 11
LENGTH: 792
TYPE: PRT
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Best Local Similarity 100.
Matches 7; Conservative
                                                                       Matches
                                                                                       Query Match
Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/995,587A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 09/604,958
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: EPO 00201872.9
PRIOR FILING DATE: 2000-05-25,
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: U$/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: RAHAOUI, HAKIM
TITLE OF INVENTION: NOVEL FRUCTOSYLTRANSFERASES
FILE REFERENCE: BO43667-CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VAN HIJUM, SACHA ADRIANUS FOKKE TACO
APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: MOD_RES
LOCATION: (495)...(496)
OTHER INFORMATION: Any
                                                                                                                                                                                                                                                                                                                  ORGANISM: Lactobacillus reuteri
                       343 GALGILK 349
461 GALGILK 467
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                                                                     Similarity 100. 7; Conservative
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                                                                       100.0%;
ative 0;
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                                                                                                                                                                                                                                      amino acid
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L00.0%; Pred. No. 4.8e+02
                                                                     1.4%; Score 7; DB
.00.0%; Pred. No. 5.
.ve 0; Mismatches
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                                                                                                        Length 792;
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RESULT 29
US-08-781-986A-5235
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; ORGANISM: Helicobacter pylori
US-09-882-227-308
                                                                                                                                                                                                                                                                                                                                                                                      US-08-945-749-1
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
7; Conserv
                                                    Sequence 5235, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus (NUMBER OF SEQUENCES: 5255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08945749
Publication No. US20020138880A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.4%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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TITLE OF INVENTION: I
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 06132/047002
CURRENT APPLICATION NUMBER: US/09/882,227
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/902,615
PRIOR FILING DATE: 1997-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: PCT/NZ96/0035
EARLIER FILING DATE: 1996-05-01
EARLIER APPLICATION NUMBER: NZ 272039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/945,749
CURRENT FILING DATE: 1998-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Auckland Uniservices Limited
APPLICANT: New Zealand Pastoral Agriculture Research Institut
TITLE OF INVENTION: ALUMINUM RESISTANCE GENE
FILE REFERENCE: 08/945,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GARDNER, Richard C
APPLICANT: MacDIARMID, Colin W
APPLICANT: HAY, Robert J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1995-05-01
NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                 CORRESPONDENCE ADDRESS:
   STREET:
                  ADDRESSEE:
                                                                                                                                                                                                                                                             349 KVEGEEN 355
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3: Human Genome Sciences,
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                       394
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                                                                                                                                                                                                                                                                                                                             1.4%;
                                                      Staphylococcus aureus Polynucleotides 5255
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Pred. No.
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; ORGANISM: Bovine US-10-188-308-21
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                                                                                                                          CURRENT APPLICATION NUMBER: US/10/188,308
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US/09/694,777
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: ECT/EP99/02695
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EP 98 10 7268.9
PRIOR APPLICATION NUMBER: EP 98 10 7268.9
PRIOR FILING DATE: 1998-04-21
                                                   NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/101 Publication No. US20030077735A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BRUGGEMANN, ANDREA
APPLICANT: FERNANDEZ-MIRANDA, DONATO DEL CAMINO
APPLICANT: PEREZ, ARACELI SANCHEZ
APPLICANT: WESELOH, RUDIGER
TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC
TITLE OF INVENTION: APPLICATIONS
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: !
                                      TYPE: PRT
                                                                                                                                                                                                                                                                                FILE REFERENCE: MPG-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PARDO-FERNANDEZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 886 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 STUHMER, WALTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/10188308
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Pred. No.
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Query Match

1.4%;

Score

7;

DB 15;

Length 960;

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; ORGANISM: Bovine sp.
US-10-188-296-21
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Best Local Similarity 100.0%; F
Matches 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21, Appropriate Publication No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Application US/101 Publication No. US20030087377A1
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Matches 7; Conservative (
                                     PRIOR APPLICATION NUMBER: US/09/694,777
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: PCT/EP99/02695
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EP 98 10 7268.9
                                                                                                                                                           APPLICANT: FERNANDEZ-MIRANDA, DONATO DEL CAMINO
APPLICANT: WESELOH, RUDIGER
APPLICANT: WESELOH, RUDIGER
TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE APPLICATION WESEL, US/10/188,341
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PRIOR FILLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: PCT/EP99/02695
PRIOR FILLING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EP 98 10 7268.9
PRIOR FILLING DATE: 1998-04-21
PRIOR FILLING DATE: 1998-04-21
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TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: MGG-8
CURRENT APPLICATION NUMBER: US/10/188,296
CURRENT FILING DATE: 2002-07-01
                                                                                                                                                  CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                   APPLICANT:
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PRIOR FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 24
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BRUGGEMANN, ANDREA
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BRUGGEMANN, ANDREA
FERNANDEZ-MIRANDA, DONATO DEL CAMINO
PEREZ, ARACELI SANCHEZ
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o. 6.2e+02;
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Best Local Similarity 100.0%;
Matches 7; Conservative (
                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: PARDO-FERNANDEZ,
APPLICANT: STUMMER, WALTER
APPLICANT: BECKH, SYNNOVE
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LENGTH: 960
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Publication No. US20030077735A1
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FILE REFERENCE: MPG-8
CURRENT APPLICATION NUMBER: US/10/188,308
CURRENT APPLICATION 2002-07-01
                                                      APPLICANT: WESELOH, RUDIGER
TITLE OF INVENTION: NOVEL HUMAN K+
TITLE OF INVENTION: APPLICATIONS
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WESELOH, RUDIGER
TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS
TITLE OF INVENTION: THEREOF,
FILE REFERENCE: MPG-8
CURRENT APPLICATION NUMBER: US/10/188,297
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US/09/694,777
PRIOR APPLICATION NUMBER: US/09/694,777
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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TYPE: PRT
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NUMBER OF SEQ ID NOS: 24
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PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EP 98 10 7268.9
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APPLICANT: STUHM
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ORGANISM: Bovine sp.
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                                                                                                                              PEREZ, ARACELI SANCHEZ
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ER, WALTER
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No. 6.2e+02;
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CURRENT APPLICATION NUMBER: US/10/188,308
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US/09/694,777
PRIOR FILING DATE: 2000-10-23
PRIOR ETLING DATE: 2000-10-23
PRIOR ETLING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: ECT/EF99/02695
PRIOR APPLICATION NUMBER: ECT/EF99/02695
PRIOR APPLICATION NUMBER: ECT/EF99/02695
PRIOR APPLICATION NUMBER: ECT/EF99/02695
PRIOR FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 24
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US-10-188-296-3
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US-10-188-308-24
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; ORGANISM: Rattus sp.
US-10-188-308-24
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                                                                                     Sequence 3, Application US/10188296 Publication No. US20030087377A1 GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 6.2e+02;
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APPLICANT: PARDO-FERNANDEZ, LUIS ANGEL APPLICANT: STUHNER, WALTER APPLICANT: BECKH, SYNNOVE APPLICANT: BRUGGEMANN, ANDREA
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TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC
TITLE OF INVENTION: APPLICATIONS
TITLE OF INVENTION: THEREOF
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: PCT/EP99/02695
PRIOR FILING DATE: 1999-04-21
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TYPE: PRT
ORGANISM: Homo mapienm
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FERNANDEZ-MIRANDA, DONATO DEL CAMINO
PEREZ, ARACELI SANCHEZ
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US-10-188-296-24
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US-10-188-296-24
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CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US/09/694,777
PRIOR FILING DATE: 2000-10-23.
PRIOR APPLICATION NUMBER: PCT/EP99/02695
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EP 98 10 7268.9
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PRIOR APPLICATION NUMBER: EP 98 10 7268.9
PRIOR APPLICATION NUMBER: EP 98 10 7268.9
PRIOR APPLICATION NUMBER: EP 98 10 7268.9
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Best Local :
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Publication No.
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Best Local Similarity 100.0%; F
Matches 7; Conservative 0;
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                                                                                   Matches
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PRIOR APPLICATION NUMBER: US/09/694,777
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: PCT/EP99/02695
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EP 98 10 7268.9
PRIOR APPLICATION NUMBER: EP 98 10 7268.9
PRIOR FILING DATE: 1998-04-21
NUMBER: FILING DATE: 1998-04-21
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APPLICANT: STUHMER, WALTER
APPLICANT: BECKH, SYNNOVE
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APPLICANT: WESSIOH, RUDIGER
TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: MPG-8
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TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: MPG-8
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 24
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CURRENT FILING DATE: 2002-07:01
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TYPE: PRT
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TYPE: PRT
ORGANISM: Homo sapiens
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200 QEAPKTP 206
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No. US20030087377A1
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                                                                                 1.4%; Score 7; DB 15; L
100.0%; Pred. No. 6.2e+02;
1ve 0; Mismatches 0;
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RESULT 38

US-10-188-341-3

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                                                                                             ; ORGANISM: Rattus sp. US-10-188-341-24
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CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US/09/694,777
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: PCT/EP99/02695
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1998-04-21
PRIOR FILING DATE: 1998-04-21
PRIOR FILING DATE: 1998-04-21
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Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 0;
Query Match 1.4%; Score 7; DB 15; Le Best Local Similarity 100.0%; Pred. No. 6.2e+02; Matches 7; Conservative 0; Mismatches 0;
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Publication No. US20030087378A1
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APPLICANT: FERNANDEZ-MIRANDA, DONATO DEL CAMINO
APPLICANT: PEREZ, ARACELI SANCHEZ
APPLICANT: WESELOH, RUDIGER
TITLE OF INVENTION: NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS
FILE REFERENCE: MPG-8
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PRIOR APPLICATION NUMBER: EP 98 10 7268.9
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CURRENT FILING DATE: 2002-07-01
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BECKH, SYNNOVE
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PEREZ, ARACELI SANCHEZ
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LENGTH: 962;
; TYPE: PRT;
; ORGANISM: Homo sapiens
US-10-188-297-3
Search completed: August 27, Job time: 72 secs
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US-10-188-297-3
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Publication No. US20030092120A1
                                                                                                                                            Best Local Similarity
Matches 7; Conserv
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SOFTWARE: PatentIn Ver. 2.1
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: PCT/EP99/02695
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EP 98 10 7268.9
PRIOR FILING DATE: 1998-04-21
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CURRENT APPLICATION NUMBER: US/10/188,297
CURRENT FILING DATE: 2002-07-01
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NOVEL HUMAN K+ ION CHANNEL AND THERAPEUTIC APPLICATIONS
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BECKH, SYNNOVE
BRUGGEMANN, ANDREA
FERNANDEZ-MIRANDA, DONATO DEL CAMINO
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RESULT 3
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The present invention provides the protein and coding sequences of proteins from Moraxella catarrhalis. These can be used to produce vaccines which protect against M. catarrhalis infection, which can otitis media, respiratory infection, sinusitus, and pneumonia. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                               29-AUG-
29-AUG-
                                                                                  Moraxella polypeptide and polynucleotides useful as vaccinimmunizing a host e.g. humans against disease e.g. otitis pneumonia, caused by infection of the bacteria
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                                                                Claim
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N-PSDB; AAL46493.
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Matches 34; Conserv
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                                                                                                                                                              The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N. gonorrhoeae amino acid sequence SEQ ID 1784.
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                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New protein from Neisseria gonorrheae, useful for the manufacture of medicament for treating or preventing N. gonorrheae infection
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                                                                                                                                                                                                                                                                                                                                                                                                                   Page 316;
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Matches Query Match Best Local

Similarity 8; Conserv

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Mismatches

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Score 8; Pred. No.

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Length 10; Indels

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                             that protect against cancer. The invention provides: vectors and chost cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a patient.
                                                                                                                                                                                                                                                                                 (see AAY05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1 (CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-87), are useful as cancer vaccines
                                                                                                                                                                                                                                                                                                                                  The present sequence represents a cancer peptide that is based on amino acid residues 55-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965), a new and potent tumour_antigen capable of elicit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; hu leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung ca metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer antigen NY ESO1/CAG-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-277270/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosenberg SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang RF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0061428.
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ATGPGGGA

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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CT fre polypeptide and polynucleotide sequences have applications in CC clagnostice, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity amino acid sequences. Abgound-Abg30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this pattent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO
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                                                                                                                               RESULT 6
ABG18127
                                                               Matches
                                                                               Query Match
Best Local
                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 48486; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS82314.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                               Similarity
HARAASIV 257
                               HARAASIV 441
                                                                                                                               415
                                                               Conservative
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                                                                             1.6%;
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                                                        Score 8; DB 22; ; Pred. No. 65; 0; Mismatches
                                                              0
                                                                                             Length 415;
                                                              Indels
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RESULT 7
AAY74923
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                                                                          Query Match
Best Local
                                                                                                                                       the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                Sequence
                                                                                                                                                                                                                                                     represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ54737 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of polypeptides, the polynucleotides, antibodies and compositions of
                                                                                                                                                                                                                                                                                              AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotid
                                                                                                                                                                                                                                                                                                                                       Claim 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                  vaccines
                                                                                                                                                                                                                                                                                                                                                                               Novel Neisserial polypeptides predicted to be useful antigens for
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-062150/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petersen J,
Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser C,
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02-SEP-1998;
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        454
                                  35 SSTVDAAA 42
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INST GENOMIC RES.
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SSTVDAAA 461
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                                                                                                                                                                                                                                                                                                                                                                 and diagnostics
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Pizza M, Rappuoli R,
                                                                                                                  497 AA;
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC;
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98US-0103749.
98US-0103794.
98US-0103796.
99US-0121528.
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98US-0094869
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                                                                          1.6%;
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                                                           Score 8; DB 2; Pred. No. 76; 0; Mismatches
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Ratti G,
                                                                          DB 21;
o. 76;
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Scalato E,
                                                                                     Length 497
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RESULT

SEQ ID

NO:1324

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Query Match
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Matches 8
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31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
                                                                                                                                                                                  AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the mapufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                   Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                        Novel Neisserial polypeptides predicted to be useful antigens vaccines and diagnostics -
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-062150/05.
N-PSDB; AAZ53686.
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Tettelin H,
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INST GENOMIC
                                                                                                              Similarity 100
8; Conservative
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                                                               SSTVDAAA 461
                                                                                    SSTVDAAA 42
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Pizza M, Rappuoli R,
                                                                                                                                                                 497
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                                                                                                                                                                                                                                                                                                                                                                  725; 1453pp; English.
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98US-0098062.
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98US-0103794.
98US-0103796.
98US-0103796.
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Ratti G,
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Scalato E, Scarselli
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09-OCT-1998;
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31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
                                                                                                                                                                                                             polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
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                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Novel Neisserial polypeptides predicted to be useful antigens vaccines and diagnostics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-062150/05.
N-PSDB; AAZ53687.
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Tettelin H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1999
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                                                                                       454
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                                                                                                        35 SSTVDAAA 42
                                                                                                                                       Similarity
8; Conserv
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INST GENOMIC RES.
                                                                                        SSTVDAAA
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                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0103749.
98US-0103794.
98US-0103796.
99US-0121528.
                                                                                                                                                                                          Ŗ,
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98US-0094869.
98US-0098994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US09346.
                                                                                        461
                                                                                                                                                   1.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grandi G,
Rappuoli R,
                                                                                                                                       0;
                                                                                                                                                    Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hickey
Ratti
                                                                                                                                                    DB 21;
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Masignani V, Mora M; Scalato E, Scarselli M;

for

RESULT 9
AAY74925
ID AAY7

AAY74925 standard; Protein; 497

B

ABP80199;

ABP80199 standard; Protein;

508

B

0

Indels

0

Gaps

0

Length 497;

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RESULT 11
AAY93290
ID AAY93
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                                                                                                                                                                                                                                                                                          Query Match
Best Local &
Matches &
 (INMR )
                                                                                                       Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy.
                            30-OCT-1998;
                                                                                      WO200026375-A2
                                                                                                                           Pathogenic
                                                                                                                                            Amino acid sequence
                                                                                                                                                                                   AAY93290;
                                                                                                                                                                                                     AAY93290 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         medicament
                                               28-OCT-1999;
                                                                                                                                                                04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                   molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                      Drsclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fontana MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-2001; 2001GB-0003424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-FEB-2002; 2002WO-IB02069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gonorrhoeae amino acid
                                                                                                                                                                                                                                                      465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003-058415/05.
                                                                                                                                                                                                                                                                       35
PASTEUR MERIEUX SERUMS & VACCINS SA. INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                     SSTVDAAA 472
                                                                                                                                                                                                                                                                      SSTVDAAA 42
                                                                                                                                                                                                                                                                                                                                                  of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gonorrhoeae
                                                                                                                                                                                                                                                                                                                                508
                                                                                                                         strain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                       from Neisseria gonorrheae, useful for the manufacture of for treating or preventing N. gonorrheae infection
                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 690;
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                A,
                                               99WO-FR02643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection;
                             98FR-0013693
                                                                                                                                                                                                                                                                                                                                                           in records ABP76736-ABP81046 represent
                                                                                                                         Neisseria;
                                                                                                                                                                                                    Protein;
                                                                                                                                            of a polypeptide of a Neisseria pathogenic strain.
                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                  1.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      815pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masignani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                     697
                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                  Score 8;
Pred. No.
                                                                                                                         vaccine; Neisseria infection
                                                                                                                                                                                                     ₽
                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monaci
                                                                                                                                                                                                                                                                                                DB
77,
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                                                                                                                                                                                                                                                                                                            24;
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                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                           Length 508;
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                                                                                                                                                                                                                                                                                                                                                           nucleic
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                                                                                                                                                                                                                                                                                                                                                            acid
                                                                                                                                                                                                                                                                                         Gaps
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RESULT 12
AAY93303
ID AAY93
      당. 왕
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Best Local S
Matches 8
                                                                                                                                                                                   Aujame L,
Tinsley C,
The present sequence represents a protein that is specific for pathogenic strains of Neisseria. The polynucleotides, polypeptides, or their antigenic fragments, are used in vaccines to treat or protect against Neisseria infections, particularly by N. meningitidis. The polynucleotide sequence is also used for recombinant production of the polypeptide and to produce attenuated Neisseria strains that
                                                                                                                                                WPI; 200
N-PSDB;
                                                                                                             New polypeptide specific or preventative vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a protein that is specific for pathogenic strains of Neisseria. The polynucleotides, polypeptides, or their antigenic fragments, are used in vaccines to treat or protect against Neisseria infections, particularly by N. meningitidis. The polynucleotide sequence is also used for recombinant production of the polypeptide and to produce attenuated Neisseria strains that overexpress it, or express it in a non-toxic mutant form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aujame L
Tinsley
                                                                                     Claim 6; Page 173-175; 187pp; French.
                                                                                                                                                                                                                                                              30-OCT-1998;
                                                                                                                                                                                                                                                                                                              11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                            Neisseria gonorrheae
                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide specific or preventative vaccines
                                                                                                                                                                                                                                                                                      28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                     WO200026375-A2.
                                                                                                                                                                                                                                                                                                                                                                                    Pathogenic strain; Neisseria; vaccine; Neisseria infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY93303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY93303 standard;
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                                                                                                                                                                                                                         (INMR ) PASTEUR MERIEUX (INRM ) INSERM INST NAT
                                                                                                                                                   2000-365622/31.
DB; AAA15333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA15321.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSTVDAAA 42
                                                                                                                                                                                    Bouchardon Perrin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bouchardon Perrin A;
                                                                                                                                                                                                                                                                                                                                                                                                            sequence of a polypeptide of a Neisseria pathogenic strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               697 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                              98FR-0013693
                                                                                                                                                                                                                                                                                      99WO-FR02643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 697 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.6%; or
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
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                                                                                                                                                                                                                         SERUMS & VACCINS SA.
SANTE & RECH MEDICALE
                                                                                                              for
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and
                                                                                                                                                                                                 Renauld-Mongenie G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Renauld-Mongenie G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 8; DB 2; Pred. No. 1e+
0; Mismatches
                                                                                                             pathogenic Neisseria useful for diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathogenic Neisseria useful
for diagnosis -
                                                                                                           diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
). 1e+02;
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                                                                                                                                                                                                 Rokbi
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                                                                                                                                                                                                 B, · Nassif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       697
                                                                                                                           in therapeutic
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ABP65660
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 RESULT 13
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Best Local S
Matches 8
                                                                                                                                                                                                                 The present invention describes a polynucleotide (I) comprising a sequence of a Bifidobacterium genome selected from the nucleotide sequences given in ABQ81842 and ABQ81843, or a sequence exhibiting at least 90% identity or which hybridises with the sequences given in ABQ81842 and ABQ81843. Also described is a polynucleotide (II) encoding a fusion protein, comprising a sequence selected from 1997 sequences given in ABP65258 to ABP66354 ligated in frame to a polynucleotide encoding a heterologous polypeptide. (I) has antidiarrheic and antibacterial activities, and can be used as an inhibitor of Salmonella. (I) (which is a probe) is useful for the detection and/or identification of Bifidobacterium longum in a biological sample. A carrier containing the lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618) can be used for preventing and/or treating diarrhoea brought about by
                              pathogenic bacteria and/or rotavirus. The carrier is a food composition selected from milk, yogurt, curd, cheese, fermented milks, milk based fermented products, ice-creams, fermented cereal based products, milk based powders, infant formula, pet food or a pharmaceutical composition selected from tablets, liquid bacterial suspensions, dried oral supplement, wet oral supplement, dry tube feeding or wet tube feeding.

(I) is useful in DNA arrays or chips to carry out analysis of the expression of the Bifidobacterium gene. AB081844 to AB081850 represent Bifidobacterium related nucleotide sequences given in the Sequence Listing from the present invention but not mentioned further within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              overexpress it,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotide comprising Bifidobacterium genome sequence useful as a probe or primer for detecting and/or identifying Bifidobacterium longum in a biological sample \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bifidobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antidiarrheic; antibacterial; inhibitor of Salmonella; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP65660 standard; Protein; 995
                   specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-668397/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001EP-0102050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001EP-0102050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rotavirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bifidobacterium longum NCC2705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35
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8; Conserv
sequence data for this patent is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID 404; 80pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           food composition; pharmaceutical composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROD NESTLE SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              express it in a non-toxic mutant form
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 8; DB 2; Pred. No. 1e+
0; Mismatches
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hhibitor of Salmonella; dete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2.
40. 1e+02;
 not represented in the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID NO:404.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacteria;
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RESULT 14
AAB12246
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Query Match
Best Local Similarity
7; Conserv
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-1998;
08-FEB-1999;
04-NOV-1999;
                                                                                                               HIV group 0. The present sequence is the descending helix of 9941. This sequence was used in a sequence homology alignment, which in turn was used to derive consensus sequence peptides (AAB12259 and AAB12260). The peptides of AAB12259 and AAB12260 were used as group O replacement peptides. The peptides of AAB12259 and AAB12260 were used to construct mosaic 9941 proteins, in which the group M immunodominant region was replaced by the peptides of AAB12259 or AAB12260. The mosaic 9941 proteins (AAB12261 and AAB12262) would be useful as antigens, which would be used for the detection of anti-group O HIV antibodies produced
                                                                                                                                                                                                                                      The present sequence is a partial gp41 protein of Human Immunodeficiency Virus Type 1 (HIV-1) strain DUR. HIV is the principle aetiological agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV envelope protein, and may be used as an antigen for the detection of antibodies produced in response to HIV infection. DUR is a member of HIV group O. The present sequence is the descending helix of gp41. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV-1; AIDS; human immunodeficiency virus type 1; group O HIV; acquired immunodeficiency syndrome; group M HIV; gp41; DUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification but is based 
European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                             virus
                                                                                                                                                                                                                                                                                                                                                                                          New antigenic peptides and peptide functional derivatives, useful for detection of antibodies produced in response to human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     De Leys R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1013766-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Partial sequence of HIV-1 strain DUR gp41 descending helix.
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                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                 Example 4; Fig 4; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-402205/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-NOV-1999;
                                                                                                    in response to HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC
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                                                                        \mathfrak{S}_{\mathfrak{S}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zheng
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99US-0119138.
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                                                                                                      infection
            1.4%; Score 7; DB 100.0%; Pred. No. 69 tive 0; Mismatches
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Pred. No. 1.4e+02
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RESULT 15
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                                                                            RESULT 16
ABG55536
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Best Local Similarity
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ABG55536;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a human protein . The human protein, preferably originated from tumour cell line, is applicable as a drug, a reagent for studying intracellular protein networks and a protein source for screening proteins for binding low molecular weight drugs. The human protein coding sequence is useful for gene diagnosis and gene therapy, expression vectors and transformant cells for detection of ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein originated from tumor cell line, applicable as drug, reagent for studying intracellular protein networks and protein source for drug screening, also encoded cDNA for gene diagnosis and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 416; 471pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAH68604.
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                                                ABG55536 standard; Peptide; 71 AA.
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14-MAR-2000;
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                                                                                                                                                                                   GGGAEAS 12
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                                                                                                                                                                                                                                                                                                                                                                                         39 AA;
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2000JP-0034091.
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2000JP-0071161.
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, 100.0%; Pred. No.
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RESULT 17
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Best Local Similarity
Matches 7; Conserv
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Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                          Sequence
                                                                   04-FEB-2002
                                                                                              ABB40293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID No 34184; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
                                     Peptide #7799 encoded by human foetal liver single exon probe
                                                                                                                         ABB40293 standard; Peptide; 71
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                                                                                                                                                                                                                                                                                                                                       from WIPO
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                                                                                                                                                                                                                      494 AKAKKTK 500
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                                                                                                                                                                                             AKAKKTK 34
                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                                          71
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2000GB-0024263.
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2000US-0234687.
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2000US-0207456.
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                                                                   (first entry)
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100.0%; Pr
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0; Mismatches
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Human; foetal liver; gene expression; single exon nucleic acid probe.

Homo

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RESULT 18
AAM61086
ID AAM61
AC AAM61
AC AAM61
XX AAM61
XX DT O5-NC
XX Humar
XX Humar
XX Humar
XX Humar
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XX Homo
XX Homo
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XX WO200
XX O9-Al
XX O4-FE
PR 26-MJ
PR 30-JI
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exo nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                      30-JAN-2001;
                                                                                                                                Homo sapiens.
                                                                                                                                                                   Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                       Human brain expressed single
                                                                                                                                                                                                                                 05-NOV-2001
                                                                                                                                                                                                                                                         AAM61086;
                                                                                                                                                                                                                                                                               AAM61086 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157277-A2.
                                                                                                       WO200157275-A2
                                                                                                                                                       epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                                                                                                   494 AKAKKTK 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome-derived single
                                                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                           AKAKKTK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                              71
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2000US-0608408.

2000US-063256.

2000US-0234687.

2000US-0234687.

2000US-0236359.

2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
      2000US-0180312.
2000US-0207456.
2000US-0608408.
                                                       2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001WO-US00669
                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO 32928;
                                                                                                                                                                                                                                                                                                                                                                                                         1.4%; Score 7; DB 22; Lo
100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     le exon nucleic acid probes useful for in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                  71
                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                       probe encoded protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 71;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
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RESULT 19
AAM73789
ID AAM73
XX AAM73
XX AAM73
XX O6-NC
XX Human
XX Micro
DS Homo
PN W0200
XX 09-AU
XX 30-JA
PF 04-FE
PR 04-FE
PR 27-SE
PR 27-SE
PR 21-SE
PR 21-SE
PR 21-SE
PR 21-SE
PR 21-SE
PR 21-SE
PR 04-OC
XX WPI;
XX MPI;
XX Human
DR WPI;
XX Human
PI Human
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Matches
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                            03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                    Human; bone microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone {\tt marrow} -
                                                                                                                                                                                                                                                                                                                                        Human bone marrow expressed probe encoded protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single
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                                                                                                                                                                                                              30-JAN-2001; 2001WO-US00668
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                                                                                                                                                                                                                                                                                                                                                                                       AAM73789;
                                                                                                                                                                                                                                                                                                                                                                                                            AAM73789 standard; Protein; •71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4;
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                                                                                                                 04-OCT-2000;
                                                                                                                                                                                                                                                         WO200157276-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           494 AKAKKTK 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon nucleic acid
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                                                                                            MOLECULAR DYNAMICS INC
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                                                                   Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4%;
ilarity 100.0%
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
; 2000GB-0024263.
                                                                                                               ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                      marrow expressed exon;
cancer; leukaemia; lymp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention provides a number of single
                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                   DK,
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                                                                     Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.0%;
O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7; DB 2; Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank
                                                                                                                                                                                                                                                                                                      lymphoma; myeloma.
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                                                                      Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   analyzing gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; LC.
No. 1.3e+02; 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic ac
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8 X S S S S S S S X &

Example

4

SEQ ID

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34095; 658pp + Sequence Listing;

English

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RESULT 20
AAM33976
Query Match
Best Local Similarity
Thes 7; Conserve
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide #8013 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM33976 standard; Protein; 71 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                        see AAI31115-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes see AAI31315-AAI57546). The present sequence is a peptide encoded
                                                                                                                                                                                                                                                                                   Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157272-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe; microarray;
                                                                                                                                         numan genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         494 AKAKKTK 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
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                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                   SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 AA;
                                                                                                   71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
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                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000GB-0024263.
                                                                                                 A
                                                                                                                                                                                                                                                                                                                           expression
                                                                                                                                                                                                                                                                               No 34245; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                               봈
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.4%;
                   1.4%; Score 7; DB (
100.0%; Pred. No. 1.0
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W,
                                                                                                                                                                                                                                                                                                                   in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7; DB 2; Pred. No. 1.3
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antenatal diagnosis;
                                    DB 22; L
o. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Le
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                                                       Length 71;
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                   Indels
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                   Gaps
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RESULT 21
ABG43675
ID ABG4
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CC The invention relates to a spatially-addressable set of single exon concluded acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 crombes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a concleic acid expressed in the human lung; measuring gene expression in a csample derived from human lung; comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung measuring the expression in a csample derived from human lung. The labeled nucleic acids derived from human lung measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising comprising comprising the array; identifying exons in a eukaryotic genome, comprising comprising comprising the example exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably claim a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method cabove and (b) measuring the expression of each of the exon in several classes and/or cell types using hybridisation to a single exon from factor above and by measuring the expression of each of the exon in several comprising the expression of each of the exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human peptide encoded by genome-derived single
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ ID No 33340; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pulmonary alveolar proteinosis; fibrocystic pulmona
primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chronic obstructive pulmonary disease; interstitial lung dis
familial idiopathic pulmonary fibrosis; neurofibromatosis;
tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; single exon probe; asthma; lung cancer; COPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG43675 standard; Peptide; 71 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyaline membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression in human lung samples
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
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; 2000US-0608408.
; 2000US-0632366.
; 2000US-234687P.
; 2000US-236359P.
; 2000GB-0024263.
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RESULT 22
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               capable of detecting 1000 or more genes from Drosophila. The invent
useful in developmental biology and in elucidating cell signalling
cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                    New isolated nucleic acid genes from Drosophila and
                                                                                                                      Disclosure; SEQ ID NO 8928; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
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11-JUL-2000;
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)B; ABL04815.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    melanogaster polypeptide SEQ ID NO 8928.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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2000US-0614150.
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                                                                               relates to an isolated nucleic acid detection reagent
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Pred. No. 1.3e+02;
                                                                                                                                                                                      ection reagent
elucidating c
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                                                                                                                                                                                                                The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
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                                                                                                                                                                                       activity, tissue growth factor activity, immunomodulatory activity activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosing disorders .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAI90858
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18-MAY-2000;
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                                                                                    Note: The sequence data for this patent did not specification, but was obtained in electronic for
                                                                                                                                                                   treatment of cancer, leukaemia, nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 24819; 1399pp + Sequence Listing; English
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                                                                                                                                          inflammation.
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o. 1.6e+02;
                                                                                                                                                                   system disorders,
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Sequence

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Score 7; Pred. No.

DB 22; L
5. 1.7e+02;

Length 94;

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RESULT 24
AAW07245
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Best Local S
Matches 7
                                                              Matches
                                                                            Query Match
Best Local :
                                                                                                                                                             immunodeficiency virus (HIV) type 1, designated group 0. In particular, the inventors have isolated 2 new strains of the group 0 virus: strains VAU and DUR. Strain VAU was isolated from a French AIDS patient and has homology to the recently characterised Cameroonian HIV strains ANT70 and MVP5180. The DUR strain was isolated from a seropositive patient from the Cameroons who showed atypical seroreactivity. The sequence presented here represents the amino acid sequence of the DUR strain gp41 immunodominant region. The DNA and protein sequences are used to generate peptides for detection of antibodies from patients infected with the new group 0 strains, as well as primers and probes to detect the viral nucleic acids. The peptides and nucleic acid sequences derived from these strains are able to distinguish between the group 0 and group
                                                                                                                                                                                                                                                                                                                                                                                                          New antigenic HIV-1 group O strain proteins and related nucleic acids - useful in diagnosis, vaccines, therapy etc., of infection by HIV-1 group O strains VAU or DUR
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                Claim 24; Fig 12; 108pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borman A,
Donjon de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus; subgroup; strain; AIDS; homology; envelop; gp120; gp41; seropositive; antibody; primer; probe; group O; group M.
                                                                                                                                                    M viral strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-230610/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAR-1995;
20-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV-1 group O strain DUR gp41 immunodominant region peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW07245 standard; Protein; 104
                                                                                                                                                                                                                                                                                                                                                The invention relates to the isolation of a novel subgroup of the human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 TGPGGGA 153
                               467 DOQIANV 473
. 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunodeficiency virus type 1.
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                                                           Similarity 7; Conserv
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    DOQIANV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGPGGGA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charneau P,
                                                                                                                        104 AA;
                                                              Conservative
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94FR-0012554.
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                                                            Score 7; DB 1; Pred. No. 1.9
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                                                                            DB 17; I
o. 1.9e+02;
                                                                                        Length 104;
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RESULT 26

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RESULT 25
ABG26287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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food supplement; medical imaging; diagnostic; genetic d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
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                                                                        434 HARAASI 440
82
                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                        105 AA;
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                                                                                                                                             100.0%;
                                                                                                                                                          1.4%; Score 7; DB:
100.0%; Pred. No. 1.:
1ve 0; Mismatches
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                                                                                                                                             DB 22; L.,
No. 1.9e+02;
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RESULT 27
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                                                                                               Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulce vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disoneurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                    A sequence including the ORFs coding for the large and small subunits of the rubisco enzyme has been isolated from Agmenellum quadruplicatum RR-6 (Synechbococcus sp. strain PCC7002). The region coding for the rubisco small subunit is claimed; the enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Promoter sequence of Synechococcus PCC7002-originated rubisco geused in a vector to produce Cyano:bacterium with improved carbon di:oxide fixation
18-MAY-2001; 2001WO-US16450.
                                                      WO200190304-A2
                                                                                                                                                                        Human polypeptide SEQ ID
                                                                                                                                                                                                 24-MAY-2002
                                                                                                                                                                                                                                              ABB89496 standard; Protein; 114
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Page 25; 28pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-157852/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agmenellum quadruplicatum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR72394 standard; Protein; 111
                              29-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KANT ) KANSAI DENRYOKU KK
                                                                                                                                                                                                                                                                                                                             465 LSDQQIA 471
                                                                                                                                                                                                                                                                                                        19 LSDQQIA 25
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bunit; carbon dioxide fixation; Synechococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                    111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           in carbon
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                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                . 7;
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0. 2e+02;
                                                                                                                                    neuroprotective; antiviral; antiinflammatory; antiulcer;
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12-MAR-1999; 11-JUN-1999;

99US-0124095 99US-0138598

09-MAR-2000; 2000WO-US06014.

WO200055199-A1 Homo sapiens. cardiant; gene therapy; cancer; immune disorder; cardiova neurological disease; infection; human; secreted protein.

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                  Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasicic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia an epilepsy; and (f) infectious diseases such as viral, bacterial, fung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                   Sequence homologous to protein fragment encoded by
                                                                                                                                                                                                                                                                                                                      29-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                        AAB27869 standard; Protein; 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epilepsy; and (f) infecti
and parasitic infections;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 1872; 2081pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALMLSGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isolated polypeptides, useful for diagnosis, treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23;
. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 29
ABG08519
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Best Local Similarity
Matches 7; Conserv
                    WPI; 2001-639362/73
                                                             Drmanac RT,
                                                                                                                                                  31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                         WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #8510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG08519 standard; Protein; 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 417; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-572359/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    494 AKAKKTK 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                                                                      HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKAKKTK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                           Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.4%;
                                                           Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Komatsoulis
                                                             ΥT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>.</u>
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Pred. No. 2.1e+02;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 8
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X44444X8X9999999999999999998
                                                                                                                                                                                                           polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCM) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                          and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID No 38878; 103pp;
124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotide (I) and suseful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
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Query Match
Best Local
                                      Matches
                  326 PGDYVLV 332
 87
                                               Similarity
PGDYVLV 93
                                     Conservative
                                              1.4%; Score 7; DB 22; L
100.0%; Pred. No. 2.2e+02;
                                .
0;
                                     Mismatches
                                                       Length 124;
                                     Indels
                                    <u>..</u>
                                    Gaps
                                    0;
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Human polypeptide SEQ ID NO 15412.
                                            06-NOV-2001 (first entry)
                                                                                                                                       AAO01520 standard;
                                                                                                                                       Protein; 124 AA
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Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation. domo sapiens

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WO200164835-A2
26-FEB-2001; 2001WO-US04927.
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WPI; 2001-514838/56.
N-PSDB; AAI81451.
         Tang YT,
                        28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                HYSEQ
          Liu C,
                 INC
          Drmanac
          RT
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ABB55608
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibit activity and may be useful in the diagnosis and/or
The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic diagnosing and tradisorders -
                                                                                                                                                                                                                             New nucleotide sequence useful in lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                     Claim 6;
                                                                                                                                                                                                                                                                                                                                              Bolotine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FR2807446-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactococcus lactis protein rpsI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB55608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                           (INRG ) INRA INST NAT RECH AGRONOMIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                    2002-043418/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 7; Conserv
                                                                                                                                                                                   SEQ ID No 2310; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APEVPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APEVPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lactis IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                              Sorokine
                                                                                                                                                                                                                                                                                                                                                                                                                                        2000FR-0004630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000FR-0004630.
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treating e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO 15412; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%;
                                                                                                                                                                                                                                                                                                                                              A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e.g.
                                                                                                                                                                                                                                                                                                                                              Renault P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides, useful for p
g. leukaemia, inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                       identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                 Ehrlich SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccines or
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RESULT 32
AAG07374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
          08-APR-1999
16-APR-1999
19-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
30-APR-1999
30-APR-1999
06-MAY-1999
06-MAY-1999
06-MAY-1999
11-MAY-1999
                                                                                                                                                                                                                                                            23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
                                                                                                                                                                                                                                                                                                            25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                   25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                      06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                     hybridisation assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG07374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG07374 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447 GKITVNG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKITVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                   2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
99US-0125788
99US-0126785
99US-0127462
99US-0128734
99US-0128734
99US-0129845
99US-0130510
99US-0130510
99US-013044
99US-013044
99US-0130449
99US-013048
99US-0132484
99US-0132487
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                                                                                                                                                                                                                                                                                             A,
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99US-0162866.
                                                                                                                                 1.4%; 5cc
100.0%; Pr
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                                                                                                                                            Score 7; DB 2; Pred. No. 2.6
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                                                                                                                                                                              DB 21; L
                                                                                                                                                                                                                 Length 156;
                                                                                                                                                Indels
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ABB58068 ID ABB5 XX

ABB58068 standard; Protein; 167 AA.

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RESULT

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                                                                                                                                                                       ABP38126
                                                                                                                                                                                 RESULT 36
                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                               Matches
                                                      Staphylococcus antibacterial;
                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form specification, but was obtained in electronic fat ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                           insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic a genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000;
11-JUL-2000;
           US6380370-B1
                                 Staphylococcus epidermidis
                                                                                       Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:2971.
                                                                                                               24-JUL-2002
                                                                                                                                     ABP38126;
                                                                                                                                                           ABP38126 standard; Protein; 172
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB58068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interactions -
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                                                                                                                                                                                                                                                                                                                                                                  (ABB57737-ABB72072)
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                                                                                                                                                                                                                                                             1.4%;
Similarity 100.0%;
7; Conservative
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                                                                                                                                                                                                                    VPPPVDR 124
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                                                                                                                                                                                                                                                                                                           167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 996; 21pp + Sequence Listing; English.
                                                                                                              (first entry)
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                                                      epidermidis; open gene therapy.
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Mismatches
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                                                                 reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                           DB 22; L. (o. 2.8e+02; 0;
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                                                                                                                                                                                                                                                                                  Length 167;
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RESULT 37
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life
                                                                                                                                                                                                                                        Corn; soybean;
branched chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-381255/41.
N-PSDB; ABN90671.
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08-NOV-1997;
                       28-OCT-1997;
                                                20-OCT-1998;
                                                                                                                                       Misc-difference
                                                                                                                                                               Misc-difference
                                                                                                                                                                            Key
                                                                                                                                                                                                     Triticum aestivum.
                                                                                                                                                                                                                             3-isopropylmalate dehydratase.
                                                                                                                                                                                                                                                                               Wheat branched chain amino acid transaminase amino acid sequence.
                                                                                                                                                                                                                                                                                                                                 AAY28428;
                                                                                                                                                                                                                                                                                                                                                        AAY28428 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
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                                                                         06-MAY-1999.
                                                                                                  WO9921880-A2
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(DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENO-) GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                      151 FYTKGKY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                              219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 100 7; Conservative
                                                                                                                                                                                                                                        ybean; wheat; rice; dihydroxyacid dehydratase; leuC; leuD; chain amino acid transferase; biosynthetic enzyme; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                              FYTKGKY 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                      (first entry)
                       97US-0063423
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97US-064964P.
                                                 98WO-US22081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID 2971;
                                                                                                                                                                           Location/Qualifiers
                                                                                                                          /note=
                                                                                                                                                   note= "encoded by TAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epidermidis infection.

ata for this patent did not form part of the printed was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; ...
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                                                                                                                                                                                                                                                                                                                                                          180
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0; Mismatches
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2.9e+02;
0;
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RESULT 38
AAM86749
ID AAM86
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Best Local S
Matches 7
                                      16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUN-2000;
                                                                                                                                         31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY28418-Y28431 are fragments of corn, soybean, wheat and rice branched chain amino acid transaminase, amino acid sequences. Sequences AAX89442-X89465 are nucleic acid fragments that encode all or a substantial portion of dihydroxyacid dehydratase, a branched chain amino acid transferase, a leuC or a leuD subunit of 3-isopropylmalate dehydratase from wheat, corn, soybean or rice. These enzymes are involved in biosynthesis and utilization of branched-chain amino acids. The nucleic acid sequences can be used to alter the level of expression of a branched chain amino acid biosynthetic enzyme in a host cell. They can also be used to obtain a nucleic acid fragment encoding a branched chain amino acid biosynthetic enzyme, and to identify inhibitors of a branched chain amino acid biosynthetic enzyme. The encoded proteins may be used to prepare antibodies for detecting the proteins in situ in cells, or in a call extracts.
                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                   Human immune/haematopoietic
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                                                                                                                                                                                                                                                                                                                                                                                                                                AAM86749 standard; Protein; 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell extracts.
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2000US-0189874.

2000US-019076.

2000US-0198123.

2000US-0205515.

2000US-0209467.

2000US-0211335.

2000US-0211647.

2000US-02174880.

2000US-0217487.

2000US-0217487.
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                                                                                                                                                                                                          2001WO-US01354
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                                                                                                                                                                                                                                                                                                                                                                           entry)
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                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:14342.
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  29-SEP-2000

29-SEP-2000

29-SEP-2000

29-SEP-2000

02-OCT-2000

02-OCT-2000

02-OCT-2000

13-OCT-2000

13-OCT-2000

20-OCT-2000

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26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
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21-SEP-2000;
25-SEP-2000;
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30-AUG-2000
01-SEP-2000
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08-SEP-2000
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22-AUG-2000
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2000US-0240960.
2000US-0241221.
2000US-0241786.
2000US-0241786.
2000US-0241787.
2000US-0241808.
2000US-0241808.
2000US-0241808.
2000US-0241826.
2000US-0241826.
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2000US-0224519.
2000US-0225213.
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2000US-0236370
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2000US-0234997
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2000US-0234223
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAW82170 to AAW91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the
                                                                                                                                                                     useful for metastasis
                                                                                                                                                                                            Nucleic
                                                                                                                                                                                                                   N-PSDB; AAK59530.
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17-NOV-2000;
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                                                                                                                                                                       acids encoding for preventing, sis -
                                                                                                                                               SEQ ID
                                                                                                                                                                                                                                                     Barash
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2000US-0249264.
2000US-0249265.
2000US-0249297.
2000US-0249297.
2000US-0249299.
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2000US-0249212.
2000US-0249213.
2000US-0249214.
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2000US-0249217.
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                                                                                                                                                                              human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
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                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
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                                                                                                                                                               Sequence
                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid genes from Drosophila and interactions -
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N-PSDB; ABL15311.
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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## ALIGNMENTS

RESULT 1 US-09-252-991A-8682

Sequence 8682, Application US/09252991A Patent No. 6551795

Percent Similarity:
Best Local Similarity:
Query Match: US-10-088-045-2 (1-502) Score: Alignment Scores: US-09-252-991A-8682 PATERIC NO. TOTAL PATERIC DISCONDINE GENERAL INFORMATION:

APPLICANT: MARC J. Rubenfield et al.

APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 8682 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 LENGTH: 1938
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa No.: 1.99e-07 163.50 33.96% 21.78% 6.23% x US-09-252-991A-8682 Mismatches: Indels: Matches: Conservative: (1-1938) TO PSEUDOMONAS

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                                                                                                                       HisAsnIleGlnThrThrLeuIleProAlaGlyGlyAlaAlaIleThrGluPheLysVal
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                                                          AspValProGlyAspTyrValLeuValAspHisAlaIlePheArgAlaPheAsnLysGly
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8564
LENGTH: 1971
TYPE: DNA
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Best Local Similarity:
Query Match:
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US-09-252-991A-8564/c
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US-09-252-991A-8564
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GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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CURRENT FILING DATE: 1999-02-18
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                                                                               1728 ---AAGCTGCGTGAAGCCACATCCATTCACTGGCACGGGATCATCCTGCCGTATCAGATG
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
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RESULT 3
US-09-296-284-23
; Sequence 23, Application US/09296284A
; Patent No. 6204040
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APPLICANT: Choi, Eui-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase,
TITLE OF INVENTION: and Methods of Use Thereof
FILE REFERENCE: 1533.087000
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
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     hrGlnGluAla-----
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                                                                                                                TGAAGACGACATTGCCGAGTTCCTGAAG---AGCGGCCGTATCGACCATTCTGCCGTCTT
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Oy  171 LeuGlnProGlyLeuTyrValTyrHis	GANISM: Gluconobacter suboxydans 296-284-2 296-284-2 ent Scores: 1.41e-07 Ler No.: 163.00 Cor t Similarity: 35.85% Cocal Similarity: 6.21% Gar Match: 3 Gar	Rhee, E Lee, E Lee, E Lee, E ENCE: I PLICATION LING DAT LING DAT SEQ ID N Patenti	1187 AGCTCCGC SULT 4 -09-296-284-2 Sequence 2, Applicati Patent No. 6204040 GENERAL INFORMATION: APPLICANT: Choi. Eu	Qy 459 alMetProAlaIleAlaLeuSerAspGlnGlnIleAlaAsnValIleThrT 476	Db 774 CGCAACG-GCCAAGTACCTGAAGAGCATGCCGGCCGTTCCGGAAGGCAAAAACCTGGGTC 832  Qy 392 InGluGInIleLys
Qy 439 erilevalalaAsnGlyLeuSerGlyLysIleThrValAsnGlyAsnGlnTyrGluSerV 459	Qy 392 lnGluGlnIleLys	Qy 347	317 alleThrGluPheLysValAspValProGlyAspTyrValLeu	Db 495GCCGTTGGCCATCTGGCGGCGCGCGTTGTTCCGACTGTCACACCAGGCCTCGA 548  Qy 281 rSerSerPheHisVallleGlyGluIlePheAspLysValHisPheGl 297  Db 549 CAAGAGCATCCCGATCCGGAAGTGGCGCGTGGCAATACCTCGTGAATGGCCC 602  Qy 297 uGlyGlyLysGlyGluAsnHisAsnIleGlnThrThrLeuIleProAlaGlyGlyAlaAl 317	Qy 215 MetGlnGlyAspPheTyrThrLysGlyLysTyrGlyGluGlnGlyLeuGlnProPheAsp 234 ::::::  Db 295 CTCGAAGATTTCACGAAGGCG

US-02-26-244-7  IS SEQUENCE 7, Application US/09296284A  FRANCH No. 2204040  GENERAL INFORMATION: APPLICANT: (Doi: Dai: Sung' All APPLICANT: (Doi: Dai: Sung' All APPLICANT: (Doi: Dai: Sung' All APPLICANT: (Doi: Dai: Sung' All APPLICANT: (Doi: Dai: Sung' All APPLICANT: (Doi: Dai: Sung' All APPLICANT: (Doi: Dai: Sung' All APPLICANT: (Doi: Dai: Dai: Sung' All APPLICANT: (Doi: Dai: Dai: Dai: Dai: Dai: Dai: Dai: Da	Qy 495 ysAlaLys 497 .     ::: Db 1295 AGCTCCGC 1302
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235 METCHLYSALAILEATGGGGGGGCCACCGGTTTATCCCGGCCATGCCGTAGCTGAGGTGGGGGCCACCGGTTTATCCCGGCCATGCCGTAGCTGAGGGGGGGCCACCGGTTTATCCCGGCCATGCCGGAGGGGGGGCCACCGGTTTATCCGGCCATGCCGGAGGGGGGGG	3213 ACCAACATCACGCCTGACCCGAAATACGGTATCGGCAACTATACA 3257 215 MetGlnGlyAspPheTyrThrLysGlyLysTyrGlyGluGlnGlyLeuGlnProPheAsp 234

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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DAN SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 4403765
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Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
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                                                                                               SerLysMetProHisAsnValAspPheHis-----AlaAlaThrGlyProGlyGlyGly
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GGCACCATGGCCAAGTACGACTGGACAATCAACGGGGAACCCTACAGCACGACCAATCCA
                          GlyLeuSerGlyLysIle-----ThrValAsnGlyAsnGlnTyrGluSerValMetPro
                                                                                                                LeuAlaAsnSerAspTyrLeuAsnAlaAspHisAlaArgAlaAlaSerIleValAlaAsn
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US-09-103-840A-1/c ; Sequence 1, Application ; Patent No. 6294328

US/09103840A

GENERAL INFORMATION:

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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE OF INVENTION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1
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224 LysTyrGlyGluGlnGlyLeuGlnProPheAspMetGluLysAlaIleArgGluAspAla 243
                                                                                                                                                                                                                                                                                                                                  153 AlaGluAlaSerPheThr-----AlaProGlyHisThrSerThrPheSerPheLysAla 170
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                                           GAATGGATCATCCTCGACGAT---TGGACGGACGGCATCGGGAAGTCCCCCGCAACAG 943569
                                                                                   GluTyrTyrValMetGlnGlyAspPheTyrThrLysGly-------
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                                                                                                                            ---GGCCTATATCTGCCTGTCGTCGTCGACGATCCGACTGAGCCAGGCCACTACGACGCC 943626
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1/c pplication US/09252991A 95 1ON: ION: C J. Rubenfield et al. ION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS 107196.136 107196.137 TION NUMBER: US/09/252,991A DATE: 1999-02-18 ON NUMBER: US 60/074,788 TE: 1998-02-18 ON NUMBER: US 60/074,788 ON NUMBER: US 60/074,788 TE: 1998-07-18 ON NUMBER: US 60/094,190 TE: 1998-07-27 D NOS: 33142	GlyLeuSerGlyLysIle*ThrValAsnGlyAsnGlnTyrGluSerValMetPro			SerAsnCysAlaAlaCysHisGlnProAspGlyLysGlyValProAsnAlaPheProPro 	ACCGCCGCAACGACTGCCAACCTG	LysThrProAlaProAlaAsnLeuGlnGluGlnIleLysAlaGlyLysAlaThrTyrAsp	ThrAspAlaValTyrLeuProGluGlyAlaProGlnAlaIleAspThrGlnGluAlaPro	GGCGCCGGCAGCCCA	AlaLeuGlyIleLeuLysValGluGlyGluGluAsnHisGluIleTyrSerHisLysGln 	AACGCGCTGGCGCTGCGCTGCTGTCTACC	AlaIl	GTGACCGCCGCTGGCGGGGGTCTTTCCCCTGGTCGCACTCGCGGAAGGCAAG	ThrThrLeuIleProAlaGlyGlyAlaAlaIleThrGluPheLysVal	GlyLyGlyGluAsnHisAsnIleGln		ThrSerSerPheHisVallleGlyGluIlePheAspLysValHisPheGluGly	TTTAAGGCCAAGCCTGGCCAGCGAATCCGGGATCATCAACAGCGCCGCCGACACC	LeuLysAlaLysValGlyGluThrValArgLeuPheValGlyAsnGlyGlyProAsnLeu	ATCGCCTACCCGTACTGATCAACGGGCGAATCCCCGTGGCGGCCACGTCT	GluTyrValValPheAsnGlySerValGlyAlaLeuThrGlyGluAsnAla	ACAGGTATGCCCGAAGGCGAAGGCGTTGACAGCAACCTGCTCGGCGGCGACGGAGGGGAC		
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ORGANISM: Pseudomonas
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                lTyrLeuProGluGlyAlaProGlnAlaIleAspThrGlnGluAlaProLysThrProAl
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                                                      eLeuLysValGluGluGluAsnHisGluIleTyrSerHisLysGlnThrAspAlaVa
                                                                                                                                                                                                    nThrThrLeuIleProAlaGlyGlyAlaAlaIleThrGluPheLysValAspValProGl
                                                                                                                                                                                                                                                          eGlyGluIlePheAspLysValHisPheGluGlyGlyLysGlyGluAsnHisAsnIleGl
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US-10-088-045-2 (1-502) x US-09-252-991A-6490 (1-963)
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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CAAGTTCGCCGCGATGCCCATCGAGGAAGTCGCCAAGGATCCGCAGGCGGTGAAAATGGG
                                           ySerValGlyAlaLeuThrGlyGluAsnAlaLeuLys-----AlaLysValGl
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1314)
; OTHER INFORMATION: I
US-09-252-991A-9169
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US-09-252-991A-9169/c
; Sequence 9169, Application US/09252991A
; Patent No. 6551795
; Patent No. 6551795
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LENGTH: 1470
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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Best Local Similarity:
Query Match:
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US-09-252-991A-8797
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APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SEQ ID NO 8797
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Patent No. 655179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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TYPE: DNA
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                                                                          1019 GCACCGTCGAGCTTCACCATGCCGCCGTTCGGCTGGCGGATGAACGACCAGGAGATCGCC
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AsnValIleThrTyrThrLeuAsnSerPheGlyAsnLysGlyGlyGlnLeuSerAlaAsp :::|||::: :::||| |||
                                                                                                                                                                                                                      AlaArgAlaAlaSerIleValAlaAsnGlyLeuSerGlyLysIleThrValAsnGlyAsn
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Conservative:
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RESULT 13
US-07-985-458-2
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Best Local Similarity:
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                    Sequence 2, Application US/07985458 Fatent No. 5344777 GENERAL INFORMATION:
APPLICANT: Tamaki, Toshimi;
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LENGTH: 2256
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GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
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  APPLICANT:
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    Takemura, Hiroshi;
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153.00
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Matches:
Conservative:
Mismatches:
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Gaps:
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Percent Similarity:
Best Local Similarity:
                                                                              Alignment Scores:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tayama, K
APPLICANT: Fukaya, M
APPLICANT: Okumura,
APPLICANT: Kawamura,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19921203
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/658,221
FILING DATE: 20-FEB-1991
APPLICATION NUMBER: 73440/1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.72
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION:
AUTHORS: Tamaki, Toshimi;
AUTHORS: Fukaya, Masahiro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)972-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                          NO.:
                                                                                                                                                                                                                                                                                                                                                                       AUTHORS:
AUTHORS:
AUTHORS:
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OPERATING SYSTEM: MS
OPERATING ASCII Form
                                                                                                                                      DATE:
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REGISTRATION NUMBER: 1
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                                                                                                                                                                                                                TITLE:
                                                                                                                                                                                                                                                                                                                                   AUTHORS:
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                                                                                                                                                      PAGES: 292-300
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Cloning and Sequencing of the Gene Clus
Encoding Two Subupits of Membrane-Bound
Alcohol Dehydrogenase from Acetobacter
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                                                                                                                                                                                                                                                                                                                                                 Takemura, Hiroshi;
Tayama, Kenji;
Okumura, Hajime;
Kawamura, Yoshiya;
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Horinouchi, Suehar
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Okumura, Hajime a
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Alcohol Dehydrogenase Complex, Plasmid
Containing The Same And Transformed Ac
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Best Local Similarity:
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GENERAL INFORMATION:
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LENGTH: 1335
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142;
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas
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BER: US 60/074,788
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RESULT 15

US-09-252-991A-737

Sequence 737, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCY.

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190
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APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO I

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 646

LENGTH: 1641

TYPE: DNA

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Best Local Similarity:
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Sequence 4893, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4910
LENGTH: 2139
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Best Local Similarity:
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                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                          Sequence 4910, Application US/09252991A Patent No. 6551795
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LENGTH: 1554
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                            US-09-252-991A-8339
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS A
FILE REFERENCE: 107196.136
                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SEQ ID NO 8339
LENGTH: 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8339, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                             ORGANISM: Pseudomonas
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Best Local Similarity:
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 14102
LENGTH: 1782
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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CURRENT FILING DATE: 1999-02-18
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                                    ProGlyHisThrSerThrPheSerPheLysAlaLeuGlnPro
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TyrGluSerValMetProAlaIleAla-----LeuSerAspGlnGlnIleAlaAsnVal 473
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                                                                          AATCTGTTGCGAGTGATCGAAGACGGCATCGTCGAACAG---CAGTTCACCGGCTTCGAA 1611
                                                                                                                     ArgAlaAlaSerIleValAlaAsnGlyLeuSerGlyLysIleThrValAsnGlyAsnGln 455
                                                                                                                                                                                                                                                                                                           AlaGlγLysAlaThrTγrAspSerAsnCγsAlaAlaCγsHisGlnProAspGlγLysGlγ 416
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Patent No. 5
                                                                                                                                                                                                                                                                                            No.:
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LOCATION:
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US-10-088-045-2 (1-502)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: UFFILING DATE: 30-AUG-11 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UFFILICATION NUMBER: UFFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
LENGTH: 1588 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Berka, Randy M.
APPLICANT: Wahleithmer, Jill A.
TITLE OF INVENTION: BLUE COPPER OXIDASE
TITLE OF INVENTION: ENHANCED ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
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CITY: New York
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CTACCTTTGCTCGCTGCGGTCTCAACC--
                                                                 LeuProValIleAspAlaIleValThrHisAlaProGluValProProProValAspArg
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_	84 LysThrProAlaProAlaAsnLeuGlnGluGlnIleLysAlaGlyLysAlaThrTyrAsp 403	38
	85 GCTATCGGTACTGCACTCGTTGAAGAGAACCTCCATGCGCTCATCAACCCTGGCGCTCCG 1044	98
	.82Alapro 383	. 38
	25 TTTGCCGTATTGCACTACGAGGGAGCGCCCAACGCCGAACCCACGACGGAACAAGGCAGT 984	92
	65 AspAlaValTyrLeuProGluGlyAlaProGlnAlaIleAspThrGlnGlu 381	36
	45 LeuGlyIIeLeuLysValGlüclyGlüclüAsnHisGlüIleTyrSerHisLysGlnThr 364 :::	865
	GCTGGACAACGCTACTCTGTCATCGTTGAAGCCAAACCAAACCGCCGCCAACTACTGGATT	80
		325
	10 LeuileProAlaGlyGlyAlaAlaIleThrGluPheLysValAsp 324	310 745
	90 IlePheAspLysValHisPheGluGlyGlyLysGlyGluAsnHisAsnIleGlnThrThr 309	727
		676
	70 ArgLeuPheValGlyAsnGlyGlyProAsnLeuThrSerSerPheHisValIleGlyGlu 289	270
	20 GIYSETVATGIYATAHEUINITGIYGIHASHALAHEUIYSATANYSVALGIYGIUTNIVAT 269	622
		J n
	30 LeuGlnProPheAspMetGluLysAlaIleArgGluAspAlaGluTyrValValPheAsn 249	230 571
	 TACCATACTCCGGCACCCGT	511
	20 Τ̈́γr̈ 229	220
	02LysGluGlyLeuProLysValAspLysGluTyrTyrValMetGlnGlyAspPhe 219	202
_	B5 ValGlyMetHisIleAlaAsnGlyMetTyrGlyLeuIleLeuValGluPro 201 :::	185 391
	55 ThrPheSerPheLysAlaLeuGlnProGlyLeuTyrValTyrHisCysAlaValAlaPro 184	165 343
	50 GlyGlyGlyAlaGluAlaSerPheThrAlaPro	150 283
	34 AspSerLysMetProHisAsnValAspPheHisAlaAlaThrGlyPro 149 	134 223
0 11 4	17 IleArgValArgGluGlyAspThrIleGluValGlnPheSerAsnHisPro 133     ::          :: ::: 63 ATCACGGCCAACAAGGGTGACACCTTGCGCATTAATGTCACGAATCAACTCACGGACCCT 222	117 163
O E (	97 LeuAlaAspGlyValGluTyrGlnPheTrpThrPheGlyGlyGlnValProGlyGlnMet 116	97
	79 AspHisProAlaLysValValValLysMetGluThrValGluLysValMetArg 96	4 7

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ic)	; TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic)
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24:	; INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
ION:	; TELECOMMUNICATION INFORMATION ; TELEPHONE: 212-867-0123 ; TELEPHONE: 212-867-0123
,711 4526.200-US	REGISTRATION NUM
 J.	ORMATI n, Jan
60/002,800	ATION NUMBER: DATE: 1-SEP-1
08/706,037 6	LICATION NUMB
US/09/005,397 .	CATION NUMBER:
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of America	Y: UI
	; CITY: New York
o No. 5972670disk of No. 5972670th America, Inc. Avenue, 64th Floor	No. 5972670 D5 Lexington
	; CORRESPONDENCE ADDRESS: 29
COPPER OXIDASE MOTANTS WITH	유무
4.	CANT: Berka, R
	AH
09005397	RESULT 22 US-09-005-397-24 ; Sequence 24, Application US/0 ; Patent No. 5972670
1341	Db 1327 GGTGGTACCCCGAAC :
.02	Qy 498 LysThrLysProAsn 5
TGTGTTTGATATCGTCAAATCACTC 132	Db 1285 ATCCATCTCCACGCCAT
sGlyGlyGlnLeuSerAlaAspAspValAlaLysA	euAsnSerPheGlyA
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uSerA	et
TIGAAGATTTTGGCAAACAATGCGAGCAATGACGCCGATTTCACGCCAAATGAGCACACT 122	Db 1165 TTGAAGATTTTGGCAA
ValAlaAsmGlyLeuSerGlyLysIleThrValAsnGlyAsmGlnTyrGlu 457	Qy 438 AlaSerIleValAlaA
GCTC 116	Db 1150TCGTTGCCCACGCTC
roProLeuAlaAsnSerAspTyrLeuAsnAlaAspHisAlaArgAla 437	Qy 418 ProAsnAlaPheProP
GGGATTCTTAGGTTCACATTTAATAACATCAAGTACGAGGCTCCT 1149	Db 1105 GGGATTCTTAGGTTCA
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                                                                                                                                                                                                                                                                                                LeuGlnProPheAspMetGluLysAlaIleArgGluAspAlaGluTyrValValPheAsn
                                                                                                                                                                                                                                                                                                                                                                                                      CCACACAAGTCGCGCTACGACGTGGATGATGCCGAGCACAGTAGTCATGCTTGAGGACTGG
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                                                                                                                                                         ArgLeuPheValGlyAsnGlyGlyProAsnLeuThrSerSerPheHisValIleGlyGlu
                                                                                                                                                                                           -----GGCGGTCCCGCAGTTCCCCGGTCAGTAATCAACGTAAAACGTGGGAAACGATAT
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                                                                                    IlePheAspLysValHisPheGluGlyGlyLysGlyGluAsnHisAsnIleGlnThrThr 309
                                                                                                                        CGCTTGCGCGTAATCAACGCTTCTGCTATCGGGTCGTTTACCTTTTCGATC-----
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                                         ZIP: 101/4-03-1
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V(
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08172331B Patent No. 5480801
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Wahlei
APPLICANT: Christ
                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PURIFIED PH NEUTRAL TITLE OF INVENTION: ACIDS ENCODING SAME NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICATION NUMBER: US/0 FILING DATE: 22-DEC-1993 CLASSIFICATION: 435
                                                                                                                                                       COUNTRY: USA
ZIP: 10174-6401
                                                                                                                                                                                           STATE: New York
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Schneider, Palle
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                                    US/08/172,331B
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Percent Similarity:
Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: LOWING Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4052.020-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
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LOCATION:
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IOR APPLICATION DATA:
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                                                                     ValGlyMetHisIleAlaAsnGlyMetTyrGly----LeuIleLeuValGluPro-----
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-----LysGluGlyLeuProLysValAspLysGluTyrTyrValMetGlnGlyAspPhe
                                   CTTGCGAGTCAATATGTCGATGGATTGCGAGGCCCTTTGGTCATCTATGATCCAAACGAC
                                                                                                                                                                                         AspHisProAlaLysValValValLys-----MetGluThrValGluLysValMetArg
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                                                                                                                 GAGATCCCATTGCGCGGC---CAAACAGGAACCATGTGGTATCAC---
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03-DEC-1993
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Mismatches:
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SOFTWARE: FastSEQ for
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TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin (
FILE REFERENCE: 11000.1003c4U
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
SEQ ID NO 8410
LENGTH: 1203
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas
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                                                        ProHisAsnValAspPheHisAlaAlaThrGlyProGlyGlyGlyAlaGluAlaSerPhe
                                                                                                                                                 ValGlnPheSerAsnHis----ProAspSerLys----
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                       ----GGCGTGCCGGGCCTCAGCTTCGAGGGC---
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Matches:
Conservative:
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Sequence 1877, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ITITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ITITLE OF INVENTION: NUMBER: US/09/328,352

FILE REFERENCE: GTC99-03PA
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1877
LENGTH: 2016
TYPE: DNA
ORGANISM: Acinetobacter baumannii
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 ProLysGluGlyLeuPro----
                                                                 AlaValAlaProValGlyMetHisIleAlaAsnGlyMetTyrGlyLeuIleLeuValGlu
                                                                                                      AATGGAGATTTTGTTTACCGCTTTAAGGTGAAACAAAATGGCACATATTGGTATCAC---
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                                                                                                                                                                                                                                                                                      -AlaAsnSerAspTyr--
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CAATCTGAGAATAAGCCTAAAAAGGATGAACCA 1479

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PATENT FILING DATE: 1999-06-04

I CURRENT FILING DATE: 1999-06-04

I CURRENT FILING DATE: 1999-06-04

I NUMBER OF SEQ ID NOS: 8252

JENGTH: 1908

TYPE: DNA

ORGANISM: Acinetobacter baumannii

US-09-328-352-3903
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Best Local Similarity:
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                              GlySerValGlyAlaLeuThrGlyGluAsnAlaLeuLysAlaLysValGlyGluThrVal
                                                               CAGATGCGAATGCTTAAGACAGATATGTCTGATGTAACAAACTATACGTTTTTAATGAAT
                                                                                                                                                              GluLysAlaIleArgGluAsp---
 GGTAAGACTCCAGAACAAAATTGGACTGGAAATTTTAAAGCT-----
                                                                                                                            TTCAAGCAGATTAAAAAGAGATGGTTTAAAAGCAACATGGAAAGATCGTTCCATGTGGAAT 648
                                                                                                                                                                                              AGTAATCTCAAGAAAGAAGCTGATTATTACCAGAATCGAAGAGAAACGGTTATTGATGTT 588
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                                                                                                                                                                                                                                                                                       AspLysGluTyrTyrValMetGlnGlyAspPheTyr-----ThrLysGlyLys-----
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                                                                                               -AlaGluTyrVal----ValPheAsn
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 -GGAGAAAAAGTA
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 14169
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; Sequence 14169, Application US/09252991A
; Patent No. 6551795
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ORGANISM: Pseudomonas
US-09-252-991A-14169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                TCTTACCGAGGGCAAGCGCAAGGACGGCGCCTACCTCTATCCGGCGATGCCCTACACC--
                                                                                                             -ProAspSerLysMetProHisAsnVal-----
                                                                                                                                             GTTCGCCGGCGGGCTGCCGATCCAGTCGCCGTTCGGCACCATCTACGGCACCAACATCAC
                                                                                                                                                                             IleArgValArgGluGlyAspThrIleGluVal-----
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                                               aThrGlyProGlyGlyAlaGluAlaSerPheThrAlaProGlyHisThrSerThrPh
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eSerPheLysAlaLeuGln--

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182 lAlaProVal-----

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452 nGlyAsnGlnTyrGluSerValMetProAlaIleAla-----LeuSerAspGlnGlnIl
                                                                                                                                                                                                                                                  432 aAspHisAlaArgAlaAlaSerIleValAlaAsnGlyLeuSerGlyLysIleThrValAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 sValHisPheGluGlyGlyLysGlyGluAsnHisAsnIleGlnThrThrLeuIleProAl
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                                        CACGGACCTGCTCAACTACCTGCGCCAGACCTGGGGCGGATTGCCCCGGTGACCTCGGTCC
                                                                               eAlaAsnVallleThrTyrThrLeuAsnSerPheGlyAsnLysGlyGlyGlnLeuSerAl
                                                                                                                                                                                                           AGACCCGCGTAATCTGTTGCGAGTGATCGAAGACGGCATCGTCGAACAG----CAGTTCAC
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                                                                                                                          CGGCTTCGAACGCATGCAACCGATGCCCGGGTTTCGCCGGGAAACTCGACGACGAGCAACT
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US-08-030-096-5
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                                                                                                                                                                                                                                                                   Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-08-030-096-5
                                                                                                                                                                                                         US-10-088-045-2 (1-502) x US-08-030-096-5 (1-3641)
                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores
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Patent No. 542604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fabijansk
APPLICANT: Arnison,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 20-JUL-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                      No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 22-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3000 K Street, CITY: Washington, D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 22 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                 179 HisCysAlaValAlaProValGlyMetHisIleAlaAsnGlyMetTyrGlyLeuIleLeu 198
                                                                                                                                                                160 ProGlyHisThrSerThrPheSerPheLysAlaLeu---GlnProGlyLeuTyrValTyr 178
199 ValGluProLysGluGlyLeuPro------LysValAspLysGluTyrTyrVal 214
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EDNESS: double
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3000 K Street, N.W.,
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Paul G.
BIMARY CRYPTOCYTOTOXIC METHOD OF HYBRID
SEED PRODUCTION
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Matches:
Conservative:
Mismatches:
Indels:
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RESULT 30
US-08-746-111-4
                                                                                                                                                                                                        COMMUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,111
FILING DATE: 06-NOV-1996
CLASSIFICATION:
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application Patent No. 6066778
              TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 6585 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ginsburg, David
APPLICANT: Ginsburg, David
APPLICANT: Gui, Jisong
TITLE OF INVENTION: Compositions And Methods For Screening
TITLE OF INVENTION: Compounds For Anticoagulant Activity
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                   AGGTCCCTGGACCAGAGGGGGTGTACAGAGGGTGGCAGACATCGAGCAGCAGCCGTGTTT
                                                                                                                                                                                                                                                                                                                                                      GluGlyLeuProLys--
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                                                                                                                                                       AATCCTGATGAGGTGAAGCGTGATGATCCCAAGTTT-----
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                                                                                                                                                                                                                                                                        GlyAspPhe---TyrThrLysGlyLysTyrGlyGluGlnGlyLeuGlnProPhe-----
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                                    GlyAsnGlyGlyProAsnLeuThrSerSerPheHisValIleGlyGluIlePheAsp---
                                                                                                              AlaLeuThrGlyGluAsnAlaLeuLysAlaLysValGlyGluThrValArgLeuPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ValGlyMetHisIleAlaAsnGlyMetTyrGlyLeuIleLeuValGluProLys
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Db 1162 GAAGTCATTTGGGACTATGCACCTGTAATACCAGGGGAATATGGACAAAAAAATACAGGTCT 1221  Qy 79	-804-196-1 ( sAlaProGluVa	/ Match: 4.89% Indels: 2 Gaps:	128.50 imilarity: 33.02% l Similarity: 20.05%	ment Scores: 0.00732 Length:	PE	; LENGTH: 6909 Dairs ; TYPE: nucleic acid ; STRANDEDNESS: both TOPOLOGY: unknown	: (301) 948 FOR SEQ ID CHARACTERIST	우꽃	- C	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/454,353 ; FILING DATE: 06-UN-1995	'APPLICATION NUMBER: US/08/804,196 FILING DATE:	- 6	; ZIE: 20850 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: TAM DC COMPATIBLE	38.	H 10	OF INVENTION: thrombosis and kit for use with the same R OF SEQUENCES: 14 SPONDENCE ADDRESS:	Reitsma, NVENTION: NVENTION:	o. 5874256 INFORMATION: CANT: Bertina.	US-08-804-196-1 ; Sequence 1, Application US/08804196	DD 1938 CGTGGTGAATCTGTGACAGTTACAATGGATAATGTTGGAACTTGGATGTTG 1988	314 GlyGlyAlaAlaIleThrGluPheLysValAspValProGlyAspTyrValLeu 331	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	1818 ACTGTCCAGTGGCACTTCTGCAGTGTGGGAACTCATGATGATATTTTGACCATCCACTC	Qy 293LysVallisphe 296
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2074 AIGITAACTTCCAIGAATTCTAGTCCAAGAAGCAAAAGCTGAAGCTGAAATTCAGGGAT 2133 366 AlaValTyrLeuProGluGlyAlaProGlnAlaIleAspThrGlnGluAlaProLysThr 385 :::   :::	46 GlyIleLeuLysValGluGlyGluGluAsnHisGluIleTyrSerHisLysGlnThrAsp	326 ProGlyAspTyrValLeuValAspHisAlaIlePheArgAlaPheAsnLysGlyAlaLeu 345	05 GACACCTTGACCCTTTCCCCATGCGTGGAGAATCTGTGACG	1945 AARGAAARTTTGACCATCCACTTCACTGGGCACTCATTCATCTARGGAAAGAGGCATGAG 2004 306 IleGlnThrThrLeuileProAlaGlyGlyAlaAlaIleThrGluPheLysValAspVal 325	93GlyGluAsnHisAsn :::	286 ValileGlyGlullePheAsp292	:::     46 ATGAGCACTATCAATGGCTATGTG	66 GlyGluThrValArqLeuPheValGlyAsnGlyGlyProAsnLeuThrSerSerPheHis 2	246 ValValPheAsmGlySerValGlyAlaLeuThrGlyGluAsmAlaLeuLysAlaLysVal 265		GlnGlyLeuGlnProPheAspMetGluLysAlaIleArgGluAspAlaGluTyr	209 AspLysGluTyrTyrValMetGlnGlyAspPheTyrThrLysGlyLysTyrGlyGlu 227	195 GlyLeuIleLeuValGluProLysGluGlyLeuProLys	1591 TTAACAAGACCATACTACAGTGACGTGGACATCATGAGAGACATCGCCTCTGGGCTAATA 1650	181 AlaValAlaProValGlyMetHisIleAlaAsnGlyMetTyr 194	176 TyrValTyrHisCys 180	TICACCTCAGGCAGGAACACACCATGATCAGAGCAGTTCAACCAGGGGAAACC	1426 TACCCTCATGGAGTGACCTTCTCGCCTTATGAAGATGAAGTCAACTCTTCT 1476	137 MetProHisAsnValAspPheHisAlaAlaThrGlyProGlyGlyGlyAlaGluAlaSer 156	120 ArgGluGlyAspThrIleGluValGlnPheSerAsnHisProAspSerLys 136	1339 GGGATTTTGGGTCCTATTATCAGAGCC 1365	100 GlyValGluTyrGlnPheTrpThrPheGlyGlyGlnValProGlyGlnMetIleArgVal 119	28 CAGTACGAAGATGAGTCCTTCACCAACATACAGTGAATCCCCAATATGAAAGAAGAT 1338	ATTTGGATAATTTCTĆAAACCAAATTGGAAAACATTATAAGAAAGTTATGTACACA

<pre></pre>	Qy 79	Qy 63 AspAlaIleValThrHisAlaProGluValProProValAspArg 78 :::	US-10-088-045-2 (1-502) x US-08-658-340-1 (1-6909)	y Match: 4.89% Indels: 2.89% Gaps:	128.50 Matches: 8 e: 128.50 Matches: 8 ent Similarity: 33.02% Conservative: 5 Local Similarity: 20.05% Migmatches: 1	Length:	ä	; IXFE: NUCLEIC ACID ; STRANDEDNESS: both ; TOPOLOGY: unknown	E CHARACTERISTICS:	; TELEPHONE: (301) 948-7400 ; TELEPAX: (301) 948-9751 ; INFORMATION FOR SEQ ID NO: 1:	; REGISTRATION NUMBER: 34,409 ; TELECOMMUNICATION INFORMATION:	ATTORNEY/AGENT INFORMATIN: NAME: Gormley, Mary E.	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/454,353 ; FILING DATE: 06-TUN-1995	APPLICATION NUMBER: US/08/658,340 FILING DATE:	; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) ; CURRENT APPLICATION DATA:	: 21F: 20850 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTED: TEM DC Compatible	STATE: Maryland COUNTRY: USA	; ADDRESSE: AKZO NO. 59109/6 SUB18981 FACENC DEPARTMENT: 1300 Piccard Drive, Suite 206 : CTTV: Bockville	QUENCES: 14 CE ADDRESS:	OF INVENTION: A method for diagnosing an increased OF INVENTION: risk for thrombosis or a genetic decrease or tributation.	; APPLICANT: Bertina, Rogier ; APPLICANT: Reitsma, Pieter	; GENERAL INFORMATION:	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	RESULT 32	Db 2254 GCTGACTATGAT 2265	Db 2194 ACAGTCATGGCTACACGGAAAATGCATGATCGTTTAGAACCTGAAGATGAAGAGAGTGAT 2253  Qy 400 AlaThrTyrAsp 403	386 ProAlaProAlaAsnLeuGlnGluGlnIleLysAlaGlyLys
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386 ProAlaProAla	ALAVALTYTLEUPTOGLUGIYALAFTOGINALALLEASPITEGLUGIWALAFTOGYSILL :::   ::::   ::::: GTTAAATGTATCCCAGATGATGATGAGACTCATATGAGATTTTTGAACCTCCAGAATCT		GlvIleLeuLysValGluGlyGluGluAsnHisGluIleTyrSerHisLysGlnThrAsp	326 ProGlyAspTyrValLeuValAspHisAlaIlePheArgAlaPheAsnLysGlyAlaLeu 345	GACACCTTGACCCTCTTCCCCATGCGTGGAGAATCTGTGACG	TleGlnThrThrLeuTleProAlaGlvGlvAlaAlaIleThrGluPheLvsValAspVal	293LysValHisPheGluGlyGlyLysGlyGluAsnHisAsn 305	1885 ACTCTTGGATTCTGCTTTGATGACACTGTCCAGTGGCACTTCTGTAGTGTGGGGACCCAG 1944	286 ValileGlyGluIlePheAsp 292	266 GLYGLUTDRYALARGLEUPREVALGIYASDGIYGLYPROASDLEUTDRSETSETEREHIS 285		246 ValValPheAsnGlySerValGlyAlaLeuThrGlyGluAsnAlaLeuLysAlaLysVal 265	1771 GACAACATCAACAAGTTTTGTGAAAATCCTGATGAGGTGAAACGTGATGACCCCCAAGTTT 1830	GlnGlyLeuGlnProPhe:AspMetGluLysAlaIleArgGluAspAlaGluTyr	209 AspLysGluTyrTyrValMetGlnGlyAspPheTyrThrLysGlyLysTyrGlyGlu 227.	195 GAYDEULEEBEWAATGIURIOHYSGIUGAYBEURIOHYS   100   1   1   1   1   1   1   1   1	1591 TTAACAAGACCATACTACAGTGACGTGGACATCATGAGAGAGA	181 AlaValAlaProValGlyMetHisIleAlaAsnGlyMetTyr 194	TATACTTATAAGTGGAACATCTTAGAGTTTGATGAACCCACAGAAAATGATGCCCAGTGC	1477 TTCACCTCAGGCAGGAACAACACCATGATCAGAGCAGTTCAACCAGGGGAAACC 1530	PheThrAlaProGlyHisThrSerThrPheSerPheLysAlaLeuGlnProGlyLeu	1426 TACCCTCATGGAGTGACCTTCTCGCCTTATGAAGATGAAGTCAACTCTTCT 1476	yG1yG1	1366 CAGGTCAGAGACACCTCAAAATCGTGTTCAAAAATATGGCCAGCCGCCCCTATAGCATT 1425	120 ArgGluGlyAspThrIleGluValGlnPheSerAsnHisProAspSerLys 136	100 GJyVAIGIUTYTGINPHETTPINTPHEGJYGIYGINVALPTOGJYGINMETIHEATGVAI 119	

	-10-088-045-2 (1-502) x US-08-746-111-26 (1-6909) 63 AspAlaIleValThrHisAlaProGluValProProPro :::                 ::            1162 GAAGTCATTTGGGACTATGCACCTGTAATACCAGCGAAT	Alignment Scores: Pred. No.: 128.50 Score: 128.50 Percent Similarity: 33.02% Best Local Similarity: 20.05% Mismatches: 145 Query Match: 139 DB: 139 Canc. 139 Canc. 130	: TELEFAX: (415) 397-8338 ; INFORMATION FOR SEQ ID NO: 26: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 6909 base pairs ; TYPE: nucleic acid ; TYPE: nucleic acid ; TYPE: nucleic acid ; TYPE: nucleic acid ; TYPE: nucleic acid ; TYPE: nucleic acid	; ATTORNEY/AGENT INFORMATION: ; NAME: Ingolia, Diane E. ; REGISTRATION NUMBER: 40,027 ; REFERENCE/DOCKET NUMBER: UM-02536 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (415) 705-8410	2 25652	ADDRESSEE: Medien & Carroll, LLP STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco STATE: California COUNTRY: United States of America ZIP: 94104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	ATION: ATION: Ginsburg, David Chi, Jisong ENTION: Composition ENTION: Compounds i QUENCES: 54 CE ADDRESS:	SULT 33 -08-746-111-26 Sequence 26, Application		Db 2194 ACAGTCATGGCTACACGGAAAATGCATGATCGTTTAGAACCTGAAGATGAAGAGAGTGAT 2253
9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	D	Q B Q B	Q	Oy DD OY	B Q B Q	B & B &	p	Q da	Qy .:	-
366 AlaValTyrLeuProGluGlyAlaProGlnAlaIleAspThrGlnGluAlaProLysThr 385.  2134 GTTAAATGTATCCCAGATGATGATGAAGACTCATATGAGATTTTTGAACCTCCAGAATCT 2193  386 PROALaProAla	2047	1945 AATGAAATTTTGACCATCCACTTCACTGGCACTCATTCAT	ATGAGCACTATCAATGGCTATGTG	ValValPheAsnGlySerValGlyAlaLeuThrGlyGluAsnAlaLeuLysAlaLysVal::::::::::::::::::::::::::::::::::::	209 AspLysGluTyrTyrValMetGlnGlyAspPheTyrThrLysGlyLysTyrGlyGlu 227	181 AlaValAlaPro	157 PheThrAlaProGlyHisThrSerThrPheSerPheLysAlaLeuGliProGlyLeu 175	MetProHisAsnValAspPheHisAlaAlaThrGlyProGlyGlyGlyAlaGluAlaSer	120 ArgGluGlyAspThrIleGluValGlnPheSerAsnHisProAspSerLys 136	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,353A
APPLICATION NUMBER: US/08/454,353A
FILING DATE: 06-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 948-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (301) 948-9751
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
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MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
CORERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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                                                                                                                                                                                                     1282 CAGTACGAAGATGAGTCCTTCACCAAACATACAGTGAATCCCAATATGAAA---GAAGAT 1338
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              MetProHisAsnValAspPheHisAlaAlaThrGlyProGlyGlyGlyAlaGluAlaSer 156
                                                                                                                                                                   GlyValGluTyrGlnPheTrpThrPheGlyGlyGlnValProGlyGlnMetileArgVal 119
                                                                CAGGTCAGAGACACTCAAAATCGTGTTCAAAAATATGGCCAGCCGCCCTATAGCATT 1425
                                                                                                 ArgGluGlyAspThrIleGluValGlnPheSerAsn------HisProAspSerLys 136
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Matches:
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RESULT 35
US-09-165-019-1
; Sequence 1, Application US/09165019
; Patent No. 6558913
; GENERAL INFORMATION:
; APPLICANT: Bertina, Rogier
; APPLICANT: Reitsma, Pieter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-088-045-2 (1-502) x US-09-165-019-1 (1-6909)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6909 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
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STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                            TACCCTCATGGAGTGACCTTCTCGCCTTATGAAGATGAA-----GTCAACTCTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGTACGAAGATGAGTCCTTCACCAAACATÁCÁGTGAATCCCAATÁTGAAA----GAAGAT 1338
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                                       GlyLeuIleLeuValGluProLysGluGlyLeuProLys-----
                                                                                 TTAACAAGACCATACTACAGTGACGTGGACATCATGAGAGACATCGCCTCTGGGCTAATA 1650
                                                                                                                                                                                                  TyrValTyr-----
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    GGACTACTTCTAATCTGTAAGAGCAGATCCCTGGACAGGCGAGGAATACAGAGGGCAGCA 1710
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Matches:
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                       Alignment Scores:
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                                                                                                SEQ ID NO 6517
LENGTH: 933
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO FELT
                                                                                                                                                                                                                     TITLE OF INVENTION: NUCLEIC ACID AND AMING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US'60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                        APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                 ORGANISM: Pseudomonas
    No . :
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RESULT 37
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APPLICANT: Cameron, Cherie
APPLICANT: Cameron, Cherie
APPLICANT: Horrocks, L. Suzanne Hoyle
APPLICANT: Horrocks, L. Suzanne Hoyle
APPLICANT: Horrocks, L. Suzanne Hoyle
APPLICANT: Horrocks, Canine Factor VIII Gene,
TITILE OF INVENTION: Canine Factor VIII Gene,
TITILE OF INVENTION: UNMBER: US/09/324,867A
CURRENT APPLICATION NUMBER: US/09/324,867A
CURRENT FILING DATE: 1999-06-03
EARLIER APPLICATION NUMBER: 09/035,141
EARLIER APPLICATION NUMBER: 60/039,953
EARLIER FILING DATE: 1997-03-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 7032
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                        ATTGGCCCTCTTCTCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACCAGATGATG 1740
                                                                                                     ATATTCAAGTATAAATGGACAGTGACCGTAGAAGATGGACCAACTAAATCAGATCCTCGG 1620
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RESULT 38
US-09-252-991A-8062/c
Sequence 8062, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
               PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6506
                                                                                                                                                                                                                                                     Sequence 6506, Application US/09252991A Patent No. 6551795
                                                                                     TITLE OF INVENTION: NUCLEIC ACID AND AMINOTITILE OF INVENTION: AERUGINOSA FOR DIAGNO: FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18
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                                                                  TITLE OF INVENTION: NUCLEIC ACID AND AMINO A TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTI FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-19 PRIOR FILING DATE: 1998-07-27
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NUMBER OF SEQ ID NOS:
SEQ ID NO 1456
LENGTH: 1494
TYPE: DNA
                                                                                                                                                                                                                                                                        Sequence 1456, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Marc J.
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ORGANISM: Pseudomonas
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
NEPHATINASA FOR DIAGNOSTICS AND THERAPEUTICS
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690 AACCTGCCCAACGGCGAGGCGAGGATC----TATGCCATCGATGGCCATCCGGTG
                         272 PheValGlyAsnGlyGlyProAsnLeuThrSerSerPheHisValIleGlyGluIlePhe
                                                                                                                                                   810 GGCACCCGCGGCGCTATTCGACGATCAACGGCAAGCATGTGCCGACCATCGACCTGCCG
                                                                                                                                                                                       242 Asp-----AlaGluTyrValValPheAsnGlySer----
                                                                                                                                                                                                                                                                                                            897
                                                                                                                                                                                                                                                                                                                                            206 ProLysVal-----AspLysGluTyrTyrValMetGlnGlyAspPheTyrThrLysGly 223
                                                                                                                                                                                                                                                                                                                                                                                    957
                                                                                                                                                                                                                                                                                                                                                                                                                      190 AlaAsnGlyMetTyrGlyLeuIleLeuValGluProLysGluGlyLeu-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 AlaLeuGlnProGlyLeuTyrValTyrHisCysAlaValAlaProValGlyMetHisIle 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 AlaSerPheThrAla-------ProGlyHisThrSerThrPheSerPheLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 GlnMetIleArgValArgGluGlyAspThrIleGluValGlnPheSerAsnHisProAsp 134
                                                                       750 GCCGGGCAGATCGTCCGGGTGCGCCTGCTGAACGTCGACAACACCGTCACCTACCGTCTC
                                                                                                           252 ValGlyAlaLeuThrGlyGluAsnAlaLeuLysAlaLysValGlyGluThrValArgLeu 271
                                                                                                                                                                                                                                                                 224 LysTyrGlyGluGlnGly---LeuGlnProPheAspMet---GluLysAlaIleArgGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 MetArgLeuAlaAspGlyValGluTyrGlnPheTrpThrPheGlyGlyGlnValProGly 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCCGCGGACTGGTCGGCCCGCTGATCATCGAGGAGCGTGAACCCACCGGGTTCCGCCAC 898
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520 GAC 518	328 Asp 328	579 CTGAAGGTGCCGGAAGCGGGCAC-CGAGCTGTCCCTGCGCGACGGGCCGGTACGCCTGGC 521	308 ThrThrLeuIleProAiaGlyGlyAlaAlaIleThrGluPheLysValAspValProGly 327	639 GAACCACGCGGCTTCGAGGGGCAGTACTGGATCGGTCCCGGGATGCGCCTGGAGCTGGCG 580	292 AspLysValHisPheGluGlyGlyLysGlyGluAsnHisAsnIleGln 307

Search completed: September Job time : 27346 secs

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Result
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-Q=/Ggn2 I/USPTO_Spool1VG11008045/runat 04092003 083147 4078/app query.fasta_1.647
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=US10088045 @CGN 11 244 @runat 04092003 083147 4078
-NCPU=6 -TCPU=3 -NO MAAP -LARGGOURERY -NEG SCORES=0 -WAIT -DSPEDCOK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Listing first 45 summaries
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-MODEL=frame+_p2n.model -DEV=xlh
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Copyright (c) 1993 - 2003 Compugen Ltd.
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6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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US-10-127-032-31
Sequence 31, Application US/10127032
Publication No. US20030113742A1
GENERAL INFORMATION:
APPLICANT: Whiteley, Marvin
APPLICANT: Whiteley, Marvin
APPLICANT: Lory, Stephen
APPLICANT: Lory, Stephen
TITLE OF INVENTION: MITHODS AND COMPOSITIONS FOR THE MODULATION OF INTEL OF INVENTION: BIOFILM FORMATION
FILE REFERENCE: UIZ-070CP
CURRENT APPLICATION NUMBER: US/10/127,032
CURRENT APPLICATION NUMBER: US 60/285,190
PRIOR APPLICATION NUMBER: US 60/285,190
PRIOR APPLICATION NUMBER: US 60/344,142
PRIOR APPLICATION NUMBER: US 60/344,142
PRIOR APPLICATION NUMBER: US 60/344,142
PRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 31
LENGTH: 1125
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-10-127-032-31
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US-10-127-032-31

Sequence 31, Appl

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pSerAsnCysAlaAlaCysHisGlnProAspGlyLysGlyValProAsnAlaPheProPr 423
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                                                                                                                       -GAGGCGGCGAAGGTCAAGGAA------CTGACCAGCAAGGAGTGGAC
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Best Local Similarity:
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: J000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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SEQ ID NO 1053
LENGTH: 1533
TYPE: DNA
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APPLICANT:
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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                                                                                                                     AsnAlaAlaSerGlnGluHisGlnGlyGlu-----LeuProValIleAspAlaIle
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TATEISHI, NAOKO
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OCHIAI, KEIKO
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sAlaGlyLysAlaThrTyrAspSerAsnCysAlaAla 408
                                                                                                                                                                                         ValTyrLeuPro-------GluGlyAlaProGlnAlaIleAsp
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                                                                                            ThrGlnGlu-AlaProLys-----ThrProAlaProAlaAsnLeuGlnGluGlnIleLy
                                                                                                                                            GCGCAAGCACCTGCTTTGCCGGGCGTGCTGGTGAAATCCACCGAACCTGACGTCATCGAT
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Query Match:
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver: 3.0
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LENGTH: 3309400
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Publication No. US20020197605A1
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AlaSerPheThrAlaProGlyHisThrSerThrPheSerPheLysAlaLeuGlnProGly
                                                                                                                                             GAGGCCACCGCCGGCGACGTCCTCCAGGTCGATATCACCCAATGAACTGCCTGAGAGCACC
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YOKOI, HARUHIKO
TATEISHI, NAOKO
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APPLICANT: HAYASHI, MIKIRO
APPLICANT: YOCHIAL, KEIKO
APPLICANT: OCHIAL, KEIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: ISENOH, AKHHIRO
APPLICANT: SENOH, AKHHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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                                                                                                                                                                                                                                                                                            Sequence 3280, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                        APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSI
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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3280
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PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
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                                                                                           -AlaIleArgGluAspAlaGluTyrValValPheAsnGlySerValGlyAlaLeu
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Qy 100 GlyValGluTyrGlnPheTrpThrPheGly 109	Qy 80 HisproAlaLysValValLysMetGluThrValGluLysValMetArgLeuAlaAsp 99	US-10-088-045-2 (1-502) x US-09-938-842A-1675 (1-1722)	Match: 5.29% Indels: 10 Gaps:	t Similarity: 33.48% ocal Similarity: 21.81%	Length:		ORGANISM: Arabidopsis thaliana	; SEQ ID NO 16/5 ; LENGTH: 1722 . TYPET: DNA	NUMBER OF	PRIOR	PRIOR		CURREN		APPLICANT: range of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t	APPLICANT: Kreps	G :	; Sequence 1675, Application US/09938842A	RESULT 5	Db 1114 GCAGACCGTGCACTCCTGCCCGAGGGCACACCA 1146	Qy 364 ThraspalaValTyrLeuProGluGlyAlaPro 374	Db 1054 CCCGATGTCGCCCGAGTTGTCGTCCACCGGACTGCTTCTGTCCTCCTGAAGCCA 1113	250	Qy 338 ArgAlaPheAsnLysGlyAlaLeuGlyIleLeuLysValGluGlyGluGluAsnHisGlu 357  Db 994 GTGGGTAAGGACGACGCTTTGGCGTTAATGGTGTGTGTGT	937	Qy 321 PheLysValAspValProGlyAspTyrValLeuValAspHisAlaIlePhe 337	Db 892 GTCCAGCCCTGGGAGACCGAATCGATCTACCTGTCGATGGGCGAG 936	Qy 301 GlyGluAsnHisAsnIleGlnThrThrLeuIleProAlaGlyGlyAlaAlaIleThrGlu 320	Db 835TTCAAGGTGGCCCTCGGTGGTCACCGCATGACTGTCACCCACACCGACGCTTCCCT 891	Qy 283 SerpheHisValIleGlyGluIlePheAspLysValHisPheGluGlyGlyLys 300	QY 2-4 LYSVALGIYGLUTINIVALATGLEUPREVALGIYASIGLYGLYPTOASILEUTINISEI 282  Db 781 CGCCCGGGCGACAAGGCCCGCCTGCGGTTTATCAACTCCGGCGGTGACACCATC 834	721 ATGTATCCGCACTACCTCATCAACGGACGTATCCCCCCGTGCTCACCGGACCTTCGAGGCT
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US-10-174-693-208
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CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: US 09/615,192
PRIOR FILING DATE: 2000-07-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FASTSEQ for Windows Version SEQ ID NO 208 LENGTH: 980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin FILE REFERENCE: 11000.1003c5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka
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GlyProGlyGlyGlyAlaGluAlaSerPheThrAlaProGlyHisThrSerThrPheSer 167
                                                                                                                                                                                                                                          AlaAspGlyValGluTyrGlnPheTrpThrPheGlyGlyGlnValProGlyGlnMetIle
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                                                       AAATACAATGTCACCATCCATTGGCATGGTATCCGGCAGTTGAGGACGGGGTGGGCCGAC 233
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                                                  TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
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 NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1910
LENGTH: 1713
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APPLICANT:
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Zhu, Tong
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                                                       ATGATCGGTCCTGGCCAAACCACTAACGTCCTCCTCACGGCAAACCAGAGACCAGGCCGC
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                                                                                                                                                                                                       PheValGlyAsnGlyGlyProAsnLeuThrSerSerPheHisValIleGlyGluIlePhe 291
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TACTACATGGCA--
                        TyrValLeuValAspHisAlaIlePheArgAlaPheAsnLysGlyAlaLeuGlyIleLeu 348
                                                                                   ProAlaGlyGlyAlaAlaIleThrGluPheLysValAspVal--
                                                                                                                                              AspLysValHisPheGluGlyGlyLysGlyGluAsnHisAsnIleGlnThrThrLeuIle 311
                                                                                                                                                                                                                                                                -----ThrGlyGluAsnAlaLeuLysAlaLysValGlyGluThrValArgLeu 271
                                                                                                                                                                                                                                                                                                                                                                                                                  TTCTCTATGCCCAAA-----CGTGACATTCCAATTCTTCTTGGGGAATGGTGGGATAGA 513
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US-10-361-460-78
                                                                                                                                                                                                                                                                                                                  US-10-088-045-2 (1-502) x US-10-361-460-78 (1-2230)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 78, Application US/10361460 Publication No. US20030163839A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PastSEQ for Windows Version SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/361,460 CURRENT FILING DATE: 2003-02-10 PRIOR APPLICATION NUMBER: 60/057,082 PRIOR FILING DATE: 1997-08-27 NUMBER OF SEQ ID NOS: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Genes Encoding Enzymes TITLE OF INVENTION: Biosynthesis and Uses FILE REFERENCE: 0709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Helentjaris, Timothy G. APPLICANT: Bowen, Benjamin A. APPLICANT: Wang, Xun
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OTHER INFORMATION: n = A,T,C
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                                                           rValMetProAlaIleAlaLeu 465
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US-10-115-563-17
                                           US-10-088-045-2 (1-502) x US-10-f15-563-17 (1-2297)
                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                 Alignment Scores:
                                                                                                     Query Match:
                                                                                                                                                                                                                                    US-10-115-563-17
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Publication No. US20030008307A1
GENERAL INFORMATION:
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                                                                                                                                                                               No.:
                                                                                                                                                                                                                                                      SEQUENCE
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APPLICATION NUMBER: US/10/115,563
FILING DATE: 02-Apr-2002
CLASSIFICATION: cUrbance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/410,488 FILING DATE: 24-MAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METHODS FOR DIAGNOSING ACTIVATED PROTEIN
C RESISTANCE ASSOCIATED WITH A FACTOR V GENETIC MUTATION
AND COMPOSITIONS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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         63
AspAlaIleValThrHisAlaProGluValProProProValAspArg--------
                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_difference
LOCATION: replace(1614, "")
OTHER INFORMATION: /label= N
/note= "Wherein "N" is a guanine in a Factor V
normal allele and an adenine in a Factor V muta
                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note= "Nuclbelow corresponds to nucleotide SEQ ID NO 13."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fitting, Thomas REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 10666 No. US20030008307A1th Torrey Pines Road, CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: 1614
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STRANDEDNESS: single
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                                        346 GlyIleLeuLysValGluGlyGluGluAsnHisGluIleTyrSerHisLysGlnThrAsp
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OTHER INFORMATION: /not;
below corresponds to nuc;
SEQ ID NO 13."
SEQUENCE DESCRIPTION: SEQ ID:
US-10-115-563-27
                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-10-115-563-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                   Query Match:
                                                                        Score:
                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/10115563
Publication No. US20030008307A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 619-554-6312 INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
                                                                                          No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOPTWARE: PRESENT Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research
                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHODS FOR DIAGNOSING ACTIVATED PROTEIN C RESISTANCE ASSOCIATED WITH A FACTOR V CAND COMPOSITIONS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Griffin, John H
Greengard, Judi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2177 GCTGACTATGAT 2188
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STREET: 10666 No. US20030008307Alth Torrey Pines Road,
CITY: La Jolla
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                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: 1614
                                                                                                                                                                                                                                                                                                                             LENGTH: 2297 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fitting, Thomas REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/410,488 FILING DATE: 24-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/115,563
FILING DATE: 02-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaThrTyrAsp 403
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                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
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0.000647
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Matches:
Conservative:
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US-10-088-045-2 (1-502) x US-10-115-563-27 (1-2297)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1694 GACAACATCAACAAGTTTTGTGAAAAATCCTGATGAGGTGAAACGTGATGACCCCAAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1514 TTAACAAGACCATACTACAGTGACGTGGACATCATGAGAGACATCGCCTCTGGGCTAATA 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 ValValPheAsnGlySerValGlyAlaLeuThrGlyGluAsnAlaLeuLysAlaLysVal 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGTACGAAGATGAGTCCTTCACCAAACATÁCÁGTGAATCCCAATÁTGAAA---GAAGÁT 1261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACATCGAACAGCAGGCTGTGTTTGCTGTGTTTGATGAGAACAAAAGCTGGTACCTTGAG
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ProGlyAspTyrValLeuValAspHisAlaIlePheArgAlaPheAsnLysGlyAlaLeu
                                                                              GACACCTTGACCCTCTTCCCCCATGCGTGGAGAATCTGTGACG
                                                                                                                                                                                ValileGlyGluIlePheAsp-----
                                                                                                                                                                                                                                                                                                                                                                                     ATGAGCACTATCAATGGCTATGTG-----
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                                                                                                                                                                                                                                  -----LysValHisPheGluGlyGlyLys---
                                                                                                                                                                                                                                                                                 ACTOTTGGATTCTGCTTTGATGACACTGTCCAGTGGCACTTCTGTAGTGTGGGGGACCCAG 186
                                                                                                                        IleGlnThrThrLeuIleProAlaGlyGlyAlaAlaIleThrGluPheLysValAspVal 325
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                                                                                                                                                                                                                                  ----GlyGluAsnHisAsn
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       Alignment Scores:
                                                         US-10-115-563-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28, Application US/10115563
Publication No. US20030008307A1
GENERAL INFORMATION:
APPLICANT: Griffin, John H
                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPARTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN:Release #1.0, Ver
CURRENT APPLICATION UNMBER: US/10/115,563
PILING DATE: 02-Apt-2002
CLASSIFICATION ENAMOND
PRIOR APPLICATION NUMBER: US/08/410,488
PILING DATE: 24-MAR-1995
PRIOR APPLICATION NUMBER: US/08/410,488
PILING DATE: 24-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Greengard, Judith S
TITLE OF INVENTION: METHODS FOR DIAGNOSING ACTIVATED PROTEIN
C RESISTANCE ASSOCIATED WITH A FACTOR V GENETIC MUTATION
C RESISTANCE ASSOCIATED WITH A FACTOR V GENETIC MUTATION
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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                                                                              OTHER INFORMATION: /note= "Nuc
below corresponds to nucleotide
SEQ ID NO 13."
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2117 ACAGTCATGGCTACACGGAAAATGCATGATCGTTTAGAACCTGAAGATGAAGAGAGTGAT 2176
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                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                               MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 AlaValTyrLeuProGluGlyAlaProGlnAlaIleAspThrGlnGluAlaProLysThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent Counsel
STREET: 10666 No. US20030008307Alth
CITY: La Jolla
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                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 619-554-6312
                                                                                                                                                                                     LOCATION:
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ValileGlyGluIlePheAsp-----
                                                                                                                                                                                                         GlyGluThrValArgLeuPheValGlyAsnGlyGlyProAsnLeuThrSerSerPheHis 285
                                                                                                                                                                                                                                                                                             ValValPheAsnGlySerValGlyAlaLeuThrGlyGluAsnAlaLeuLysAlaLysVal 265
                                                                                                                                                                                                                                                                                                                                                                                 GlnGlyLeuGlnProPhe-----AspMetGluLysAlaIleArgGluAspAlaGluTyr 245
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                                                                                 ACTCTTGGATTCTGCTTTGATGACACTGTCCAGTGGCACTTCTGTAGTGTGGGGACCCAG
                                                                                                                                                                     ATGAGCACTATCAATGGCTATGTG------
                                                                                                                                                                                                                                                                                                                                       GACAACATCAACAAGTTTTGTGAAAAATCCTGATGAGGTGAAAACGTGATGACCCCAAGTTT 175
                                                                                                                                                                                                                                                                                                                                                                                                                             GACATCGAACAGCAGGCTGTTTTGCTGTTTTGATGAGAACAAAAGCTGGTACCTTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGGTCAGAGACACTCAAAATCGTGTTCAAAAATATGGCCAGCCGCCCTATAGCATT 1348
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                                   ------LysValHisPheGluGlyGlyLys-----GlyGluAsnHisAsn 305
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DB:
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CURRENT APPLICATION NUMBER: US/9/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; SEQ ID NO 2275
; LENGTH: 6909
; TYPE: DNA
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APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2275, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
1282 CAGTACGAAGATGAGTCCTTCACCAAACATACAGTGAATCCCAATATGAAA---GAAGAT 1338
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                                                                                                                                              GTTAAATGTATCCCAGATGATGATGAAGACTCATATGAGATTTTTGAACCTCCAGAATCT 2193
                                                                                                                                                                                          AlaValTyrLeuProGluGlyAlaProGlnAlaIleAspThrGlnGluAlaProLysThr 385
                                                                                                                                                                                                                                                                                    GlyIleLeuLysValGluGlyGluGluAsnHisGluIleTyrSerHisLysGlnThrAsp 365
                                                     ACAGTCATGGCTACACGGAAAATGCATGATCGTTTAGAACCTGAAGATGAAGAGAGTGAT 225
                                                                                               ProAlaProAla------AsnLeuGlnGluGlnIleLysAlaGlyLys 399
                                                                                                                                                                                                                                             ATGTTAACTTCCATGAATTCTAGTCCAAGAAGCAAAAAGCTGAGGCTGAAATTCAGGGAT
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                                                                                                         nucleotide sequence", SEQUENCE DESCRIPTION: SEQ ID NO: US-10-115-563-13
                                                 Alignment Scores:
Pred. No.:
    Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/115,563
FILING DATE: 02-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                              FEATURE:
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REFERENCE/DOCKET NUMBER: 44
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/410,488
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office
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TITLE OF INVENTION: METHODS FOR DIAGNOSING ACTIVATED PROTEIN
C RESISTANCE ASSOCIATED WITH A FACTOR V GENETIC MUTATION
AND COMPOSITIONS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2254
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                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: 6918.6925 OTHER INFORMATION: /st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: mat_peptide LOCATION: 175..6765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 6925 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: CA
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ZIP: 92037
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91..6765
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Length:
Matches:
Conservative:
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GTCACAATGGAT

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209

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AlaValAlaPro-----

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176 TyrValTyr------

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157

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Db 1885 ACTCTTGGATTCTGCTTTGACACTGTCCAGTGGCACTTCTGTAGTGTGGGACCCAG 1944  Qy 293LysValHisPheGluGlyGlyLysGlyGluAsnHisAsn 305	Qy . 246 ValValPheAsnGlySerValGlyAlaLeuThrGlyGluAsnAlaLeuLysAlaLysVal 265  Db 1831	Qy 195 GlyLeuIleLeuValGluProLysGluGlyLeuProLysVal 208	1426 TACCCTCATGGAGTGACCTTCTCGCCTTATGAAGATGAA	Qy 88 Met	Best Local Similarity: 20.05% Mismatches: 145 Query Match: 4.89% Indels: 139 DB: 14 Gaps: 21  US-10-088-045-2 (1-502) x US-10-115-563-13 (1-6925)  Qy 63 AspAlaIleValThrHisAlaProGluValProProPoroValAspArg
; STRANDENESS: single ; MOLECULE TYPE: CDNA ; MOLECULE TYPE: CDNA SEQUENCE DESCRIPTION: SEQ ID NO: 26: US-10-115-563-26  Alignment Scores: Pred. No.: 128.50 Percent Similarity: 33.02% Conservative: 55	REGISTRATION INVMER: 34,163 REFERENCE/DOCKET NUMBER: 449.0 TELECOMMUNICATION INFORMATION: TELEFAX: 619-554-6312 INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: LENGTH: 6925 base pairs TYPE: nucleic acid	COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/115,563 FILING DATE: 02-Apr-2002 CLASSIFICATION: <unknown> PRIOR APPLICATION NUMBER: US/08/410,488 FILING DATE: 24-MAR-1995 ATTORNEY/AGENT INFORMATION: NAME: Firting Thomas</unknown>	Greenga NVENTION SEQUENCE ENCE ADI SSEE: Th SSEE: Th 10666 La Joll : CA 12 CA 37: USA 32037 EADABLE	Oy 400 AlaThrTyrAsp 403	326 ProGlyAspTyrValLeuValAspHisAlaIlePheArgAlaPheAsnLysGlyAlaLeu

mery Match: 14.89% Indexe: 115  S-10-088-045-2 (1-502) x US-10-115-563-26 (1-6925)  S-10-088-045-2 (1-502) x US-10-115-563-26 (1-6925)  P

# Copyright GenCore version (c) 1993 - 2003 5.1.6 Compugen Ltd

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spot|US10088045/runat_04092003_083142_3928/app_query.fasta_1.647
-Q=/cgn2_1/USPTO_spot|US10088045/runat_04092003_083142_3928/app_query.fasta_1.647
-DB=EST_-OPMT=fastap_-SUPFIX=rst_-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits_-START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-UTFMT=pto -NORM=ext_-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10088045_@CGN 1 1 2810 @runat_04092003_083142_3928 -NCPU=6 -ICPU=3
-NO_MMAP_-LARGEQUERY_-NEG_SCORES=0 -WAIT_-DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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## gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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G135584 EST4684	1 EST42381	95071 NF091A04	226252 BJ22625	423593 T7 end	26343 AV826343	35352 020H08	550165 NF088G08	553614 C0874E11	26844 AV826844	644576 NF015H09	44	8	553237 C0869G05	53	BZ560121 pacs2-164	8	Ų	079863 AY07986	83187 LuP12	22649 AV82	318801 952004B	550887 C0836D10	016516 PUEBD63T	648894 NF052E0	559318 pacs2-16	552719 C0861B1	551823 C0846	554730 C0889I	53053	882241 HL01E2	377723 MtBB33D10	Z574542 msh2 371	H378995 AG-ND-16	G646015 ES	Z716485 OGEAC31T	H380607 AG-ND-16	Z337383 ia87a06.	180641 LRH18E8	H380839 AG-ND-13	H404724 AG-ND-13	375921 AG-ND-1	395696 AG-ND-10	401929 AG-ND-12	BH380443 AG-ND-168	ription

#### ALIGNMENTS

RESULT 1
BH380443
LOCUS
DEFINITION ACCESSION VERSION KEYWORDS

SOURCE

ORGANISM GSS BH380443 AG-ND-168I17.TR ND-TAM Anopheles , genomic survey BH380443 BH380443.1 GI:17326585 sequence. gambiae DNA linear GSS 10-DEC-2001 genomic clone AG-ND-168I17

Anopheles gambiae (African malaria mosquito) Anopheles gambiae Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Neoptera, Endopterygota, Diptera, Nematocera, Culic Anopheles. ecta; Pterygota; Culicoidea;

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BASE COUNT
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AUTHORS
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This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center library was constructed at Texas A&M University BAC Center Mixed Sexes of Larvae.
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Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the malaria mosquito Anopheles gambiae
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Seq primer: M13
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Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Institute for Genomic Research 9712 Medical Center Dr., Rockville,
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The Institute for Genomic Researd
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sThrSerThrPheSerPheLysAlaLeuGlnProGlyLeuTyrValTyrHisCysAlaVa
                                                                                                                                                                                         TATAACTTCTGGACTTTTGGCGGAACAGTTCCGGGAAGCTTTATCAGGGCAAGAGTGGGT
                                                                                                                                                                                                              TyrGlnPheTrpThrPheGlyGlyGlnValProGlyGlnMetIleArgValArgGluGly
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                                                                       pPheHisAlaAlaThrGlyProGlyGlyGlyAlaGluAlaSerPheThrAlaProGlyHi
                                                                                                                       GACGATAATTGAATTTCATTTGAAGAATAATGAAAACAGTACATTCCCCGCATAATATAGA
                                                                                                                                            Asp-ThrIleGluValGlnPheSerAsnHisProAspSerLysMetProHisAsnValAs
                                                   CCTTCATGCTGTAAATGGCCCTGGTGGCGGTGCAGAAGCTACTTTTGTAGCTCCGGGAAA
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/mol_type="genomic DN
/strain="PEST"
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/clone="AG-ND-168117"
/clone_1lb="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
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                   Percent Similarity:
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genomic survey sequence.
BH401929
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Seq primer: M13 For
Class: BAC ends.
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Contact: Brendan J Loftus
Department of Eukaryotic Genomics
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Hong/Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J., R.,C., Huff,E.R., Carlile,J.L., Black,K., Zhang,H.-B., Gardner,M.J. and Collins,F.H.
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Anopheles gambiae
Bukaryota, Metazoa; Arthropoda; Hexapoda; In
Neoptera; Endopterygota; Diptera; Nematocera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
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                                                                                                                                                                         /clone="AG_ND-124C6"
/clone lib="ND-TAM"
/note="Vector: pECBAC1;
80 c 126 g 14
                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="PEST"
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                                                                                                                                                                                                                                                                          db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                                                                                organism="Anopheles gambiae"
                    9.36e-51
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era; Culicoidea;
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                                                                                       Other GSSs: AG-ND-105E5.TR
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 3208
Fax: 301 838 3543
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Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit
                                                                                                                                                                                                                        Construction of a BAC library and generation of BAC sequence-tagged connectors for genome sequencing of malaria mosquito Anopheles gambiae Mol. Genet. Genomics 268 (6), 720-728 (2003)
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Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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BH395696
                                                                                                                                                                                                                                                                                                                                                          Neoptera; Endopterygota; Diptera; Nematocera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyGluAsnAlaLeuLysAlaLysValGlyGluThrValArgLeuPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysAlaIleArgGluAspAlaGluTyrValValPheAsnGlySerValGlyAlaLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGATTTCTATACCAAAGGTAAATACGGAGACAAAGGTCTTCAGGAATTTGATATGGAT
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   Neoptera;
Anopheles.
                                             Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
                                                                                     , genomic survey
BH375921
BH375921.1 GI:17
                                                                                                                                  BH375921
AG-ND-119L15.TF ND-TAM Anopheles
                                                                           GSS.
                             Eukaryota;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
                                                                                                                                                                                                          GlnGlyAspPhe-TyrThrLysGlyLysTyrGlyGluGlnGlyLeuGlnProPheAspMe
                                                                                                                                                                                                                                                                                          LeuIleLeuValGluProLysGluGlyLeuProLysValAspLysGluTyrTyrValMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysMetProHisAsnValAspPheHisAlaAlaThrGlyProGlyGlyGlyAlaGluAla
TCTGGGAGATAATGAACTGAAAGA-AAGGTTGGTGAA
                         uThrGlyGluAsnAlaLeuLysAlaLysValGlyGlu
                                                                                   GGATAAAGCAATTGCAGAACATCCTGAATATGTGGTTTTTCAATGGTAAAACAGGAGCACT
                                                                                                                      tGluLysAlaIleArgGluAspAlaGluTyrValValPheAsnGlySerValGlyAlaLe
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                                                                                                                                                                                                                                                                     TTAATTCTGATAGAACCGGAAGGTGGATTGCCTAAAGTAGATAAAGAGTTCTATATCATG
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/clone="AG.ND-105E5"
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/clone_"Vector: pECBAC1; Site_1:
/note="Vector: pECBAC1; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="PEST"
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20.64%
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Matches:
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; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Endopterygota; Diptera; Nematocera; Culicoidea;

GI:17322063

sequence.

gambiae DNA

linear GSS 10-DEC-2001 genomic clone AG-ND-119L15

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Best Local Similarity:
Query Match:
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This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain to NNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universeity BAC Center Dartial digest.

Seq primer: M13 For Class: BAC ends.
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CONTACT: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the African malaria mosquito Anopheles gambiae mol. Genet. Genomics 268 (6), 720-728 (2003)
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Hong,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J.,
C., Huff,E.R., Carlile,J.L., Black,K., Zhang,H.-B., Gardner,M.,
and Collins,F.H.
                                                                                                                                                                                                                                                                   TTCCCGCATAATATAGACCTTCATGCTGTAAATGGCCCTGGTGGCGGTGCAGAAGCTACT
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                                                                                                                                                                                                                                                                                                                                              ATCAGGGCAAGAGTGGGTGACGAAATTGAATTTCATTTGAAGAATAATGAAAACAGTACA
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                                                   AATTCTGATAGAA 263
                                                                                       uIleLeuValGlu 200
                                                                                                                      GTATACCACTGTGCGACCGCTTCCGTGGGGATGCATATTGCTAATGGGATGTATGGGATT
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a 48 c 67 g
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/mol_type="genomic DNA"
/strain="PEST"
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Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3543

Email: bjlottus@rigr.org

This clone is from an A. gambiae BAC library (ND-TAM) provided by

F.H. Collins and sequenced by The Institute for Genomic Research

(TIGR). The BAC library was generated from A. gambiae PEST strain

DNA. All DNA was extracted from newly hatched first instar larvae

to minimize the inclusion of DNA from microorganisms that inhabit

the gut. The DNA is derived from mixed sexes of larvae. The BAC

library was constructed at Texas A&M University BAC Center

University, College Station, Texas 77843-2123, USA using a HindIII

Seq primer: M13 Rev

Class: BAC ends.
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                                                                                                           30 AlaAlaGlnProLysSerSerThrValAspAlaAlaAlaLysThrAlaAsnAlaAspAsn 49
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HOng,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Lo,C., Huff,E.R., Carlile,J.L., Black,K., Zhang,H.-B., and Collins,F.H.
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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                                       AlaAlaSerGlnGluHisGlnGlyGluLeuProValIleAspAlaIleValThrHisAla
                                                                                                                                                                CTTGCTGTTGTTTTGTCTGCAATTTTCACTTTGAATGCTTGTAAACAAAAACGCTTCTGAA 484
                                                                                                                                                                                               LeuIleCysAlaLeuSerAlaLeuMet---LeuSerGlyCysSerAsnGlnAlaAspLys
                                                                               GCTTCACAA----TCCGGAAGTACTGAAGGTATTACTGTTCAGGGAAATGCAGAA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="AG-ND-139F12"
/clone_lib="ND-TAM"
/note="Vector: pEGBAC1; Site_1: HindIII"
132 c 176 g 210 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA'
/strain="PEST"
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Matches:
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                                                                                                                                                                                                                       partial digest.
Seq primer: M13 Rev
Class: BAC ends.
                                                                                                                                                                                                                                                                                   This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center
                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Dr.,
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Other_GSSs: AG-ND-138F14.TF
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Construction of a BAC library and generation of BAC sequence-tagged connectors for genome sequencing of malaria mosquito Anopheles gambiae
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Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
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                                                                                                                                                                                                                                                                       University, College Station, Texas 77843-2123, USA using a HindIII
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                                                                                                                                                                                                                                                                                                                                                                                     ail: bjloftus@tigr.org
is clone is from an A.
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                                                               /clone="AG-ND-138F14"
/clone_11b="ND-TAM"
/clone_Tector: pECBAC1; Site_1:
/note="Vector: pECBAC1; Site_1:
129 c 177 g 211 t
                                                                                                                                           /mol_type="genomic
/strain="PEST"
                                                                                                                                                                          organism="Anopheles gambiae"
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era; Culicoidea;
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                                                                                                                                                                                                                                  Contact: Hui Peng, MD. & PhD. Dr. Archibald Perkins' Lab Yale University School of Medicine 310 Cedar Street, LH. 305, New Haven, Tel: 203-764-9977
                                                                                                                                                                                                                                                                                                                                                  Ma,X.Y., Husain,T., Peng,H., Lin,S., L
, Johnson,S., Krause,D. and Perkins,A.
Development of a murine myeloid cDNA m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI180641
BI180641.1
                                                                                                                                                                  IMAGE Consortium (info@image.llnl
Seq primer: M13AEK as 3' primer, 7
                                                                                                                                                                                                 Email: hui.peng@yale.edu
This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Mus musculus
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1 (bases 1 to 653)
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/tissue_type="Primary
/dev_stage="Adult"
                                                /db_xref="taxon:10090"
/clone="3216873(5')"
                                    sex="Female"
                                                                                  mol_type="mRNA"
strain="BALB/c"
                                                                                                                                                 ocation/Qualifiers
                                                                                                                 organism="Mus musculus"
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50.72%
36.23%
8.00%
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Conservative:
Mismatches:
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Fulus cDNA clone
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BASE COUNT ORIGIN

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US-10-088-045-2 (1-502) x BI180641 (1-653)
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               Sorghum bicolor (sorghum)
Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                           BZ337383
BZ337383.1 GI:24731977
GSS.
                                                                                                                                                                                              BZ337383
719 bp
ia87a06.gl WGS-SbicolorF (JM107
bicolor genomic clone ia87a06 5'
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/note="Vector: pZL1; Site 1: SalI site; Site 2: EagI site;
LRH library was constructed from CDNA of primary bone
marrow cells depleted of lineage-committed cells and
enriched for primitive cells by FACS sorting for cells
with low level staining with rhodaminel23 and Hoechst
33342 dyes. CDNA from 5000 cells derived from 30 mice,
5000 cells were were directionally cloned into SalI-EagI
restriction site of the (ZipLox (Gibco BRL). The ligated
cDNA fragments were transformed into BHDB host cells.
The original library had an initial plating complexity of
1.44X107 clones. "

18 a 200 c 208 g 125 t 2 others
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186.50
48.25%
37.06%
7.10%
       O'Shaughnessy, A.L.,
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Conservative:
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5', genomic survey sequence.
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       Balija, V.,
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ORIGIN
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JOURNAL
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genomic survey sequence.
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REFERENCE AUTHORS

SOURCE ORGANISM

KEYWORDS ACCESSION DEFINITION

ERSION

RESULT 8 BZ337383

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US-10-088-045-2 (1-502) x BZ337383 (1-719)
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353 bp AG-ND-164017.TF ND-TAM Anopheles
                                      BH380607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mccombie@cshl.org
Plate: ia87 row: a column: 06
Seq primer: -21M13UnivRev
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished Contact: W. Richard McCombie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 516 367 8884
Fax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., Palmer, L., McCombie, W.R. and Martienssen, R.A. Genomic shotgun sequences from Sorghum bicolor (methyl-filtere
                                                                                                                                                                                                                                                         AsnVallleThrTyrThrLeuAsnSerPheGlyAsnLysGlyGlyGlnLeuSerAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyValProAsnAlaPheProProLeuAlaAsnSerAspTyrLeu---AsnAlaAspHis 434
                                                                                                                                                                     AspValAlaLysAlaLysLys
                                                                                                                                                                                                                  GATGTGGTCAGTTTCGTGCGTGGCAGTTGGGGTAACAAGGGCACGCCTGTGAAGGCCAGT
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                                                                                                                              GACGTGGCGGACCTGCGCAAG
                                                                                                                                                                                                                                                                                                           GCGCCGTCTACCTTCACCATGCCCGCGTTTGCGTGGCGCCCTGTCGGACCAGGAAGTGGCG
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/note="Site_1: Xba I; Site_2: Xba I; The vector was
digested with XbaI and one nucleotide was added by fill in
in the recessive 3' end. The genomic DNA was nebulized,
end repaired, adaptor ligated and size fractionated using
sephadex The resulting fragments were between 0.8 and 3
kb and were cloned into the vector (.x/y reads in M13mp19,
b/g reads in pUC19). The same ligation was transformed in
either JM107 or DH5a."

232 c 214 g 125 t
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/mol_type="genomic DNA"
/db_xref="taxon:4558"
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41.12%
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Matches:
Conservative:
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              clone
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one AG-ND-164017
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This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University. College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J., C., Huff, E.R., Carlile, J.L., Black, K., Zhang, H.-B., Gardner, M.C. and Collins, F.H.

Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the African malaria mosquito Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               partial digest.
Seg primer: M13 For
Class: BAC ends.
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Fax: 301 838 3543
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BH380607.1
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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Anopheles gambiae
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ProGluValProProValAspArgAspHisProAlaLysValValValLysMetGlu
                                                                                           AlaAlaSerGlnGluHisGlnGlyGluLeuProValIleAspAlaIleValThrHisAla
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/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
76 c 64 g 125 t
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/strain="PEST"
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OGEAC31TC ZM_0.7_1.5_KB
genomic_survey sequence.
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Tel: 301-838-5843
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Cathy Whitelaw
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/clone=lib="ZM_0.7_1.5_KB"
/clone=lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
176 g 60 t
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/mol_type="genomic DNA"
/strain="B73"
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  Rohlfing, T.,
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Citek
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                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 612 625 1738
Email: kvandenb@cbs.umn.edu
M394422e TIGR sequence name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner
Tel: 612 624 2755
Fax: 612 625 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VandenBosch, K., Endre, G., Hur, J., Beremand, P., C.L., Craven, M.B., Cho, J. and Fraser, C.M. ESTs from roots of Medicago truncatula 72 h afinoculation, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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EST507634 KV3 Medicago truncatula
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Seg primer: SKmod (CTA gAA CTA
Location/Qualifiers
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Medicago truncatula
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                             /clone_lib="KV3"
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing CDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                              /tissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with
                                                                                                                                                                                                                                                                                                 /organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="genotype_A17"
                                                                                                                                                                                  /lab_host="E. coli strain XLOLR"
/clone_lib="KV3"
                                                                                                                                                                                                                                                                clone="pKV3-48A4"
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one="pKV1-40"
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genomic survey sequence.
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This clone is from an A. gambiae BAC library (ND-TAM) provided by Fhe Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University. College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          partial digest.
Seq primer: M13 For
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryg
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301 838 0208
Fax: 301 838 3543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., L., C., Huff, E.R., Carlile, J.L., Black, K., Zhang, H.-B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Brendan J Loftus
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uThrValGluLysValMetArgLeuAlaAspGlyValGluTyrGlnPheTrpThrPheGl 109
                              TCCAATGGTGCCTGAACCAATAGGAAACAGAGCTGCAAAAAAAGCTGATTGTACGTCTGGA
                                                              aProGluValProProProValAspArgAspHisProAlaLysValValValLysMetGl
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/clone="AG-ND-162A8"
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/note="Vector: pECBAC1; Site_1: HindIII"
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Best Local Similarity:
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msh2_3719
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Fax: 2066857244
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Box 352145, Seattle, WA 98105-2145,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spencer, D.H., Raymond, C.K., Smith, Burns, J.L., Kaul, R. and Olsen, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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/note="Environmental isolate.
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/clone="msh2_3719"
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                                                                                                                                                                                                                                                                                              BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire Biologie Moleculaire des Relations Plantes-Microorganismes, CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email: http://sequence.toulouse.inra.fr/Mtruncatula.html).
                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago truncatula

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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413 bp mRNA linear EST 03-AU MtBB33D10F1 MtBB Medicago truncatula cDNA clone MtBB33D10 T3,
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/Clone lib="WLBB"
//clone lib="WLBB"
/note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2:
XhoI; Plants were grown in an aeropomic chamber on
nitrogen-rich medium for 21 days. Three days before
inoculation with Sinorhizobium mellloti, the medium was
replaced by N-free medium. Root nodules (+ short adjacent
                                                                                                             /tissue_type="symbiotic root nodules"
/dev_stage="harvested 4 days post inoculation with
Sinorhizobium meliloti"
                                                                                                                                                                     /db_xref="taxon:3880"
/clone="MtBB33D10"
                                                                                                                                                                                                       /mol_type="mRNA"
/cultivar="Jemalong"
                                                                                                                                                                                                                                            organism="Medicago truncatula"
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Stein, N., Potckina, E. and Graner, A.
Barley ESTs from pooled RNAs of ger
length transcripts)
                                                                                                                                                                                                       Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                         CB882241 612
HL01E24w HL Hordeum vulgare
     Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant |
Corrensetr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
                                                                                                                                                                                                                                                                                                                       CB882241
                                                                              Contact: Stein Nils
                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                                                            3-PRIME,
                                                                                                                                                                                          Triticeae; Hordeum.
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                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
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GI:30084234

germinating

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for

Pooideae

Research

(IPK)

subsp. ď

mRNA vulgare

cDNA linear E

EST 23-APR-2003 ne HL01E24

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US-10-088-045-2 (1-502) x AL377723 (1-413)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValGluLysValMetArgLeuAlaAspGlyValGluTyrGlnPheTrpThrPheGlyGly 110
                                                                                                                                    ValAlaProValGlyMetHisIleAlaAsnGlyMetTyrGlyLeuIleLeuValGluPro
                                                                                                                                                                                            GAAACTTTTCAATACAAATTCAAAGTTGACAGGCCTGGTACATATTTCTATCAT-----
                                                                                                                                                                                                                                                                                                                                               ProGly----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnValProGlyGlnMetileArgValArgGluGlyAspThrIleGluValGlnPheSer 130
                                             LysGluGlyLeuProLysValAspLysGluTyrTyrValMetGlnGlyAspPhe
                                                                                                                                                                                                                                                                                            TTTGGAACTCCTTGGGCTGATGGAACTGCTGCAATATCTCAATGTGCTATAAATCCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Asn-----HisProAspSerLysMetProHisAsnValAspPheHisAlaAlaThrGly 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAATTTCCAGGCCCAACTATTAGAGCTGAAGTTGGTGACACTCTTGTTATTGACCTCACC 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            root segments) were harvested 4 days post inoculation cDNA was prepared from polyA+ enriched RNA. The cDNA directionally ligated into Unizapa KR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mass-excised from phage stocks using Exassit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France)."
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-TTACCAAAGAGCCAAAGAGAGCCATTTCATTACGATGGTGAGTTC
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152.50
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Query Match:
                                    DEFINITION
                                                                    CA553053/c
                                                                                        RESULT 16
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           CA553053 501 bp mRNA linear .EST 1 C0866F05-5N NIA Mouse Blastocyst cDNA Library (Long) Mus cDNA clone NIA:C0866F05 IMAGE:30031360 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: stein@ipk-gatersleben.de
Insert Length: 612 Std Error:
Plate: 1 row: E column: 24
Seq primer: T7.
CA553053
                                                                                                                                                                                                                                                                                                                                                                                                                                            ValAspPheHisAlaAlaThrGlyProGly-----
                                                                                                                       GAGCTGAACCTGCTCCTCAGCGACTGGTAC 599
                                                                                                                                                                                          TACGGCTCTCTGATCGTGGATGTGGCAGATGGGGAAGAGCCGTTCAAGTATGACGGC
                                                                                                                                                                                                                TyrGlyLeuIleLeuValGluProLysGluGlyLeuPro-----LysValAspLys
                                                                                                                                                                                                                                                              GGGACATATTTCTACCAT------GGGCACTACGGCATGCAGAGGGCGGCAGGGCTG
                                                                                                                                                                                                                                                                                               GlyLeuTyrValTyrHisCysAlaValAlaProValGlyMetHisIleAlaAsnGlyMet
                                                                                                                                                                                                                                                                                                                                    TCCCAATGCGCCATCAACCCCGAGGAAACCTTCACTTACCGATTTGTCGTCGACAAGCCG
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/note="Vector: pSPORT1, Site_1: SalI (5-end of cDNA);
/note="Vector: pSPORT1, Site_1: SalI (5-end of cDNA);
Site_2: Not1 (3-end of cDNA); average insert size is 1.6 -.
1.7 kb, library was created by RZED, Heidelberg (Dr.
1.7 kb, library was created by RZED, Heidelberg (Dr.
Bernhard Korn, Im Neuenheimer Feld 506, D-69120 Heidelberg
, Germany, http://www.rzpd.de)"
a 187 c 187 g 124 t
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/lab_host="DH10B"
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/dev_stage="seeds, 12 h and 62 h after imbibition"
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/cultivar="barke"
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8 B

80 HisProAlaLysValVal----

498

CCGATCATGGACAAG---GCGACGATGCAGCCACCGTTGCATCCCACGTCCGGTCCCGAC

--LysMetGlu-----

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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Spite 4000, Baltimore, MD.21224-6820, U
Email: cdna@lgsun.grc:nia.nih.gov
Plate: C0866 row: F column: 05
Seg primer: M13 Reverse
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Ko,M.S.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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ProVallleAspAlaIleValThrHisAlaProGluValProProProValAspArgAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98
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/note="Vector: pspORT1 (Invitrogen); Site 1: Sall; Site 2:
Not1; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
extracted from a pool of 20 Blastocysts. Double-stranded
cDNAs were synthesized with an Oligo(dT) primer
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/dev_stage="3.5-dpc"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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/strain="C57BL/6J"
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                                                                                                                                         cDNA Library (Long)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C0899D07-5N NIA Mouse Blastocyst cDNA Library (Long) Mus cDNA clone NIA:C0889D07 IMAGE:30033546 5', mRNA sequence. CA554730 CA554730.1 GI:25099041
                                                                                                                                                                                                                                                                                                                 National Institute on Aging/National Institut
333 Cassell Drive, Suite 4000, Baltimore, MD
Email: cdna@igsun.grc.nia.nih.ggv
Plate: C0889 row: D column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 513)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Systematic Analyses of NIA
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                                                                                                                                                                                                                                                                                                                                                                                      Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrIleGluValGlnPheSerAsnHisProAspSerLysMetProHisAsn-----Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATCTCTGGGGTTACAACGGCCAATCCCCGGGTCCCACCATTGAGGCAGTAGAAGGCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnPheTrpThrPheGlyGlyGlnValProGlyGlnMetIleArgValArgGluGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATCGGCCGGTGACGCTGAACGGCTGGTCGTTGCCATGGCGCATGAACGGCGACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATTGGCATGGCGTGCTTTCGCCGAGCGGTATGGACGGGGTCGGCGGCCTCAACCAGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGGAGTTTCACCTGGTGGCCGAACCTGTGGTGCGCAATTTGCCGAAGGCATGAAGGCT
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                                                                                                                                                                                                                                                                                                    primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus
                                                                                                                                                                                                                                                                                   quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y., Kargul,G.J.,
/clone_lib="NIA Mouse Blastocyst cDNA Library (Long)" (note="Vector: pSPORT1 (Invitrogen); Site_I: Sali; Site_NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This:
                                                                                                 /clone="NIA:C0889D07 IMAGE:30033546"
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/dev_stage="3.5-dpc"
                                                                                                                                                                     db_xref="niaEST:C0889D07-5N"
                                                                                                                                                                                      /strain="C57BL/6J"
                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                       xref="taxon:10090"
                                                                                    host="DH10B"
                                                                                                                                                                                                                                                                                   stop: 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse
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more, MD 21224-6820, I
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COMMENT

TITLE AUTHORS

REFERENCE

KEYWORDS

FEATURES

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US-10-088-045-2 (1-502) x CA554730 (1-513)
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                                                                                                                                                                                                      195 GlyLeuIleLeuValGluProLysGlu | | | | ::::| | | | | | | | :::::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 ACCGTACATTGGCATGGCGTGCTTTTGCCGAGCGGTATGGACGGGGGTCGGCGGCCTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 --- ValAspPheHisAlaAlaThrGlyProGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 GlyAspThrIleGluValGlnPheSerAsnHisProAspSerLysMetProHisAsn---
                                                                                                                                                                                                                                                                                        99 ACGTTTATGTACCAC---CCGCACTCCGACGAAATGGTGCAGATGGCGATGGGCATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA551823 515 bp mRNA linear EST 19-NOV-201 C0849A06-5N NIA Mouse Blastocyst cDNA Library (Long) Mus musculus cDNA clone NIA:C0849A06 IMAGE:30029669 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCGACTATCGGCCGGTGTGACGCTGAACGGCTGGTCGTTGCCATGGCGCATGAACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGCGCCGATCATGGACAAG----GCGACGATGCAGCCACCGTTGCATCCCACGTCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACTGGAAGGAGTTTCACCTGGTGGCCGAACCTGTGGTGCGCGAATTTGCCGAAGGCATG
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                                                                                                                                                                                                                                                                                                                                           LeuTyrValTyrHisCysAlaValAlaProValGlyMetHisIleAlaAsnGlyMetTyr 194
                                                                                                                                                                                                                                                                                                                                                                                                         CAGCCTCACATCAAACCTGGCGAGACCTTCGTCTACGAGTTCCAGATGAAGCATAGCGGG
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                                                                                                                                                                              GGCATGATTGTGGTGCATCCACGTGAT
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National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0849 row: A column: 06
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 515)
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CA551823.1
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GAAGCGCCGATCATGGACAAG---GCGACGATGCAGCCACCGTTGCATCCCACGTCCGGT 448
                                          GluLeuProValIleAspAlaIleValThrHisAlaProGluValProProProValAsp 77
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/note="Vector: pSPORT1 (Invirrogen); Site_1: Sall; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1533-1558 (2001). [PMID: 11544199]). Total RNAs were
extracted from a pool of 20 Blastocysts. Double-stranded
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/dev_stage="3.5-dpc"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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C0861B10-5N NIA Mouse Blastocyst cDNA Library (Long) Mus
cDNA clone NIA:C0861B10 IMAGE:30030837 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                   National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov plate: C0861 row: B column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Dawood B. Dudekula
Laboratory of Genetics
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1 (bases 1 to 515)
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                                                                                                                                                                                                                                                                                                                             quality sequence stop: 515
              /clone_lib="NIA Mouse Blastocyst cDNA Library (Long)" /note="Vector: pSPORT1 (Invitrogen); Site_1: Sal1; Site Not1; Mouse cDNA project by the Laboratory of Genetics
National Institute on Aging (NIA), Intramural Research
                                                                          /tissue_type="Blastocyst"
/dev_stage="3.5-dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                      /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                            clone="NIA:C0861B10 IMAGE:30030837"
                                                                                                                                                                              db_xref="njaEST:C0861B10-5N"
                                                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                               db_xref="taxon:10090"
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Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 20 Blastocytes. Double-stranded contracted from a pool of 20 Blastocytes.

cDNAs were synthesized with an Oligo(dT) primer

purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the CDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The CDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation

mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed

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ACCESSION
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                           396 LysAlaGlyLysAlaThrTyrAspSerAsnCysAlaAlaCysHisGlnProAspGlyLys 415
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BZ559318
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Spencer,D.H., Raymond,C.K., Smith,E.E.,
Burns,J.L., Kaul,R. and Olsen,M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Box 352145, Seattle,
Tel: 2062216954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol., (2002) In Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whole-Genome-Sequence variation among multiple isolates Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
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University of Washington
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                                                                                                                                                                                                                                     HisGluIleTyrSerHisLysGlnThrAspAlaValTyr-----
                                                                                                                                                                                                                                                                  CGCAACCTGTGGACGTGGAGGACACCGTGCAGTTGCTGAAGACC---GGGCAGAACTCG
                                                                                                                                                                                                                                                                                                                                      GTTCCGGGGCAGTTCTACCTCGCCGGAGAAACCGTCGAACAATGGCAAGCCCCTGAGCCTG
                                                                                                                                                                                                                                                                                                                                                                  ValProGlyAspTyrValLeuValAspHisAlaIle-----PheArgAlaPheAsn---
TCGCGGGGCGGTCGTCGGTACGCGCAGTTCTGCTCCGACTGCCACCGCAAGGACGGCAGC 308
                                                                                                 AlaIleAspThrGlnGluAlaProLysThrProAlaProAlaAsnLeuGlnGluGlnIle
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a 352 c
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/clone_lib="pacs2-164"
/note="clinical isolate 2-164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Pseudomonas"
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DB: RESULT 20 BZ559318/c LOCUS DEFINITION र् 밁 á 밁 δ 밁 ঠ 밁 ş 밁 გ 밁 S US-10-088-045-2 (1-502) x CA552719 BASE COUNT ORIGIN 밁 밁 ð Alignment S No. 141 267 447 504 159 155 219 122 327 102 387 195 90 78 99 42 BZ559318 1145 bp DNA linear GSS 17-pacs2-164_1405.s1 pacs2-164 Pseudomonas aeruginosa genomic GluTyrGlnPheTrpThrPheGlyGlyGlnValProGlyGlnMetIleArgValArgGlu GAAGCGCCGATCATGGACAAG---GCGACGATGCAGCCACCGTTGCATCCCACGTCCGGT CAGCCTCACATCAAACCTGGCGAGACCTTCGTCTACGAGTTCCAGATGAAGCATAGCGGG 100 ACCGTACATTGGCATGGCGTGCTTTTGCCGAGCGGTATGGACGGGGTCGGCGGCCTCAAC 160 GACTGGAAGGAGTTTCACCTGGTGGCCGAACCTGTGGTGCGCGAATTTGCCGAAGGCATG CCCGACTATCGGCCGGTGGTGACGCTGAACGGCTGGTCGTTGCCATGGCGCATGAACGGC ArgAspHisProAlaLysValValVal--------LysMetGlu---GluLeuProValIleAspAlaIleValThrHisAlaProGluValProProProValAsp GlyLeuIleLeuValGluProLysGlu 203 LeuTyrValTyrHisCysAlaValAlaProValGlyMetHisIleAlaAsnGlyMetTyr 194 AlaSerPheThrAlaProGlyHisThrSerThrPheSerPheLysAlaLeuGlnProGly 174 ---ValAspPheHisAlaAlaThrGlyProGly-----GGCGACAAGCTCCGTATCTTCGTCACCAAC------AAATTGCCGGAGCATACC 220 GlyAspThrIleGluValGlnPheSerAsnHisProAspSerLysMetProHisAsn---AAGGCTCATCTCTGGGGTTACAACGGCCAATCCCCGGGTCCCCACCATTGAGGCAGTAGAA GGCATGATTGTGGTGCATCCACGTGAT 16 ACGTTTATGTACCAC---CCGCACTCCGACGAAATGGTGCAGATGGCGATGGCCATGATG 43 100 γď 5.26e-05 145.50 43.20% 26.63% 5.54% Yulan Piao (NIA)." 155 c 151 g ----ThrValGluLysValMetArg---LeuAlaAspGlyVal 101 (1-515)Matches: Conservative: Mismatches: Indels: Gaps: 109 t 515 45 28 67 29 -GlyGlyAlaGlu 154 17-DEC-2002 140 121 268 328 89 77

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Contact: Dixon RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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NF052E03EC1F1021 Elicited cell culture Medicago
clone NF052E03EC 5', mRNA sequence.
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/mol type="mRNA"
/db_xref="laxon:3880"
/clone="NF052E03EC"
/tissue_type="Cell cultures derived from root tissues"
/tissue_type="Cell suspensions were subcultured every 14
/dev_stage="Cell suspensions were subcultured every 14
/days. Cells were induced six days after subculture"
/clone_lib="Elicited cell culture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
-ima point were pooled and used for mRNA isolation."
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 596)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., A., Fraser, C.M., Yuan, Y., San Miguel, P.,
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Zea mays
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Fax: 301-838-0208
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                                                                                                                                                                                                         Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                       9712 Medical Center Drive,
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/note="Vector: pCR4-TOPO; Site_1:
/not selected genomic DNA library"
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                                                                                               organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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Mammalia; Eutheria; Rodentia; Sciuro;
1 (Dases 1 to 360)
Piao, Y., Kargul,G.J., Dudekula,D.B.,
         Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0836 row: D column: 10
                                              Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National
333 Cassell Drive, Suite 4000, Baltin
                                                                                                                                          Systematic Analyses of NIA Mouse
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                145 ---AlaAlaThrGlyProGlyGlyGlyAlaGluAlaSerPheThrAlaProGlyHisThr
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                                                                                                                                                                                                                                                         131 AsnHisProAspSerLysMetProHisAsnValAspPheHis---
                                                                                                                                                                                                                                                                                                                              111 GlnValProGlyGlnMetIleArgValArgGluGlyAspThrIleGluValGlnPheSer
                                                                                                                                                                                                                                                                                                                                                                                                     92 GluLysValMetArg---LeuAlaAspGlYValGluTyrGlnPheTrpThrPheGlyGlY
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GACGAAATGGTGCAGATGGCGATGGCATGATGGGCATGATTGTGGTGCATCCACGTGAT
                            ProValGlyMetHisIleAlaAsnGlyMetTyrGlyLeuIleLeuValGluProLysGlu
                                                                        TTCGTCTACGAGTTCCAGATGAAGCATAGCGGGACGTTTATGTACCAC---CCGCACTCC
                                                                                                       SerThrPheSerPheLysAlaLeuGlnProGlyLeuTyrValTyrHisCysAlaValAla
                                                                                                                                               CCGAGCGGTATGGGCGGGGTCGGCGTCAACCAGCCTCACATCAAACCTGGCGAGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="NIA Mouse Blastocyst cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site 1: Sali; Site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs.were
extracted from a pool of 20 Blastocysts. Double-stranded
cDNAs were synthesized with an Oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA)."
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/dev_stage="3.5-dpc"
/lab_host="DH10B"
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KEYWORDS
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DB:
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                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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Plate:
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BM318801
BM318801.1 GI:18053143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 607)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                AspGly-ValGluTyrGlnPhe-----
                                                                                                     CGCCACTCGGCACCAGGAGTG----
                                                                AspHisProAlaLysValValLysMetGluThrValGluLysValMetArgLeuAla
                                                                                      California Ave, Palo
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GGAGATCAGCTACCAGTTCAAGAGCCCCGACTGCGTGCGGAAGCTGGCGGTGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  walbot@stanford.edu
952004 row: B colum
Location/Qualifiers
                                                                                                                                                                                                                                                                        carbenicillin-containing plates was used to recover positive clones."
214 c 205 g 95 t
                                                                                                                                                                                                                                                                                                                                           /note="Vector: pUC19; Site_1: EcoRI; Site_2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis Syst
                                                                                                                                                                                                                                                                                                                                                                                        clone_lib="952 -
                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="suspension culture"
/dev_stage="mixed logarithmic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/cultivar="BMS (Black Mexican Sweet)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Zea mays"
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Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SstI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Motoaki Seki
Plant Functional Genomics Research Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Large scale analysis of Arabidopsis full-length cDNA (2002b) Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 623)
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AV822649 RAFL5 Arabidopsis
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Arabidopsis thaliana
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/clone lib="RAFL5"
/note="Site_1: SstI; Site_2: XhoI; subjected to dehydration-treated(1,2,5,10,24 hr)"
142 c 168 g 149 t
                                                                                                                           /dev_stage="rosette plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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clone="RAFL05-09-003"
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                                                 Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
                                                                                                                                                                                                                                                                                                                                            CA483187
                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Malpighiales; Linaceae; Linum.
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il: scloutier@em.agr.ca
cloned using a Sall adapter. The insert is located
I and MluI sites. Not all sequences generated with r
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Average insert size is 2.07
Plate: 006 row: H column:
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                                                                                             AACCTCTTGCTCAGCGACTGGTGGCATAAAAGTGTCCACGACCAAAAAGTCGGCCTCTCT
                                                                                                                     TyrValMetGlnGlyAspPheTyrThrLysGlyLysTyrGlyGluGln---GlyLeuGln
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174 C 195 g 157.
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/dev_stage="12 days after flowering"
/lab_nost="EMDH10B-TONA"
/clone_lib="LuP12"
/note="Vector: pCMVSport6.1 (Invitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Linum usitatissimum"
/mol type="mRNA"
/cultivar="AC McDuff"
/db_xref="taxon:4006"
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Tel: 6195941336
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5500 Campanile Dr, San Diego,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Breitbart, M., Salamon, P., Andresen, B., Mahaffy, J.M., Segall, A.M., Mead, D., Azam, F. and Rohwer, Genomic analysis of uncultured marine viral communities Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14250-14255 (2002)
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                                                                                           GATGGCTCGCCCGTCGTGAACAGCGACAAGCTCAAGCAGATCACCGTCGTGCTGAAC
                                                                                                                         AlaAsnSerAspTyrLeuAsnAla---AspHisAlaArgAlaAlaSerIleValAlaAsn
                                                                                                                                                                                    AsnCysAlaAlaCysHisGlnProAspGlyLysGlyValProAsnAlaPheProProLeu
                                                                                                                                                                                                                       CCNAACAAGGTTTGGGAGCAGGCGGCCCTGATCGCCCGGGCGAGAAGGTCTATGCGAAC
                                                           GlyLeuSerGlyLysIleThrValAsnGlyAsnGlnTyrGluSerValMetProAlaIle 463
                                                                                                                                                        AACTGCGCGGTCTGCAC-AAGCCCGACGGCAAGGGCG--CCGGCCAGTTCCCCGGCCCTC
 ----AlaLeuSerAspGlnGlnIleAlaAsnValIleThrTyrThrLeuAsnSerPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Marine viruses were isolated from 200 liters of surface seawater using a combination of differential filtration and density-dependent gradient centrifugation. Linker-amplified shotgun libraries were constructed by randomly shearing the total marine viral community DNA, end-repairing, ligating dabNA linkers to the ends, and amplifying the fragments using Vent DNA polymerase. The resulting fragments were ligated into the pSMART vector and electroporated into MC12 cells (Lucigen; Middleton, W
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ed marine virus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        community"
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/mol type="genomic DNA"
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485 TCCAACAAGACCGGCCAGACCGTGCAGCCGTCCGAAGTGCTGGCCGCCAGCAAGTAATCG
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C0887A01-5N NIA Mouse Blastocyst cDNA Library (Long) Mus cDNA clone NIA:C0887A01 IMAGE:30033312 5', mRNA sequence.
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                      0.2 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using XX Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="NIA Mouse Blastocyst cDNA Library (Long)"
/note="Vector: psport] (Invitrogen); Site_1: Sali; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1533-1558 (2001). [PMID: 11544199]). Total RNAs were
extracted from a pool of 20 Blastocysts Double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNAs were synthesized with an Oligo(dT) primer
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/dev_stage="3.5-dpc"
/lab_host="DH10B"
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                                                                                                                                                        Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 600)
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RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaral Tel: 81-298-36-4359
                                                                                                                           Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
                                                                                                                                                                                                                                                 EST
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                                     Contact: Motoaki Seki
Plant Functional Genomics Research Group
                                                                                                  Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
and Shinozaki,K.
                                                                      Unpublished
                                                                                    Large scale analysis of Arabidopsis full-length cDNA
                                                                                                                                                                                                                                                                                           mRNA sequence
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BZ560121 1269 bp DNA linear GSS 17-DEC-20 pacs2-164_2164.xl pacs2-164 Pseudomonas aeruginosa genomic clone
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An Arabidopsis full-length cDNA library was constructed essentially
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
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/db_xref="taxon:3702"
/clone="RAFL08-08-J24"
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/lab_host="DH10B"
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Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library J. Bacteriol. (2002) In press
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                          gAlaAlaSerIleValAlaAsnGlyLeuSerGlyLysIleThrValAsnGlyAsnGlnTy 456
                                                                            yValProAsnAlaPheProProLeuAlaAsnSerAspTyrLeuAsnAlaAspHisAlaAr 436
                                                                                                                  GCGGGGCGGTCTCGGCTACGCGCAGTTCTGCTCCGACTGCCACCGCAAGGACGGCAGCGG
                                                                                                                                           AlaGlyLysAlaThr-TyrAspSerAsnCysAlaAlaCysHisGlnProAspGlyLysGl
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/note="clinical isolate 2-164 Whole genomic
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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OGADM08TC ZM2_0.7_1.5_KB
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Consortium for Maize Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Cathy Whitelaw
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/clone="IMBMA0036B15"
/clone lib="ZM2 0.7 1.5 KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
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                                                          Seq primer: M13 Reverse
High quality sequence stop: 515
                                                                                               Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0869 row: G column: 05
                                                                                                                                     National Institute on Aging/National Institutes 333 Cassell Drive, Suite 4000, Baltimore, MD 213
                                                                                                                                                                                                      Contact: Dawood B. Dudekula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCGACCCGCTCGTCGTCGGCGAGCCACAGTCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGATGCAGCGCGTGGCCGGGCTCGACGGCATGCTCGTCGTCGTCGGTGCCCGACGGCGTC
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                                                                                                                                                                                                                                                                                                                                                                                   musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GlyAlaGluAlaSerPheThrAlaProGlyHisThrSerThr 165
                                                                                                                                                                                                                                                                                 Kargul, G.J., Dudekula, D.B.,
Location/Qualifiers
1. .515
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                                                                                                                                                                                                                                             Mouse
                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                           Blastocyst
                                                                                                                                                                                                                                                                                   Qian, Y.,
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21224-6820, 1
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Best Local Similarity:
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                                                                                                                                                                267
                                                                                                                                                                                                      122 GlyAspThrIleGluValGlnPheSerAsnHisProAspSerLysMetProHisAsn---
                                                                                                                                                                                                                                                                              102 GluTyrGlnPheTrpThrPheGlyGlyGlnValProGlyGlnMetileArgValArgGlu
                                                                                                                                                                                                                                                                                                                        387 GACTGGAAGGAGTTTCACCTGGTGGCCGAACCTGTGGTGGCGGAATTTGCCGAAGGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 ArgAspHisProAlaLysValValVal----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 GluLeuProValIleAspAlaIleValThrHisAlaProGluValProProProValAsp
                                                                                                                                                                                                                                                                                                                                                                                                            CCCGACTATCGGCCGGTGATGACGCTGAACGGCTGGTCGTTGCCATGGCGCATGAACGGC
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      CAGCCTCACATCAAACCTGGCGAGACCTTCGTCTACGAGTTCCAGATGAAGCATAGCGGG
                                         AlaSerPheThrAlaProGlyHisThrSerThrPheSerPheLysAlaLeuGlnProGly
                                                                                   ACCGTACATTGGCATGGCQTGCTTTTGCCGAGCGGTATGGACGGGGTCGGCGGCCTCAAC
                                                                                                                      --- valAspPheHisAlaAlaThrGlyProGly---
                                                                                                                                                                  GGCGACAAGCTCCGTATCTTCGTCACCAAC----
                                                                                                                                                                                                                                               AAGGCTCATCTCTGGGGTTGCAACGGCCAATCCCCGGGTCCCCACCATTGAGGCAGTAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.2 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Glone lib="NIA Mouse Blastocyst cDNA Library (Long)" /note="Vector: pspoRT1 (Invitrogen); Site 1: Sall; Site 2: Not!; Mouse cDNA project by the Laboratory of Genetics; National Institute on Aging (NIA), Intramural Research program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PmID: 11544199]). Total RNAs were extracted from a pool of 20 Blastocysts. Double-stranded cDNAs were synthesized with an Oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Blastocyst"
/dev_stage="3.5-dpc"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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Matches:
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Indels:
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45
27
68
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-----GlyGlyAlaGlu

154 220 140

268

121 328 101 388 89 448 77

174 160

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AV826269
                                                                                                           US-10-088-045-2 (1-502) x AV826269
                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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JOURNAL
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                                                                              101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      site (ht details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
Tel: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 614)
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AV826269.1
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AV826269 RAFL8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Large scale analysis of Arabidopsis full-length cDNA (2002b)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Motoaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (thale cress)
GlnValProGlyGlnMetIleArgValArgGluGlyAspThrIleGluValGlnPheSer 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuTyrValTyrHisCysAlaValAlaProValGlyMetHisIleAlaAsnGlyMetTyr 194
                                              GTGGAGTACAAGTATTGGTCGCCGGACTGCAAAGAGGGCGCCGTTATGACCGTCAACGGC
                                                                            ValGluTyrGlnPheTrp---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyLeuIleLeuValGluProLysGlu 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGTTTATGTACCAC---CCGCACTCCGACGAAATGGTGCAGATGGCGATGGCATGATG
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                                                                                                                                                                                                                                                                      /lab host="warts"
/clone_lib="RAFL8"
/note="Site_1: BamHI; Site_2: SalI
/note="Site_1: BamHI; Site_2: SalI
dehydration=treated (1, 2, 5, 10,
dehydration=166 g 146 t
                                                                                                                                                                                                                                                                                                                                           /dev_stage="rosette plants"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                           clone="RAFL08-11-P16"
                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Arabidopsis
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                                                                                                                                         0.000285
139.50
44.07%
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Arabidopsis thaliana
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08-11-P16 5',
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580 221 7302
Fax: 580 221 7380
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NF106G08EC1F1066 Elicited cell culture Medicago truncatula
clone NF106G08EC 5', mRNA sequence.
EG448142
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                                                                                                                                                                                                                                                                                   Email: radixon@noble.org
Insert Length: 659 Std Error: 0.0
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The Samuel Roberts Noble Foundation
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Tel: 580 221 7302
Fax: 580 221 7380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/clone_lib="Blicited cell culture"
/note="Vector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 an 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."
a 136 c 135 g 217 t
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/mol_type="mRNA"
/db xref="taxon:3880"
/clone="NF015H09EC"
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                                                                                                                                                                                                                                                                                                               Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
Tel: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
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AV826844 RAFL9
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1 (bases 1 to 571)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shinozaki, K.
                                         145
                                   /dev_stage="plants at various developmental germination to mature seeds"
/lab_host="DH10B"
/clone_lib="RAFL9"
/note="Site_1: BamHI; Site_2: SalI; subjecte dehydration=[1, 2, 5, 10, 24 hr) and cold (1 hr) treatments"

133 c 154 g 136 t 3 others
                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                           db xref="taxon:3702"
                                                                                                                                                                                                                                            organism="Arabidopsis
                                                                                                                                                                                        lone="RAFL09-07-M21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA553614 489 bp mRNA linear EST 1 C0874E11-5N NIA Mouse Blastocyst cDNA Library (Long) Mus cDNA clone NIA:C0874E11 IMAGE:30032122 5', mRNA sequence.
                                                                                                           Seq primer: M13 Reverse
High quality sequence stop: 489
                                                                                                                                                Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0874 row: E column: 11
                                                                                                                                                                            Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820,
                                                                                                                                                                                                                                                              Systematic Analyses of NIA Mouse Unpublished
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Rodentia; Sciurog
1 (Dases 1 to 489)
Piao, Y., Kargul, G.J., 'Dudekula, D.B.,
                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                          Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                     KO, M.S.H
                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysAlaValAlaProValGlyMetHisIleAlaAsnGlyMetTyrGlyLeuIleLeuVal 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProGlyHisThrSerThrPheSerPheLysAlaLeuGlnProGlyLeuTyrValTyrHis 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGTTCGGAAGTCCATGGGCAGATGGAGCAGCAGGAGTTACTCAATGCGCAATTAAC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsnHisProAspSerLysMetProHisAsn-----ValAspPheHisAla-----
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GGACACTATGGCÁTGCAGAGATCAGCTGGGCTATÁCGGÁTCGTTGATTGTG
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Indels:
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                  Blastocyst
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                                                                                                                                                                                                                                                                                                                     Tanaka, T.,
                                                                                                                                                                                                                                                                                  Library
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; Murinae; Mus
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216

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389

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RESULT 38
BF650165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 GlnValProGlyGlnMetileArgValArgGluGlyAspThrIleGluValGlnPheSer 130
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NF088G08EC1F1066
clone NF088G08EC
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                                                                      BF650165
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                                                                                                                                                                                                                                                                                                    SerThrPheSerPheLyBAlaLeuGlnProGlyLeuTyrValTyrHisCysAlaValAla 183
                                                                                                                                                                                                                                                                                                                                                                                              ProGly---
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC-----AAACTGCCGGAACAGACGACCATCCATTGGCACGGTGTGCTTCTG
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                                                                                                                                                                 GACGAAATGGTCCAGATGGCGATGGCATGATGGGAATGATCGTGGTGCATCCGCGCGAT
                                                                                                                                                                                                           ProValGlyMetHisIleAlaAsnGlyMetTyrGlyLeuIleLeuValGluProLysGlu
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                                                                                                                                                                                                                                                                                                                                                       CCCAACGGCATGGACGCGTTGGTGGACTCAATCAGCCCCACATTCCCCCGGGCAAGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.2 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Plao (NIA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pSPORT1 (Invitrogen); Site 1: Sal1; Site 2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAS were extracted from a pool of 20 Blastocysts. Double-stranded cDNAs were synthesized with an Oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="3.5-dpc"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="NIA:C0874E11 IMAGE:30032122"
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"Vector: pSPORT1 (Invitrogen); Site_1: SalI; Si
                   645 bp mRNA linear EST 20-DEC-
Elicited cell culture Medicago truncatula cDNA
5', mRNA sequence.
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173 ProGlyLeuTyrValTyrHisCysAlaValAlaProValGlyMetHisIleAlaAsnGly
                                                                                          153 AlaGluAlaSerPheThrAlaProGlyHisThrSerThrPheSerPheLysAlaLeuGln 172
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J. Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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EST.
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                                              TCTCAATGTCCTATA---CTACCTGGAGACACCTTTGTTTATCGATTTGTTGATAGG
                                                                                                                                         ATCCATTGGCATGGTATTAGACAGATTGGAACTCCTTGGTTTGATGGAACAGAAGGAGTG
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/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/clone_lib="Elicited cell culture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5; 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
a 116 c 136 g 203 t 1 others
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/mol_type="mRNA"
/db_xref="taxon:3880"
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sequence
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1 (bases 1 to 737)
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Tel: +45 96358467
Fax: +45 98141808
                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Karen G. Welinder
Institut for bioteknologi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lundsgaard, M., Emmersen, J., and Welinder, K.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Aalborg Universitet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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GTATATGGAATGATTCGTGTGGCACCTAATGACCTTGAACCTTTTCTTATGACTTTGAT 488
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ValGlnPheSerAsnHisProAspSerLysMetProHisAsnValAspPheHis-----
                                    ACAATCAATGGTAAGTTTTCCAGGTCCCACCATTAAAGCTCAACAAGGTGACACCATCGTT
                                                      ThrPheGlyGlyGlnValProGlyGlnMetIleArgValArgGluGlyAspThrIleGlu
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                                                                                                                                                                                                                                        /dev stage="Plant 3 weeks old, three days post infection"
/clone lib="Infected Arabidopsis Leaf"
/note="Organ: Leaf; Vector: pBlants winded cDNA
library of Arabidopsis and E. cichoracearum infected leaf
from three weeks old Arabidopsis plants. Plants were
harvested 3 days after infection and mRNA oligo dT
                                                                                                                                                                                                                           selected."
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/dev_stage="Plant 3 w
                                                                                                                                                                                                                                                                                                                           'strain="Columbia"
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AV826343 RAFL8 Arabidopsis thaliana
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                                                                                                 GTTGAAGCAGACGGACACTACGTAGAACCATTCACGGTG
                                                                                                                                                                                                                  PheAspLysValHisPheGluGlyGlyLysGlyGluAsnHisAsnIleGlnThrThrLeu 310
                                                                                                                                          IleProAlaGlyGlyAlaAlaIleThrGluPheLysVal
                                                                                                                                                                                                                                                            CTTCGAATAGGTAGCTTGACGGCTCTCTCTGCTCTCAGTTTCCAAATC---
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        mRNA lin
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mRNA sequence.

mRNA sequence.

AV826343

AV826343.1 GI:19868403

AV826343.1 GI:19868403

EST.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Vagnoliophyta; eudicotyledons; core eudicots; rosids

Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.

1 (bases II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 612)

Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,

Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,

Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Hayashizaki,Y.,

Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.

Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp

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BASE COUNT
ORIGIN
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                    330 CCTGGAGAGACTTTTACCTACAATTTCACTGTTGAAAAGCCCGGGAACACATTTCTACCAT 389
                                                                                                                                                                                                                                                                                                                                                                                              160 ProGlyHisThrSerThrPheSerPheLysAlaLeuGlnProGlyLeuTyrValTyrHis 179
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                                                                                                                            217 GlyAspPheTyrThrLysGly---LysTyrGlyGluGlnGlyLeuGlnProPheAspMet 235
                                                                                                                                                                          441 GACGTGGCTAAAGGAAAGAGCGAGAGATTGAGATACNATGGTGAGTTTAATCTCTTACTC 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGTITCCTGGTCCCACCATAAAAGCCTTCGCCGGAGACACCATCGTCGTCAATCTCACC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC-----AAACTCACCACCGAAGGCCTTGTCATCCATTGGCATGGAATCCGT 272
TCCAAACCTATGCGCTGGATCGGTGAAGCTCAGANCATATTGATAAATGGG
                                       GluLysAlaIleArg-----GluAspAlaGluTyrValValEheAsnGly 250
                                                                                                                                                                                                                                                             AGTGACTGGTGGCATGAGGCTATTCCCTCCCAAGAACTCGGNCTTTCT---
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/note="Site 1: BamHI; Site_2: SalI; subjected dehydration-treated (1, 2, 5, 10, 24 hr)"
140 c 165 g 144 t 3 others
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| lab_host="DH10B"
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